

445

245	250	255
Ile Arg Phe Leu Gly Ser Ile Ile Ile Ala Leu Ala Ile Glu Ala Leu		
260	265	270
Met Leu Val Phe Lys Phe Ser Val Ser Glu Pro Asp Lys Ile Thr Tyr		
275	280	285
Ala Val Tyr Leu Ala Ile Gly Val Ala Val Leu Leu Ile Ser Leu Ala		
290	295	300
Ile Tyr Val Lys Phe Ala Tyr Ser Val Leu Pro Lys Arg Glu Arg		
305	310	315

## (2) INFORMATION FOR SEQ ID NO:537:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537

Met Val Ile His Glu Lys Ile Lys Ser Arg Phe Ser Arg Asn Trp Ser			
1	5	10	15
Leu Arg Asn Arg Gly Arg His Phe Ala Ser Ser Ser Val Tyr Phe Phe			
20	25	30	
Ser Leu Leu Val Ile Thr Ala Val Asn Arg Ser Ser Ala Val Ala Trp			
35	40	45	
Leu Leu Met Pro Glu His Leu Ile Gly Trp Phe Leu Ile Ser Phe Ser			
50	55	60	
Gly Glu Phe Val Ala Asp Met Ala Phe Gly Lys Lys Ser Lys Ile Phe			
65	70	75	80
Lys Thr Arg Phe Gly Ile Ser Ile Val Ser Gly Val Ser Leu Leu Leu			
85	90	95	
Gly Ala Tyr Gln Arg Phe Tyr Phe Leu Tyr Gly Leu Ala Leu Leu Ile			
100	105	110	
Gly Gly Leu Ser Phe Leu			
115			

## (2) INFORMATION FOR SEQ ID NO:538:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature

446

## (B) LOCATION 1...88

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:538

Leu His Pro Leu Ala Asp Val Phe Val Val Asn Asp Lys Arg Unk Val  
 1               5               10               15  
 Leu Ala Met Val Unk Met Leu Ile Unk Ser Leu Ala Asn Ile Phe Phe  
     20             25             30  
 Asn Tyr Leu Phe Ile Phe Unk Leu Glu Val Gly Val Gln Gly Unk Ala  
     35             40             45  
 Ile Val Thr Val Ile Gly His Ala Ile Gly Gly Leu Val Leu Met Gln  
     50             55             60  
 His Phe Trp Arg Lys Lys Gly Glu Leu Tyr Phe Ile Lys Leu Ile Phe  
     65             70             75             80  
 Phe Ile Phe Ser His Phe Phe Ser  
     85

## (2) INFORMATION FOR SEQ ID NO:538:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...88

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:538

Leu His Pro Leu Ala Asp Val Phe Val Val Asn Asp Lys Arg Unk Val  
 1               5               10               15  
 Leu Ala Met Val Unk Met Leu Ile Unk Ser Leu Ala Asn Ile Phe Phe  
     20             25             30  
 Asn Tyr Leu Phe Ile Phe Unk Leu Glu Val Gly Val Gln Gly Unk Ala  
     35             40             45  
 Ile Val Thr Val Ile Gly His Ala Ile Gly Gly Leu Val Leu Met Gln  
     50             55             60  
 His Phe Trp Arg Lys Lys Gly Glu Leu Tyr Phe Ile Lys Leu Ile Phe  
     65             70             75             80  
 Phe Ile Phe Ser His Phe Phe Ser  
     85

## (2) INFORMATION FOR SEQ ID NO:539:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

**SUBSTITUTE SHEET (RULE 26)**

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...92

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:539

Met Phe Lys Ser Arg Leu Asn Ser Trp Ile Leu Leu Gly Ile Leu Gly  
 1 5 10 15  
 Val Leu Val Val Val Phe Trp Asp Val Ile Lys Tyr Lys Ile Glu Asp  
 20 25 30  
 Leu Gln His Asp His Tyr Leu Ser Gln Val Lys Glu Arg Glu Glu Tyr  
 35 40 45  
 Tyr Lys Asn His Ile Glu Glu Ala Leu Lys Lys Asp Ser Glu Cys Phe  
 50 55 60  
 Glu Lys Gly Gly Asp Lys Val Asp Cys Ser Ala Ala Met Arg Ile Ala  
 65 70 75 80  
 Ala Gly Glu Arg Asn Arg Arg Met Leu Glu Ile Lys  
 85 90

## (2) INFORMATION FOR SEQ ID NO:540:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...138

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:540

Met Val Phe Trp Gly Ala Val Phe Phe Leu Trp Asp Arg Thr Ala Trp  
 1 5 10 15  
 Lys Arg Leu Met Val Phe Leu Asn Ser Leu Unk Unk Met Leu Ala Ala  
 20 25 30  
 Leu Ser Leu Gly Ser Phe Leu Gly Ala Trp Ile Lys Asn Glu Ala His  
 35 40 45  
 Thr Thr Gln Ile Val Leu Ile Ser Ser Leu Pro Leu Ile Phe Met Met  
 50 55 60  
 Gly Phe Val Trp Pro Phe Glu Ser Leu Pro Ser Tyr Leu Gln Val Phe  
 65 70 75 80  
 Val Gln Ile Val Pro Ala Tyr His Gly Ile Ser Leu Leu Gly Arg Leu  
 85 90 95  
 Asn Gln Met His Ala Glu Phe Ile Asp Val Ser Ile His Phe Tyr Ala  
 100 105 110  
 Leu Ile Ala Ile Phe Ile Val Ser Phe Ile Gly Cys Val Phe Lys Leu  
 115 120 125  
 Ser Ser Leu Lys Lys Ala Cys Glu Asn Ala  
 130 135

## (2) INFORMATION FOR SEQ ID NO:541:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids

448

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541

Met	Leu	Arg	Lys	Asn	Ile	Leu	Ala	Tyr	Tyr	Gly	Ala	Asn	Phe	Leu	Leu
1					5					10					15
Ile	Ile	Ala	Gln	Ser	Leu	Pro	His	Ala	Ile	Leu	Thr	Pro	Leu	Leu	Leu
					20				25					30	
Ser	Lys	Gly	Leu	Ser	Leu	Ser	Glu	Ile	Leu	Leu	Val	Gln	Thr	Phe	Phe
					35			40				45			
Ser	Phe	Cys	Val	Leu	Val	Ala	Glu	Tyr	Pro	Ser	Gly	Val	Leu	Ala	Asp
					50			55			60				
Leu	Met	Ser	Arg	Lys	Asn	Leu	Phe	Leu	Val	Ser	Asn	Val	Phe	Leu	Ile
					65			70		75				80	
Ala	Ser	Phe	Ser	Leu	Val	Leu	Phe	Phe	Asp	Ser	Phe	Ile	Leu	Met	Leu
					85				90			95			
Leu	Ala	Trp	Gly	Leu	Tyr	Gly	Leu	Tyr	Ser	Ala	Cys	Ser	Ser	Gly	Thr
					100			105				110			
Ile	Glu	Ala	Ser	Leu	Ile	Thr	Asp	Ile	Lys	Glu	Asn	Lys	Lys	Asp	Leu
					115			120			125				
Ser	Lys	Phe	Leu	Ala	Lys	Asn	Asn	Gln	Ile	Thr	Tyr	Leu	Gly	Met	Ile
					130			135			140				
Ile	Gly	Ser	Ser	Leu	Gly	Ser	Phe	Leu	Tyr	Leu	Lys	Val	His	Ala	Met
					145			150		155			160		
Leu	Tyr	Val	Val	Gly	Ile	Phe	Leu	Ile	Met	Leu	Cys	Ala	Leu	Thr	Ile
					165				170			175			
Ile	Ile	Tyr	Phe	Lys	Glu	Lys	Glu	Gly	Asp	Phe	Lys	Ser	Gln	Lys	Asn
					180			185			190				
Leu	Lys	Leu	Leu	Lys	Glu	Gln	Val	Lys	Gly	Ser	Leu	Lys	Glu	Leu	Lys
					195			200			205				
Asp	Asn	Pro	Lys	Leu	Lys	Ile	Leu	Leu	Val	Gly	His	Leu	Ile	Thr	Pro
					210			215			220				
Val	Phe	Phe	Met	Ser	His	Phe	Gln	Met	Trp	Gln	Ala	Tyr	Phe	Leu	Lys
					225			230		235			240		
Gln	Gly	Val	Lys	Glu	Gln	Tyr	Leu	Phe	Val	Phe	Tyr	Ile	Ala	Phe	Gln
					245				250			255			
Val	Ile	Ser	Ile	Pro	His	Ser	Phe	Phe	Lys	Ser	Gln	Lys	Leu	Unk	Ala
					260			265			270				
Lys	Lys	Ser	Pro		275										

(2) INFORMATION FOR SEQ ID NO:541:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 276 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

**SUBSTITUTE SHEET (RULE 26)**

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541

```

Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe Leu Leu
1           5           10          15
Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu Leu Leu
20          25          30
Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr Phe Phe
35          40          45
Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu Ala Asp
50          55          60
Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Val Phe Leu Ile
65          70          75          80
Ala Ser Phe Ser Leu Val Leu Phe Phe Asp Ser Phe Ile Leu Met Leu
85          90          95
Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser Gly Thr
100         105         110
Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys Asp Leu
115         120         125
Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly Met Ile
130         135         140
Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His Ala Met
145         150         155         160
Leu Tyr Val Val Gly Ile Phe Leu Ile Met Leu Cys Ala Leu Thr Ile
165         170         175
Ile Ile Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln Lys Asn
180         185         190
Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu Leu Lys
195         200         205
Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile Thr Pro
210         215         220
Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe Leu Lys
225         230         235         240
Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala Phe Gln
245         250         255
Val Ile Ser Ile Pro His Ser Phe Phe Lys Ser Gln Lys Leu Unk Ala
260         265         270
Lys Lys Ser Pro
275

```

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 254 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...254

450

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:542

Met His Glu Gln Gly Ser Ile Ser Phe Ile Gly Glu Gln Gly Ala Lys  
 1 5 10 15  
 Arg Leu Leu Tyr Ile Leu Tyr Lys Leu Ala Phe Asn Ala Lys Ser Asn  
 20 25 30  
 Lys Ile Ala Leu Asp Arg His Tyr Ala Lys Met Phe Leu Gln Val Val  
 35 40 45  
 Ala Arg Thr Leu Ile Lys Asn Val Asn Ile Leu Glu Glu Gln Gly Phe  
 50 55 60  
 Ile Glu Val Ile Lys Gly Lys Gln Arg Tyr Leu Tyr Val Tyr Leu Lys  
 65 70 75 80  
 Asp Tyr Arg Glu Leu Glu Cys Leu Val Lys Ser Lys Met Ala Lys Tyr  
 85 90 95  
 Val Met Tyr Leu Arg Gln Phe Phe Asp Tyr Leu Asp Arg Lys Arg Arg  
 100 105 110  
 Tyr Gly Phe Asp Phe Thr Leu Lys Asn Leu Ala Phe Ala Lys Thr Lys  
 115 120 125  
 Glu Ser Leu Pro Arg His Leu Asn Asp Lys Asp Leu Lys Ser Phe Leu  
 130 135 140  
 Lys Thr Leu Leu Asp Tyr Lys Pro Ala Thr Ser Phe Glu Lys Arg Asn  
 145 150 155 160  
 Lys Cys Ile Leu Leu Ile Val Ile Leu Gly Gly Leu Arg Lys Cys Glu  
 165 170 175  
 Val Leu Asn Ile Glu Leu Lys His Ile Gln Val Glu Glu Gln Asn Tyr  
 180 185 190  
 Ser Ile Leu Ile Gln Gly Lys Gly Arg Lys Glu Arg Lys Ala Tyr Ile  
 195 200 205  
 Lys Lys Ser Leu Leu Glu Pro Ser Leu Asn Ala Trp Ile Ser Asp Asp  
 210 215 220  
 Tyr Arg Leu Lys Tyr Phe Asn Gly Ala Tyr Leu Phe Lys Lys Asp Lys  
 225 230 235 240  
 Gln Lys Ser Gln Asn Ser Leu Thr Leu Tyr Asn Leu Ser Pro  
 245 250

## (2) INFORMATION FOR SEQ ID NO:543:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...185

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:543

Val Val Phe Lys Ile Leu Ser Leu Trp Leu Gly Val Phe Cys Phe Leu  
 1 5 10 15  
 Arg Ala Thr His Leu Tyr Leu Gly Glu Glu Pro Lys Tyr Lys Asp Asn  
 20 25 30  
 Phe Thr His Phe Glu Tyr Ala Asn Pro Asn Ala Arg Lys Gly Gly Val  
 35 40 45  
 Leu Arg Asn Asp Ala Ile Gly Thr Phe Asp Ser Leu Asn Pro Phe Ala  
 50 55 60  
 Leu Lys Gly Thr Lys Ala Glu Gly Leu Asp Leu Ile Tyr Asp Thr Leu

451

65	70	75	80
Met Val Gln Ser Leu Asp Glu Pro Phe Ala		Glu Tyr Pro Leu Ile Ala	
85	90	95	
Lys Asp Ala Glu Val Ala Lys Asp Asn Ser Tyr Val Ile Phe Thr Leu			
100	105	110	
Asp Lys Arg Ala Arg Phe Ser Asn Asn Ala Pro Ile Leu Ala Ser Asp			
115	120	125	
Val Lys Phe Ser Phe Asp Thr Ile Met Lys Leu Gly Ser Pro Leu Tyr			
130	135	140	
Arg Gln Tyr Tyr Gln Asp Val Lys Lys Ala Val Ile Leu Asp Lys His			
145	150	155	160
His Val Lys Phe Ile Tyr Lys Thr Thr Glu Asn Lys Glu Leu Pro Leu			
165	170	175	
Ile Leu Gly Gln Leu Gln Ile Phe Ser			
180	185		

## (2) INFORMATION FOR SEQ ID NO:544:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: protein
  
- (iii) HYPOTHETICAL: YES
  
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
  
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...37
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:544

Val Ala Met Ile Asp Cys Ala Ile Ile Gly Gly Gly Pro Ala Gly Leu			
1	5	10	15
Ser Ala Gly Leu Tyr Ala Thr Arg Gly Gly Val Lys Asn Ala Val Leu			
20	25	30	
Phe Glu Lys Gly Met			
35			

## (2) INFORMATION FOR SEQ ID NO:545:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 93 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: protein
  
- (iii) HYPOTHETICAL: YES
  
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
  
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...93
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:545

452

Leu Tyr Pro Pro Gly Ser Val Val Lys Met Gly Val Gly Leu Ser Phe  
 1 5 10 15  
 Leu Glu Asn Leu His Ile Thr Glu Asn Thr Thr Ile Pro Thr Pro Pro  
 20 25 30  
 Phe Ile Glu Val Gly Lys Arg Lys Phe Arg Asp Trp Lys Lys Thr Gly  
 35 40 45  
 His Gly Asn Ser Asn Leu Tyr Lys Ala Ile Arg Glu Ser Val Asp Val  
 50 55 60  
 Tyr Phe Tyr Lys Phe Gly Leu Glu Ile Ser Ile Glu Unk Leu Ser Lys  
 65 70 75 80  
 Unk Phe Lys Unk Ser Gly Leu Trp Gly Lys Asn Gly Arg  
 85 90

## (2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 93 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545

Leu Tyr Pro Pro Gly Ser Val Val Lys Met Gly Val Gly Leu Ser Phe  
 1 5 10 15  
 Leu Glu Asn Leu His Ile Thr Glu Asn Thr Thr Ile Pro Thr Pro Pro  
 20 25 30  
 Phe Ile Glu Val Gly Lys Arg Lys Phe Arg Asp Trp Lys Lys Thr Gly  
 35 40 45  
 His Gly Asn Ser Asn Leu Tyr Lys Ala Ile Arg Glu Ser Val Asp Val  
 50 55 60  
 Tyr Phe Tyr Lys Phe Gly Leu Glu Ile Ser Ile Glu Unk Leu Ser Lys  
 65 70 75 80  
 Unk Phe Lys Unk Ser Gly Leu Trp Gly Lys Asn Gly Arg  
 85 90

## (2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 182 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...182

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:546

Val Gly Lys Ser Leu Arg Tyr Ser Leu Asn Leu Asp Leu Asn Gln Lys  
 1 5 10 15  
 Ala Asp Leu Phe Phe Thr Glu Leu Glu Pro Thr Gly Leu Thr Leu Ser  
 20 25 30  
 Pro Ile Met Lys Arg Phe Thr Ile Lys Gly Asp Phe Asp Ser Gly Leu  
 35 40 45  
 Lys Ser Tyr Asp Met Ser Tyr Met Tyr Ala Ser Leu Gln Ala Ile Ser  
 50 55 60  
 Ala Ile Arg Arg Leu Pro Leu Gly Leu Tyr Asp Gly Val His Val Tyr  
 65 70 75 80  
 Ser Lys Thr Pro Met Lys Asp Ile Glu Lys Leu Arg Asn Ala Leu Lys  
 85 90 95  
 Thr Ile Asn His His Gly Ile Gly Ile Glu Gly Trp Trp Gln Gln Asn  
 100 105 110  
 Gly Asn Phe Phe Ser Ala Met Glu Leu Glu Lys Arg Ala Leu Phe Ile  
 115 120 125  
 Val Leu Met Leu Ile Ile Leu Met Ala Ser Leu Asn Ile Ile Ser Ser  
 130 135 140  
 Leu Leu Met Val Val Met Asn Arg Arg Lys Glu Ile Ala Leu Leu Phe  
 145 150 155 160  
 Ser Met Gly Ser Ser Gln Lys Glu Ile Gln Lys Thr Phe Phe Tyr Leu  
 165 170 175  
 Gly Asn Ile Ile Ser Leu  
 180

## (2) INFORMATION FOR SEQ ID NO:547:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...247

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:547

Met Lys Thr Phe Leu Ile Ala Leu Ala Leu Thr Ala Ser Leu Ile  
 1 5 10 15  
 Gly Ala Glu Asn Thr Lys Trp Asp Tyr Lys Asn Lys Glu Asn Gly Pro  
 20 25 30  
 His Arg Trp Asp Lys Leu His Lys Asp Phe Glu Val Cys Lys Ser Gly  
 35 40 45  
 Lys Ser Gln Ser Pro Ile Asn Ile Glu His Tyr Tyr His Thr Gln Asp  
 50 55 60  
 Lys Ala Asp Leu Gln Phe Lys Tyr Ala Ala Ser Lys Pro Lys Ala Val  
 65 70 75 80  
 Phe Phe Thr His His Leu Lys Ala Ser Phe Glu Pro Thr Asn His  
 85 90 95  
 Ile Asn Tyr Arg Gly His Asp Tyr Val Leu Asp Asn Val His Phe His  
 100 105 110  
 Ala Pro Met Glu Phe Leu Ile Asn Asn Lys Thr Arg Pro Leu Ser Ala  
 115 120 125

454

His Phe Val His Lys Asp Ala Lys Gly Arg Leu Leu Val Ala Ile  
 130 135 140  
 Gly Phe Glu Glu Gly Lys Glu Asn Pro Asn Leu Asp Pro Ile Leu Glu  
 145 150 155 160  
 Gly Ile Gln Lys Lys Gln Asn Leu Lys Glu Val Ala Leu Asp Ala Phe  
 165 170 175  
 Leu Pro Lys Ser Ile Asn Tyr Tyr His Phe Asn Gly Ser Leu Thr Ala  
 180 185 190  
 Pro Pro Cys Thr Glu Gly Val Ala Trp Phe Val Ile Glu Glu Pro Leu  
 195 200 205  
 Glu Val Ser Ala Lys Gln Leu Ala Glu Ile Lys Lys Arg Met Lys Asn  
 210 215 220  
 Ser Pro Asn Gln Arg Pro Val Gln Pro Asp Tyr Asn Thr Val Ile Ile  
 225 230 235 240  
 Lys Ser Ser Ala Glu Thr Arg  
 245

## (2) INFORMATION FOR SEQ ID NO:548:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...422

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:548

Met Lys Ile Ser Leu Leu Gly His Gly Lys Thr Thr Leu Ala Leu Gly  
 1 5 10 15  
 Arg Phe Phe Lys Lys Asn His Asn Glu Val Lys Phe Phe Asp Asp Lys  
 20 25 30  
 Phe Pro Ala Phe Phe Lys Asp Ser Glu Gly Phe Leu Cys Tyr Pro Ser  
 35 40 45  
 Lys Asp Phe Asn Pro Asn Asp Ser Gln Leu Glu Ile Val Ser Pro Gly  
 50 55 60  
 Ile Ser Phe Thr His Pro Leu Val Met Lys Ala Lys His Leu Met Ser  
 65 70 75 80  
 Glu Tyr Asp Tyr Ile Asp Ser Leu Phe Asp His Ser Phe Thr Pro Thr  
 85 90 95  
 Met Ile Ser Ile Ser Gly Thr Asn Gly Lys Thr Thr Thr Glu Met  
 100 105 110  
 Leu Thr Thr Leu Leu Glu Asp Phe Lys Ala Val Ser Gly Gly Asn Ile  
 115 120 125  
 Gly Thr Pro Leu Ile Glu Leu Phe Glu Lys Arg Ser Pro Leu Trp Val  
 130 135 140  
 Leu Glu Thr Ser Ser Phe Ser Leu His Tyr Thr Asn Lys Ala Tyr Pro  
 145 150 155 160  
 Leu Ile Tyr Leu Leu Ile Asn Val Glu Ala Asp His Leu Thr Trp His  
 165 170 175  
 Cys Asn Phe Glu Asn Tyr Leu Asn Ala Lys Leu Lys Val Leu Thr Leu  
 180 185 190  
 Met Pro Lys Thr Ser Leu Ala Ile Leu Pro Leu Lys Phe Lys Glu His  
 195 200 205  
 Pro Ile Val Gln Asn Ser Gln Ala Gln Lys Ile Phe Phe Asp Lys Ser

455

210	215	220													
Glu	Glu	Val	Leu	Glu	Cys	Leu	Lys	Ile	Pro	Ser	Asn	Ala	Leu	Phe	Phe
225		230				235							240		
Lys	Gly	Ala	Phe	Leu	Leu	Asp	Ala	Ala	Leu	Ala	Leu	Leu	Val	Tyr	Glu
						245			250				255		
Gln	Phe	Leu	Lys	Ile	Lys	Asn	Leu	Lys	Trp	Gln	Asp	Tyr	Arg	Glu	Asn
						260			265			270			
Ala	Leu	Lys	Arg	Leu	Asn	Ala	Phe	Lys	Ile	Gly	Ser	His	Lys	Met	Glu
						275			280			285			
Glu	Phe	Arg	Asp	Lys	Gln	Gly	Arg	Leu	Trp	Val	Asp	Asp	Ser	Lys	Ala
						290			295			300			
Thr	Asn	Ile	Asp	Ala	Thr	Leu	Gln	Ala	Leu	Lys	Thr	Phe	Lys	Asn	Gln
						305			310			315			320
Lys	Ile	His	Leu	Ile	Leu	Gly	Gly	Asp	Ile	Lys	Gly	Val	Asn	Leu	Thr
						325			330			335			
Pro	Leu	Phe	Glu	Glu	Phe	Lys	Asn	Tyr	Lys	Ile	Ser	Leu	Tyr	Ala	Ile
						340			345			350			
Gly	Ser	Ser	Ala	Ser	Ile	Ile	Gln	Ala	Leu	Ala	Leu	Glu	Phe	Asn	Val
						355			360			365			
Ser	Cys	Gln	Val	Cys	Leu	Lys	Leu	Glu	Lys	Ala	Val	Gln	Glu	Ile	Lys
						370			375			380			
Ser	Val	Leu	Leu	Gln	Asn	Glu	Val	Ala	Leu	Leu	Ser	Pro	Ser	Ala	Ala
						385			390			395			400
Ser	Leu	Asp	Gln	Phe	Ser	Ser	Tyr	Lys	Glu	Arg	Gly	Glu	Lys	Phe	Lys
						405			410			415			
Ala	Phe	Val	Leu	Lys	Asp										
						420									

## (2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549

Met	Ala	His	His	Unk	Glu	Gln	His	Gly	Gly	His	His	His	His	His	His
1				5			10			15					
His	Thr	His	His	His	Tyr	His	Gly	Gly	Glu	His	His	His	His	His	
					20		25			30					
His	Ser	Ser	His	His	Glu	Glu	Gly	Cys	Cys	Ser	Thr	Ser	Asp	Ser	His
					35		40			45					
His	Gln	Glu	Glu	Gly	Cys	Cys	His	Gly	Unk	His	Glu				
					50		55			60					

## (2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...60
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:549

Met Ala His His Unk Glu Gln His Gly Gly His His His His  
1 5 10 15  
His Thr His His His Tyr His Gly Gly Glu His His His His  
20 25 30  
His Ser Ser His His Glu Glu Gly Cys Cys Ser Thr Ser Asp Ser His  
35 40 45  
His Gln Glu Glu Gly Cys Cys His Gly Unk His Glu  
50 55 60

(2) INFORMATION FOR SEQ ID NO:550:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...54
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:550

Met Lys Glu Ile Ile Val Ala Leu Val Gly Gln Pro Asn Val Gly Lys  
1 5 10 15  
Ser Ser Leu Ile Asn Ala Leu Ser Asn Thr His Leu Lys Val Gly Asn  
20 25 30  
Phe Thr Glu Val Thr Val Asp Lys Met Glu Val Ser Leu Ile Gln Lys  
35 40 45  
Asp His Gln Ile Asn Ser  
50

(2) INFORMATION FOR SEQ ID NO:551:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 297 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551

```

Leu Val Lys Ile Arg Leu Phe Asp Phe Thr Ile Arg Leu Phe Lys Pro
1          5           10          15
Glu Phe His Ile Phe Asp Phe Leu Lys Gly Ile Arg Val Leu Met Ile
20         25          30
Glu Trp Met Gln Asn His Arg Lys Tyr Leu Val Val Thr Ile Trp Ile
35         40          45
Ser Thr Ile Ala Phe Ile Ala Ala Gly Met Ile Gly Trp Gly Gln Tyr
50         55          60
Ser Phe Ser Leu Asp Ser Asp Ser Ala Ala Lys Val Gly Gln Ile Lys
65         70          75          80
Ile Ser Gln Glu Leu Ala Gln Glu Tyr Arg Arg Leu Lys Asp Ala
85         90          95
Tyr Ala Glu Ser Ile Pro Asp Phe Lys Glu Leu Thr Glu Asp Gln Ile
100        105         110
Lys Ala Met His Leu Glu Lys Ser Ala Leu Asp Ser Leu Ile Asn Gln
115        120         125
Ala Leu Leu Arg Asn Phe Ala Leu Asp Leu Gly Leu Gly Ala Thr Lys
130        135         140
Gln Glu Val Ala Lys Glu Ile Arg Lys Thr Asn Val Phe Gln Lys Asp
145        150         155         160
Gly Val Phe Asp Glu Glu Leu Tyr Lys Asn Ile Leu Lys Gln Ser His
165        170         175
Tyr Arg Pro Lys His Phe Glu Glu Ser Val Glu Arg Leu Leu Ile Leu
180        185         190
Gln Lys Ile Ser Ala Leu Phe Pro Lys Thr Thr Thr Pro Leu Glu Gln
195        200         205
Ser Ser Leu Ser Leu Trp Ala Lys Leu Gln Asp Lys Leu Asp Ile Leu
210        215         220
Ile Leu Asn Pro Asn Asp Val Lys Ile Ser Leu Asn Glu Glu Glu Met
225        230         235         240
Lys Lys Tyr Tyr Glu Asn His Arg Lys Asp Phe Lys Lys Pro Thr Ser
245        250         255
Phe Lys Thr Arg Ser Leu Tyr Phe Asp Ala Ser Leu Glu Lys Thr Asp
260        265         270
Leu Lys Glu Leu Glu Tyr Tyr His Lys Asn Lys Val Ser Tyr Leu
275        280         285
Asp Unk Unk Gly Glu Ile Thr Gly Phe
290        295

```

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 297 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature

(B) LOCATION 1...29

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552

Met Val Lys His Tyr Leu Phe Met Ala Val Ser Gln Val Phe Phe Ser

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1	5	10	15												
Phe	Phe	Leu	Val	Leu	Phe	Phe	Ile	Ser	Ser	Ile	Val	Leu	Leu	Ile	Ser
							20		25					30	
Ile	Ala	Ser	Val	Thr	Leu	Val	Ile	Lys	Val	Ser	Phe	Leu	Asp	Leu	Val
							35		40				45		
Gln	Leu	Phe	Leu	Tyr	Ser	Leu	Pro	Gly	Thr	Ile	Phe	Phe	Ile	Leu	Pro
							50		55				60		
Ile	Thr	Phe	Phe	Ala	Ala	Unk	Arg	Leu	Gly	Unk	Ser	Arg	Leu	Ser	Tyr
							65		70				75		80
Asp	His	Glu	Leu	Leu	Val	Phe	Phe	Leu	Unk						
							85		90						

## (2) INFORMATION FOR SEQ ID NO:552:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552

Met	Val	Lys	His	Tyr	Leu	Phe	Met	Ala	Val	Ser	Gln	Val	Phe	Phe	Ser
1							5		10			15			
Phe	Phe	Leu	Val	Leu	Phe	Phe	Ile	Ser	Ser	Ile	Val	Leu	Leu	Ile	Ser
							20		25			30			
Ile	Ala	Ser	Val	Thr	Leu	Val	Ile	Lys	Val	Ser	Phe	Leu	Asp	Leu	Val
							35		40			45			
Gln	Leu	Phe	Leu	Tyr	Ser	Leu	Pro	Gly	Thr	Ile	Phe	Phe	Ile	Leu	Pro
							50		55			60			
Ile	Thr	Phe	Phe	Ala	Ala	Unk	Arg	Leu	Gly	Unk	Ser	Arg	Leu	Ser	Tyr
							65		70			75		80	
Asp	His	Glu	Leu	Leu	Val	Phe	Phe	Leu	Unk						
							85		90						

## (2) INFORMATION FOR SEQ ID NO:553:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...111

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:553

Val His Arg Phe Ser Arg Asn Pro Cys Ala Ser Cys Asn Arg Ala Arg  
 1 5 10 15  
 Ser Cys Ser Arg Leu Ser Arg Ser Leu Val Ser Ala Val Thr Trp Trp  
 20 25 30  
 Leu Ser Leu Ser Phe Ser Val Val Ser Ala Leu Phe Ser Leu Val Ser  
 35 40 45  
 Ser Val Ile Leu Trp Val Ser Ser Val Phe Ser Leu Phe Ser Leu Ser  
 50 55 60  
 Phe Ser Val Val Asn Ser Leu Phe Ser Ser Val Ser Arg Ser Leu Ala  
 65 70 75 80  
 Ala Asn Lys Arg Val Phe Ser Leu Ala Lys Met Ser Phe Ser Val Phe  
 85 90 95  
 Ser Ser Ala Phe Ser Leu Val Ser Leu Leu Phe Cys His Asn  
 100 105 110

## (2) INFORMATION FOR SEQ ID NO:554:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...137

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:554

Met Gln Lys Met Gly Val Val Ser Tyr Ser Val Phe Gln Ala Phe Glu  
 1 5 10 15  
 Lys Ala Leu Ser Arg Phe Lys Glu Gly Val Val Leu Ile Val Asp Ser  
 20 25 30  
 Leu Arg Arg Leu Ile Met Gly Ser Ala Ser Val Lys Glu Leu Ser Gly  
 35 40 45  
 Val Ile Gly Ile Val Gly Ala Leu Ser His Ala Asn Ser Val Ser Met  
 50 55 60  
 Leu Leu Leu Phe Gly Ala Phe Leu Ser Ile Asn Leu Gly Ile Leu Asn  
 65 70 75 80  
 Leu Leu Pro Ile Pro Ala Leu Asp Gly Ala Gln Met Leu Gly Val Val  
 85 90 95  
 Phe Lys Asn Ile Phe His Ile Ala Leu Pro Thr Pro Ile Gln Asn Ala  
 100 105 110  
 Leu Trp Leu Val Gly Val Gly Phe Leu Val Phe Val Met Phe Leu Gly  
 115 120 125  
 Leu Phe Asn Asp Ile Thr Arg Leu Leu  
 130 135

## (2) INFORMATION FOR SEQ ID NO:555:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(iii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555

Val	Met	Ala	Leu	Leu	Lys	Ile	Ser	Val	Val	Val	Pro	Glu	Gly	Glu	Val
1								5		10				15	
Tyr	Thr	Gly	Glu	Val	Lys	Ser	Val	Val	Leu	Pro	Gly	Val	Glu	Gly	Glu
								20		25			30		
Phe	Gly	Val	Leu	Tyr	Gly	His	Ser	Asn	Met	Ile	Thr	Leu	Leu	Gln	Ala
								35		40		45			
Gly	Val	Val	Glu	Ile	Glu	Thr	Glu	Asn	Gln	Lys	Glu	His	Ile	Ala	Ile
								50		55		60			
Asn	Trp	Gly	Tyr	Ala	Glu	Val	Thr	Asn	Glu	Arg	Val	Asp	Ile	Leu	Ala
								65		70		75		80	
Asp	Gly	Ala	Val	Phe	Ile	Lys	Lys	Gly	Ser	Asp	Asp	Arg	Asp	Asp	Ala
								85		90		95			
Ile	Ser	Arg	Ala	Lys	Lys	Leu	Leu	Glu	Asp	Ala	Ser	Ser	Asp	Arg	Leu
								100		105		110			
Ala	Val	Ser	Ser	Val	Leu	Ala	Lys	Ile	Glu	Ser	Leu				
								115		120					

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556

Met	Tyr	Ser	Leu	Leu	Leu	Asp	Leu	Asn	Lys	Lys	Thr	Ala	Leu	Leu	Gly
1								5		10			15		
Thr	Arg	Gly	Phe	Phe	Ile	Asp	Asp	Lys	His	Ile	Lys	Glu	Lys	Gly	Leu
								20		25		30			
Thr	Thr	Pro	Thr	Leu	Leu	Glu	Leu	Tyr	Ser	Asp	Leu	Glu	Glu	Ala	Ile
								35		40		45			
Arg	Leu	Lys	Cys	Glu	Tyr	Phe	Ile	Met	Glu	Val	Ser	Ser	His	Ala	Ile
								50		55		60			
Val	Gln	Asn	Ala	Ser	Leu	Gly	Leu	Ile	Ser	Leu	Leu	Lys	Phe	Ser	Pro
								65		70		75		80	
Ile	Ser	Gln	Ala	Ile	Ile										
								85							

## (2) INFORMATION FOR SEQ ID NO:557:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557

```

Met Ser Lys Arg Ala Ile Arg Phe Pro Asn Lys Leu Phe Ser Tyr Pro
1          5           10          15
Lys Pro Lys Ile Lys Ala Thr Asn Thr Ser His Thr Val Leu Phe Ala
20         25           30
Tyr Pro Leu Lys Pro His Glu Met Ala Leu Leu Ala Leu Ala Thr Ser
35         40           45
Leu Leu Ala Pro Ile Phe Asn Ala Ile His Ser Thr Asn Ala Leu Asn
50         55           60
Ala Ile Lys Pro Asp Gly Thr Gly Ser Lys Ile Asn Pro Ile Ile Met
65         70           75           80
Pro Met Lys Ile Gln Lys
85

```

## (2) INFORMATION FOR SEQ ID NO:557:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557

```

Met Ser Lys Arg Ala Ile Arg Phe Pro Asn Lys Leu Phe Ser Tyr Pro
1          5           10          15
Lys Pro Lys Ile Lys Ala Thr Asn Thr Ser His Thr Val Leu Phe Ala
20         25           30
Tyr Pro Leu Lys Pro His Glu Met Ala Leu Leu Ala Leu Ala Thr Ser
35         40           45
Leu Leu Ala Pro Ile Phe Asn Ala Ile His Ser Thr Asn Ala Leu Asn
50         55           60
Ala Ile Lys Pro Asp Gly Thr Gly Ser Lys Ile Asn Pro Ile Ile Met
65         70           75           80
Pro Met Lys Ile Gln Lys

```

## (2) INFORMATION FOR SEQ ID NO:558:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558

Met	Lys	Thr	Asn	Phe	Tyr	Lys	Ile	Lys	Leu	Leu	Phe	Ala	Trp	Cys	Leu
1				5				10					15		
Ile	Ile	Gly	Met	Phe	Asn	Ala	Pro	Leu	Asn	Ala	Asp	Gln	Asn	Thr	Asp
			20				25					30			
Ile	Lys	Asp	Ile	Ser	Pro	Glu	Asp	Met	Ala	Leu	Asn	Ser	Val	Gly	Leu
	35					40					45				
Val	Ser	Arg	Asp	Gln	Leu	Lys	Ile	Glu	Ile	Pro	Lys	Glu	Thr	Leu	Glu
	50				55			60							
Gln	Lys	Val	Thr	Ile	Leu	Asn	Asp	Tyr	Asn	Asp	Lys	Asn	Val	Asn	Ile
65		70				75			80						
Lys	Phe	Asp	Asp	Ile	Ser	Leu	Gly	Ser	Phe	Gln	Pro	Asn	Asp	Asn	Leu
	85					90			95						
Gly	Ile	Asn	Ala	Met	Trp	Gly	Ile	Gln	Asn	Leu	Leu				
	100					105									

## (2) INFORMATION FOR SEQ ID NO:559:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559

Val	Tyr	Ser	Arg	Phe	Phe	Ala	Asn	Gln	His	Glu	Phe	Asp	Phe	Glu	Ala
1				5				10				15			
Gln	Gly	Ala	Leu	Gly	Ser	Asp	Gln	Ser	Ser	Leu	Asn	Phe	Lys	Ser	Thr
			20			25				30					
Leu	Leu	Gln	Asp	Leu	Asn	Gln	Ser	Tyr	Asn	Tyr	Leu	Ala	Tyr	Ser	Ala
	35				40				45						

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Thr	Ala	Arg	Ala	Ser	Tyr	Gly	Tyr	Asp	Phe	Ala	Phe	Phe	Arg	Asn	Ala
50				55					60						
Leu	Val	Leu	Lys	Pro	Ser	Val	Gly	Val	Ser	Tyr	Asn	His	Leu	Gly	Ser
65				70				75				80			
Thr	Asn	Phe	Lys	Ser	Asn	Ser	Gln	Ser	Gln	Val	Ala	Leu	Lys	Asn	Gly
							85		90				95		
Ala	Ser	Ser	Gln	His	Leu	Phe	Asn	Ala	Asn	Ala	Thr	Trp	Lys	Arg	Val
					100			105				110			
Ile	Ile	Met	Gly	Thr	Leu	His	Thr	Phe	Ile	Cys	Met	Trp	Glu	Phe	Tyr
					115			120				125			
Lys	Ser	Ser	Leu	Thr	Leu	Asp	Arg	Met	Met	Trp	Arg	Leu			
					130			135				140			

## (2) INFORMATION FOR SEQ ID NO:559:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...141

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:559

Val	Tyr	Ser	Arg	Phe	Phe	Ala	Asn	Gln	His	Glu	Phe	Asp	Phe	Glu	Ala
1				5				10				15			
Gln	Gly	Ala	Leu	Gly	Ser	Asp	Gln	Ser	Ser	Leu	Asn	Phe	Lys	Ser	Thr
					20			25				30			
Leu	Leu	Gln	Asp	Leu	Asn	Gln	Ser	Tyr	Asn	Tyr	Leu	Ala	Tyr	Ser	Ala
					35			40				45			
Thr	Ala	Arg	Ala	Ser	Tyr	Gly	Tyr	Asp	Phe	Ala	Phe	Phe	Arg	Asn	Ala
					50			55			60				
Leu	Val	Leu	Lys	Pro	Ser	Val	Gly	Val	Ser	Tyr	Asn	His	Leu	Gly	Ser
					65			70		75		80			
Thr	Asn	Phe	Lys	Ser	Asn	Ser	Gln	Ser	Gln	Val	Ala	Leu	Lys	Asn	Gly
							85		90			95			
Ala	Ser	Ser	Gln	His	Leu	Phe	Asn	Ala	Asn	Ala	Thr	Trp	Lys	Arg	Val
						100		105				110			
Ile	Ile	Met	Gly	Thr	Leu	His	Thr	Phe	Ile	Cys	Met	Trp	Glu	Phe	Tyr
					115			120				125			
Lys	Ser	Ser	Leu	Thr	Leu	Asp	Arg	Met	Met	Trp	Arg	Leu			
					130			135				140			

## (2) INFORMATION FOR SEQ ID NO:560:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560

```

Met Ile Asp Asn Leu Asp Gly Ala Lys Asp Ala Gln Leu Ile Lys Lys
1      5          10          15
Ala Tyr Ala Phe Leu Cys Leu Gly Gly Asp Gly Thr Ile Leu Gly Ala
20     25          30
Leu Arg Met Thr His Ala His Asn Lys Pro Cys Phe Gly Val Arg Ile
35     40          45
Gly Asn Leu Gly Phe Leu Ser Ala Val Glu Leu Asn Gly Leu Lys Asp
50     55          60
Phe Leu Gln Asp Leu Lys Gln Asn Arg Ile Lys Leu Glu Glu His Leu
65     70          75          80
Ala Leu Glu Gly Arg Ile Gly Asn Thr Ser Phe Tyr Ala Ile Asn Glu
85     90          95
Ile Val Ile Ala Lys Lys Ala Leu Gly Val Leu Asp Ile Lys Ala
100    105         110
Cys Ala Gly His Thr Pro Phe Asn Thr Tyr Lys Gly Asp Gly Leu Ile
115    120         125
Ile Ala Thr Pro Leu Gly Ser Thr Ala Tyr Asn Leu Ser Ala His Gly
130    135         140
Pro Ile Val His Ala Leu Ser Gln Ser Tyr Ile Leu Thr Pro Leu Cys
145    150         155         160
Asp Phe Ser Leu Thr Gln Arg Pro Leu Val Leu Gly Ala Glu Phe Cys
165    170         175
Leu Ser Phe Cys Ala His Glu Asp Ala Leu Val Val Ile Asp Gly Gln
180    185         190
Ala Thr Tyr Asp Leu Lys Ala Asn Gln Pro Leu Tyr Ile Gln Lys Ser
195    200         205
Pro Thr Thr Thr Lys Leu Leu Gln Lys Asn Ser Arg Asp Tyr Phe Lys
210    215         220
Val Leu Lys Glu Lys Leu Leu
225    230

```

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 185 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561

```

Met Unk Glu Asn Gly Arg Gly Val Pro Lys Asp Tyr Lys Lys Ala Val
1      5          10          15
Glu Tyr Phe Gln Lys Ala Val Asp Asn Asp Ile Pro Arg Gly Tyr Asn
20     25          30

```

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Asn	Leu	Gly	Val	Met	Tyr	Lys	Glu	Gly	Lys	Gly	Val	Pro	Lys	Asp	Glu
35						40						45			
Lys	Lys	Ala	Val	Glu	Tyr	Phe	Arg	Ile	Ala	Thr	Glu	Lys	Gly	Tyr	Thr
50						55				60					
Asn	Ala	Tyr	Ile	Asn	Leu	Gly	Ile	Met	Tyr	Met	Glu	Gly	Arg	Gly	Val
65					70			75			80				
Pro	Ser	Asn	Tyr	Ala	Lys	Ala	Thr	Glu	Cys	Phe	Arg	Lys	Ala	Met	His
85						90					95				
Lys	Gly	Asn	Val	Unk	Ala	Tyr	Ile	Leu	Leu	Gly	Asp	Ile	Tyr	Tyr	Ser
100						105					110				
Gly	Met	Ile	Asn	Trp	Val	Leu	Ser	Arg	Thr	Lys	Ile	Arg	Leu	Val	His
115						120			125						
Tyr	Lys	Met	Ala	Ala	Asp	Val	Ser	Ser	Ser	Arg	Ala	Tyr	Unk	Gly	Leu
130						135			140						
Ser	Glu	Ser	Tyr	Unk	Tyr	Gly	Leu	Gly	Val	Glu	Lys	Unk	Unk	Lys	Lys
145						150			155			160			
Ala	Glu	Glu	Tyr	Met	Gln	Lys	Ala	Cys	Asp	Phe	Asp	Ile	Asp	Lys	Asn
165							170					175			
Cys	Lys	Lys	Lys	Asn	Thr	Ser	Ser	Arg							
180						185									

## (2) INFORMATION FOR SEQ ID NO:561:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...185

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:561

Met	Unk	Glu	Asn	Gly	Arg	Gly	Val	Pro	Lys	Asp	Tyr	Lys	Ala	Val	
1					5			10			15				
Glu	Tyr	Phe	Gln	Lys	Ala	Val	Asp	Asn	Asp	Ile	Pro	Arg	Gly	Tyr	Asn
					20			25			30				
Asn	Leu	Gly	Val	Met	Tyr	Lys	Glu	Gly	Lys	Val	Pro	Lys	Asp	Glu	
					35			40			45				
Lys	Lys	Ala	Val	Glu	Tyr	Phe	Arg	Ile	Ala	Thr	Glu	Lys	Gly	Tyr	Thr
					50			55			60				
Asn	Ala	Tyr	Ile	Asn	Leu	Gly	Ile	Met	Tyr	Met	Glu	Gly	Arg	Gly	Val
					65			70			75			80	
Pro	Ser	Asn	Tyr	Ala	Lys	Ala	Thr	Glu	Cys	Phe	Arg	Lys	Ala	Met	His
					85			90			95				
Lys	Gly	Asn	Val	Unk	Ala	Tyr	Ile	Leu	Leu	Gly	Asp	Ile	Tyr	Tyr	Ser
					100			105			110				
Gly	Met	Ile	Asn	Trp	Val	Leu	Ser	Arg	Thr	Lys	Ile	Arg	Leu	Val	His
					115			120			125				
Tyr	Lys	Met	Ala	Ala	Asp	Val	Ser	Ser	Ser	Arg	Ala	Tyr	Unk	Gly	Leu
					130			135			140				
Ser	Glu	Ser	Tyr	Unk	Tyr	Gly	Leu	Gly	Val	Glu	Lys	Unk	Unk	Lys	Lys
					145			150			155			160	
Ala	Glu	Glu	Tyr	Met	Gln	Lys	Ala	Cys	Asp	Phe	Asp	Ile	Asp	Lys	Asn
					165			170			175				
Cys	Lys	Lys	Lys	Asn	Thr	Ser	Ser	Arg							

180

185

## (2) INFORMATION FOR SEQ ID NO:562:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...183

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:562

Met	Ile	Val	Gly	Leu	Ile	Gly	Val	Val	Glu	Ile	Ser	Ala	Leu	Glu	
1									10					15	
Ala	His	Ile	Glu	Val	Gln	Gly	Val	Val	Tyr	Gly	Val	Gln	Val	Ser	Met
									20					30	
Arg	Thr	Ala	Ala	Leu	Leu	Gln	Thr	Gly	Gln	Lys	Ala	Arg	Leu	Lys	Ile
									35					45	
Leu	Gln	Val	Ile	Lys	Glu	Asp	Ala	His	Leu	Leu	Tyr	Gly	Phe	Leu	Glu
									50					60	
Glu	Ser	Glu	Lys	Ile	Leu	Phe	Glu	Arg	Leu	Leu	Lys	Ile	Asn	Gly	Val
									65					80	
Gly	Gly	Arg	Ile	Ala	Ala	Ile	Leu	Ser	Ser	Phe	Ser	Pro	Asn	Glu	
									85					95	
Phe	Glu	Asn	Ile	Ile	Ala	Thr	Lys	Glu	Val	Lys	Arg	Leu	Gln	Gln	Val
									100					110	
Pro	Gly	Ile	Gly	Lys	Lys	Leu	Ala	Asp	Lys	Ile	Met	Val	Asp	Leu	Ile
									115					125	
Gly	Phe	Phe	Ile	Gln	Asp	Glu	Asn	Arg	Pro	Ala	Arg	Asn	Glu	Val	Phe
									130					140	
Leu	Ala	Leu	Glu	Ser	Leu	Gly	Phe	Lys	Ser	Ala	Glu	Ile	Asn	Pro	Val
									145					160	
Leu	Lys	Thr	Leu	Lys	Pro	His	Leu	Ser	Ile	Glu	Ala	Ala	Ile	Lys	Glu
									165					175	
Ala	Leu	Gln	Gln	Leu	Arg	Ser									
									180						

## (2) INFORMATION FOR SEQ ID NO:563:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature

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## (B) LOCATION 1...154

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:563

Val Gly Val Leu Leu Ala Leu Phe Phe Tyr Ala Lys Asn Asn Leu  
 1 5 10 15  
 Leu Glu Asn Thr Gln Ile Arg Met Gln Tyr Thr Ala Asp Ala Ile Ala  
 20 25 30  
 Lys Ser Leu Leu Glu Leu Asn Asn Ala Ser Ser Leu Glu Pro Leu Lys  
 35 40 45  
 Ile Leu Glu Glu Arg Phe Lys Asn Thr Pro Phe Val Leu Leu Asp Ala  
 50 55 60  
 Asp Asn Arg Val Lys Phe Ser Asn Ile Gly Val Phe Val Ala Ser Phe  
 65 70 75 80  
 Lys Asn Asp Ala Leu Ile Lys Thr Pro Tyr Phe Ala Leu Lys Lys Gln  
 85 90 95  
 Gly Phe Tyr Leu Thr Asp Ser Ala Pro Thr Asn Arg Leu Gly Val Ser  
 100 105 110  
 Lys Ile Ile Ala Glu Glu Glu Ile Gln Lys Ile Phe Ile Pro Leu  
 115 120 125  
 Tyr Lys Met Ile Gly Tyr Val Phe Leu Gly Ala Ser Leu Phe Val Ala  
 130 135 140  
 Leu Ile Ala Met Trp Leu Tyr Lys Ile Pro  
 145 150

## (2) INFORMATION FOR SEQ ID NO:564:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...288

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:564

Val Val Ile Met Ile Leu Val Cys Phe Leu Ala Cys Ser Gln Glu Ser  
 1 5 10 15  
 Phe Ile Lys Met Gln Lys Lys Ala Gln Glu Gln Glu Asn Asp Gly Ser  
 20 25 30  
 Lys Arg Pro Ser Tyr Val Asp Ser Asp Tyr Glu Val Phe Ser Glu Thr  
 35 40 45  
 Ile Phe Leu Gln Asn Met Val Tyr Gln Pro Ile Glu Glu Arg Asn Ala  
 50 55 60  
 Phe Phe Gln Leu Thr Lys Asp Glu Asp Asn Ser Phe Asn Pro Glu Asn  
 65 70 75 80  
 Ser Val Ile Leu Leu Asn Glu Pro Ser Asp Asn Ser Glu Lys Asn Leu  
 85 90 95  
 Leu Ser Tyr Pro Asn Asp Pro Asn Asn Glu Asp Asn Ala Asn Asn  
 100 105 110  
 Ser Gln Lys Asn Pro Phe Leu Tyr Lys Pro Lys Arg Lys Thr Lys Asn  
 115 120 125  
 Pro Lys Leu Ile Glu Tyr Ser Gln Gln Asp Phe Tyr Pro Leu Lys Asn  
 130 135 140  
 Gly Asp Ile Ile Met Ser Lys Glu Gly Asp Gln Trp Leu Ile Glu Ile

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145	150	155	160
Gln Ser Lys Ala Leu Lys Arg Phe Leu Lys Asp Gln Asn Asp Lys Asp			
165	170	175	
Arg Gln Ile Gln Thr Phe Thr Phe Asn Asp Thr Lys Thr Gln Ile Ala			
180	185	190	
Gln Ile Lys Gly Lys Ile Ser Ser Tyr Val Tyr Thr Thr Asn Asn Gly			
195	200	205	
Ser Leu Ser Leu Arg Pro Phe Tyr Glu Ser Phe Leu Leu Glu Lys Lys			
210	215	220	
Ser Asp Asn Val Tyr Thr Ile Glu Asn Lys Ala Leu Asp Thr Met Glu			
225	230	235	240
Ile Ser Lys Cys Gln Met Val Leu Lys Lys His Ser Thr Asp Lys Leu			
245	250	255	
Asp Ser Gln His Lys Ala Ile Ser Ile Asp Leu Asp Phe Lys Lys Glu			
260	265	270	
Arg Phe Lys Ser Asp Thr Glu Leu Phe Leu Glu Cys Leu Lys Glu Ser			
275	280	285	

## (2) INFORMATION FOR SEQ ID NO:565:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...420

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:565

Met Ala Ala Pro Leu Leu Ala Leu Pro Phe Leu Ser Asn Pro Leu Val			
1	5	10	15
Leu Gly Ala Leu Ala Val Ile Gly Val Gly Ala Tyr Leu Tyr Pro Asn			
20	25	30	
Lys Gln Asp Ser Leu Val Val Gln Ala Asp Gly Leu Tyr Ser Glu Ile			
35	40	45	
Leu Gly Phe Phe Ile Ser Phe Ser Ser Lys Ile Leu Lys Gly Ile Gly			
50	55	60	
Glu Pro Leu Ala Asn Val Ile Gln Pro Phe Gly Met Val Leu Gly Met			
65	70	75	80
Leu Leu Ile Leu Tyr Ser Phe Lys Arg Tyr Gln Asn Asn Asp Leu			
85	90	95	
Phe Glu Ile Lys Thr Phe Leu Met Leu Phe Val Phe Val Gly Tyr Leu			
100	105	110	
Ser Leu Tyr His Tyr Ala Phe Lys Ser Asp Gly Ser Ser Ser Gly Asn			
115	120	125	
Gly Arg Ser Ser Phe Ala Phe Gln Asn His Val Thr Glu Ile Phe Asp			
130	135	140	
Thr Pro Ala Asn Leu Leu Asn Ala Gly Ile Ser Asn Val Val Lys Glu			
145	150	155	160
Tyr Gln Thr Asn Ser Ala Arg Glu His Lys Asn Ile Asp Thr His His			
165	170	175	
Ser Ile Thr Asn Ala Asn Ile Ser Phe His Val Arg Gln Ile Leu Thr			
180	185	190	
Ser Leu Asn Lys Leu Tyr Glu Asp Phe Lys Ile Asn Asn Gly Leu Ser			
195	200	205	

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Leu Lys Thr Leu Ile Ala Ala Val Leu Leu Val Ile Leu Gly Leu  
 210 215 220  
 Glu Leu Phe Leu Leu Phe Lys Val Phe Cys Tyr Val Phe Met Thr Tyr  
 225 230 235 240  
 Leu Glu Lys Ile Ile Tyr Leu Ser Leu Val Ile Phe Met Leu Leu  
 245 250 255  
 Gly Phe Phe Gln Gln Thr Arg Gly Phe Leu Val Ser Tyr Val Lys Lys  
 260 265 270  
 Ile Ile Ser Leu Thr Phe Tyr Met Pro Leu Leu Leu Val Leu  
 275 280 285  
 Phe Asn Ser Phe Ala Leu Gln Tyr Ala Ile Lys Val Gly Gly Ser Asn  
 290 295 300  
 Glu Ile Val Ala Lys Phe Gly Ile Ile Val Ala Ile Gly Ile Ser Leu  
 305 310 315 320  
 Thr Phe Ile Gln Lys Val Pro Glu Met Ile Asn Ala Ile Phe Gly Thr  
 325 330 335  
 Gln Gly Gly Leu Thr Asp Ala Lys Ser Phe Ile Tyr Gln Gly Val Gln  
 340 345 350  
 Met Ala Ser Ala Gly Ala Gly Ala Ile Ala Gly Ser Leu Lys Ser Val  
 355 360 365  
 Gly Arg Ser Ala Phe Gly Arg Thr Leu Glu Ala Tyr Lys Asp Ala Lys  
 370 375 380  
 Ser Thr Ile Asn Ser Thr Thr Ala Asn Met Arg Asp Met Pro Gly His  
 385 390 395 400  
 Pro Gly Val Arg Val Gly Val Glu Thr Ile Glu Leu Pro Lys Ser His  
 405 410 415  
 Arg Ala Ser Lys  
 420

## (2) INFORMATION FOR SEQ ID NO:566:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...72

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:566

Val Leu Lys Phe Gln Lys Leu Pro Leu Leu Phe Val Ser Ile Leu Tyr  
 1 5 10 15  
 Asn Gln Ser Pro Leu Leu Ala Phe Asp Tyr Lys Phe Ser Gly Val Ala  
 20 25 30  
 Glu Ser Val Ser Lys Val Gly Phe Asn His Ser Lys Leu Asn Ser Lys  
 35 40 45  
 Glu Gly Ile Phe Pro Thr Ala Thr Phe Val Thr Ala Thr Ile Lys Leu  
 50 55 60  
 Gln Val Asn Tyr Lys Ser Ala Pro  
 65 70

## (2) INFORMATION FOR SEQ ID NO:567:

## (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 205 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567

Met	Gly	Asn	His	Phe	Ser	Lys	Leu	Gly	Phe	Val	Leu	Ala	Ala	Leu	Gly
1							5				10				15
Ser	Ala	Ile	Gly	Leu	Gly	His	Ile	Trp	Arg	Phe	Pro	Tyr	Met	Thr	Gly
							20			25				30	
Val	Ser	Gly	Gly	Gly	Ala	Phe	Val	Leu	Leu	Phe	Leu	Phe	Leu	Ser	Leu
							35		40			45			
Ser	Val	Gly	Ala	Ala	Met	Phe	Ile	Ala	Glu	Met	Leu	Leu	Gly	Gln	Ser
					50		55			60					
Thr	Gln	Lys	Asn	Val	Thr	Glu	Ala	Phe	Lys	Glu	Leu	Asp	Ile	Asn	Pro
					65		70			75				80	
Lys	Lys	Arg	Trp	Lys	Tyr	Ala	Gly	Ile	Met	Leu	Ile	Ser	Gly	Pro	Leu
					85		90			95					
Ile	Leu	Thr	Phe	Tyr	Gly	Thr	Ile	Leu	Gly	Trp	Val	Leu	Tyr	Tyr	Leu
					100		105				110				
Val	Ser	Ile	Ser	Phe	Asn	Leu	Pro	Ser	Ser	Ile	Gln	Glu	Ser	Glu	Gln
					115		120				125				
Ile	Phe	Thr	Gln	Thr	Leu	Gln	Ser	Ile	Gly	Leu	Gln	Ser	Ile	Gly	Leu
					130		135			140					
Phe	Ser	Val	Leu	Phe	Ile	Thr	Gly	Trp	Ile	Val	Ser	Arg	Gly	Ile	Lys
					145		150			155				160	
Glu	Gly	Ile	Glu	Lys	Leu	Asn	Leu	Val	Leu	Met	Pro	Leu	Leu	Phe	Ala
					165		170			175					
Thr	Phe	Phe	Gly	Leu	Leu	Phe	Tyr	Ala	Met	Ser	Met	Asp	Ser	Phe	Ser
					180		185			190					
Lys	Ala	Phe	His	Phe	Met	Leu	Ile	Ser	Ser	Gln	Ile				
					195		200			205					

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 328 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568

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Met Glu Lys Val Cys Val Ser Ala Trp Gly Leu Pro Lys Ile Leu Glu  
 1 5 10 15  
 Glu Arg Leu Lys Glu Lys Tyr Gly Asp Asp Trp Glu Lys His Val Lys  
 20 25 30  
 Ala Lys Ala Ile Asn Glu Glu Leu Glu Glu Gln Val Lys Ala Lys  
 35 40 45  
 Ala Lys Glu Gln Gln Lys Thr Gln Arg Glu Lys Thr Leu Asn Gly Phe  
 50 55 60  
 Leu Lys Lys Val Gly Leu Lys Lys Arg Asp Met Leu Gln Ser Thr Met  
 65 70 75 80  
 Leu Phe Asp Glu Val Lys Glu Ala Asp Val Leu Phe Gln Ala Glu Arg  
 85 90 95  
 Lys Ile Gly Asp Trp Ile Phe Ser Ser Ala Val Phe Phe Ala Leu  
 100 105 110  
 Ala Leu Ile Glu Ala Ile Ile Ile Val Cys Leu Leu Pro Leu Lys Glu  
 115 120 125  
 Lys Val Pro Tyr Leu Val Thr Phe Ser Asn Ala Thr Gln Asn Phe Ala  
 130 135 140  
 Ile Val Gln Arg Ala Asp Lys Ser Ile Arg Ala Asn Gln Ala Leu Val  
 145 150 155 160  
 Arg Gln Leu Val Ala Ser Tyr Val Asn Asn Arg Glu Asn Ile Ser Ser  
 165 170 175  
 Ile Lys Glu Gln Asn Glu Ile Ala His Glu Thr Ile Arg Leu Gln Ser  
 180 185 190  
 Ala Phe Glu Val Trp Asp Phe Phe Glu Lys Leu Val Ser Tyr Glu His  
 195 200 205  
 Ser Ile Tyr Thr Asn Ile Asn Leu Thr Arg Lys Ile Ser Ile Ile Asn  
 210 215 220  
 Ile Ala Leu Ile Ser Lys Thr Gln Ala Asn Ile Glu Ile Ser Ala Gln  
 225 230 235 240  
 Leu Phe His Lys Glu Lys Leu Glu Ser Glu Lys Arg Tyr Arg Ile Ile  
 245 250 255  
 Met Thr Phe Glu Phe Glu Pro Ile Glu Ile Asp Thr Lys Ser Val Pro  
 260 265 270  
 Leu Asn Pro Thr Gly Phe Ile Val Thr Gly Tyr Asp Val Thr Glu Ile  
 275 280 285  
 Ala Ile Leu Lys Asp Leu Asp Glu Lys Asn Lys Val Lys Asp Asp Gly  
 290 295 300  
 Val Lys Ser Arg Ile Ile His Val Glu Lys Lys Asp Pro His Met Ser  
 305 310 315 320  
 Gln Tyr Lys Asp Val Lys Glu Gln  
 325

## (2) INFORMATION FOR SEQ ID NO:569:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...139

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:569

Leu Leu Asn Met Trp Asp Glu Ala Lys Glu Gly Ile Asn Ile Asn

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1	5	10	15
Thr Glu Lys Leu Ser Gln Glu Leu Gly Val Val Cys Val Pro Thr Ser			
20	25	30	
Ala Arg Unk Lys Glu Asp Arg Leu Asn Thr Glu Leu Leu Asp Glu			
35	40	45	
Ile Val Arg Leu Tyr Ser Gln Asn Thr Thr Asn Asn Glu Asn Ile Lys			
50	55	60	
Val Pro Ser Gln Ser Phe Lys Glu Ser Leu Lys Tyr Ser Gln Ser Ala			
65	70	75	80
Gln Arg Ile Ala Lys Ser Val Ile Ser Glu Asn Lys Gln Asn Ala Ser			
85	90	95	
Phe Glu His Thr Tyr Lys Ile Asp Lys Ile Phe Asn Ala Pro Ala Leu			
100	105	110	
Trp Asp Phe His Phe Phe Unk Val Tyr Val Tyr His Leu Phe Phe Glu			
115	120	125	
Leu Phe Asn Arg Arg Gly Ser Ala Lys Ser Pro			
130	135		

## (2) INFORMATION FOR SEQ ID NO:569:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...139

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:569

Leu Leu Asn Met Trp Asp Glu Ala Lys Lys Glu Gly Ile Asn Ile Asn			
1	5	10	15
Thr Glu Lys Leu Ser Gln Glu Leu Gly Val Val Cys Val Pro Thr Ser			
20	25	30	
Ala Arg Unk Lys Glu Asp Arg Leu Asn Thr Glu Leu Leu Asp Glu			
35	40	45	
Ile Val Arg Leu Tyr Ser Gln Asn Thr Thr Asn Asn Glu Asn Ile Lys			
50	55	60	
Val Pro Ser Gln Ser Phe Lys Glu Ser Leu Lys Tyr Ser Gln Ser Ala			
65	70	75	80
Gln Arg Ile Ala Lys Ser Val Ile Ser Glu Asn Lys Gln Asn Ala Ser			
85	90	95	
Phe Glu His Thr Tyr Lys Ile Asp Lys Ile Phe Asn Ala Pro Ala Leu			
100	105	110	
Trp Asp Phe His Phe Phe Unk Val Tyr Val Tyr His Leu Phe Phe Glu			
115	120	125	
Leu Phe Asn Arg Arg Gly Ser Ala Lys Ser Pro			
130	135		

## (2) INFORMATION FOR SEQ ID NO:570:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570

Met	Leu	His	Lys	Ala	Lys	Val	Gly	Ile	Val	Phe	Gln	Ala	Leu	Leu	Gly
1						5			10				15		
Ile	Phe	Cys	Val	Phe	Leu	Leu	Leu	Phe	Tyr	Leu	Ser	Ala	Phe	Leu	Met
						20			25				30		
Val	Ala	Phe	Lys	Asp	Thr	Lys	Arg	Met	Phe	Ile	Ser	Val	Leu	Ile	Gly
						35			40				45		
Ser	Val	Val	Phe	Leu	Trp	Ser	Asp	Leu	Leu	Val	Phe	Val	Gly	Phe	Lys
						50			55				60		
Asn	Ile	Ser	Phe	Val	Leu	Asp	Ile	Gly	Tyr	Glu	Ile				
						65			70				75		

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571

Met	Gln	Glu	Ala	Leu	Leu	Arg	Phe	Gln	Glu	Gly	Phe	Lys	Glu	Trp	Gly
1						5			10				15		
Tyr	Leu	Ile	Leu	Phe	Leu	Tyr	Ser	Leu	Gly	Gly	Tyr	Val	Gly	Ile	
						20			25				30		
Val	Ile	Ala	Ser	Ile	Leu	Ser	Ala	Thr	Thr	His	Ala	Leu	Asp	Ile	Lys
						35			40				45		
Ile	Thr	Ile	Leu	Val	Ala	Phe	Gly	Asn	Leu	Ile	Gly	Ser	Gly	Ala	
						50			55				60		
Leu	Val	Ile	Phe	Ala	Arg	Tyr	Gln	Lys	Arg	Glu	Phe	Leu	Lys	Tyr	Phe
						65			70				75		80
Gln	Lys	His	Arg	Arg	Lys	Leu	Ala	Leu	Ala	Ser	Leu	Trp	Val	Lys	Arg
						85			90				95		
Tyr	Ala	Leu	Leu	Met	Ile	Phe	Val	Asn	Lys	Tyr	Leu	Tyr	Gly	Ile	Lys
						100			105				110		
Ser	Val	Val	Pro	Leu	Ala	Ile	Gly	Phe	Ser	Lys	Tyr	Pro	Leu	Lys	Lys
						115			120				125		
Phe	Leu	Trp	Leu	Asn	Val	Phe	Ser	Ser	Phe	Leu	Trp	Ala	Leu	Ile	Val
						130			135				140		
Gly	Ser	Val	Ser	Phe	Gln	Ala	Ser	Asp	Trp	Val	Lys	Thr	Leu	Tyr	Glu

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(2) INFORMATION FOR SEQ ID NO:571:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 193 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: YES
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: Helicobacter pylori
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION 1...193
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:571

```

Met Gln Glu Ala Leu Leu Arg Phe Gln Glu Gly Phe Lys Glu Trp Gly
1 5 10 15
Tyr Leu Ile Leu Phe Leu Tyr Ser Leu Gly Gly Gly Tyr Val Gly Ile
20 25 30
Val Ile Ala Ser Ile Leu Ser Ala Thr Thr His Ala Leu Asp Ile Lys
35 40 45
Ile Thr Ile Leu Val Ala Phe Leu Gly Asn Leu Ile Gly Ser Gly Ala
50 55 60
Leu Val Ile Phe Ala Arg Tyr Gln Lys Arg Glu Phe Leu Lys Tyr Phe
65 70 75 80
Gln Lys His Arg Arg Lys Leu Ala Leu Ala Ser Leu Trp Val Lys Arg
85 90 95
Tyr Ala Leu Leu Met Ile Phe Val Asn Lys Tyr Leu Tyr Gly Ile Lys
100 105 110
Ser Val Val Pro Leu Ala Ile Gly Phe Ser Lys Tyr Pro Leu Lys Lys
115 120 125
Phe Leu Trp Leu Asn Val Phe Ser Ser Phe Leu Trp Ala Leu Ile Val
130 135 140
Gly Ser Val Ser Phe Gln Ala Ser Asp Trp Val Lys Thr Leu Tyr Glu
145 150 155 160
Arg Leu Ser His Tyr Thr Ser Phe Phe Val Ile Ser Phe Val Leu Ile
165 170 175
Ala Leu Leu Ile Trp Phe Leu Leu Lys Arg Tyr Ser Arg Lys Met Gly
180 185 190
Phe

```

(2) INFORMATION FOR SEQ ID NO:572:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 140 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572

Met	Pro	Phe	Leu	Lys	Asn	Trp	Ile	Trp	Ser	Leu	Lys	Met	Ala	Leu	Ser
1							5			10			15		
Ala	Ile	Ser	Gly	Ala	Ser	Gly	Val	Gly	Lys	Ser	Val	Leu	Ile	Ala	Ser
							20			25			30		
Leu	Leu	Gly	Ala	Phe	Gly	Leu	Lys	Glu	Ser	Asn	Ala	Ser	Asn	Ile	Glu
							35			40			45		
Val	Glu	Leu	Ile	Ala	Pro	Phe	Leu	Asp	Thr	Glu	Glu	Tyr	Gly	Ile	Phe
							50			55			60		
Arg	Glu	Asp	Glu	His	Glu	Pro	Leu	Val	Ile	Ser	Val	Ile	Lys	Lys	Glu
							65			70			75		80
Lys	Thr	Arg	Tyr	Phe	Leu	Asn	Gln	Thr	Ser	Leu	Ser	Lys	Asn	Thr	Leu
							85			90			95		
Lys	Ala	Leu	Leu	Lys	Gly	Leu	Ile	Lys	Arg	Leu	Ser	Asn	Asp	Arg	Phe
							100			105			110		
Ser	Gln	Asn	Glu	Leu	Asn	Asp	Ile	Leu	Met	Leu	Ser	Leu	Leu	Asp	Gly
							115			120			125		
Tyr	Ile	Gln	Asn	Lys	Asn	Lys	Arg	Leu	Ala	Pro	Phe				
							130			135			140		

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573

Met	Pro	Gln	Asn	Gln	Leu	Val	Ile	Thr	Ile	Ile	Asp	Glu	Ser	Gly	Ser
1							5			10			15		
Lys	Gln	Leu	Lys	Phe	Ser	Lys	Asn	Leu	Lys	Arg	Asn	Leu	Ile	Ile	Ser
							20			25			30		
Val	Val	Ile	Leu	Leu	Ile	Val	Gly	Leu	Gly	Val	Gly	Phe	Leu	Lys	
							35			40			45		
Phe	Leu	Ile	Ala	Lys	Met	Asp	Thr	Met	Thr	Ser	Glu	Arg	Asn	Ala	Val
							50			55			60		
Leu	Arg	Asp	Phe	Arg	Gly	Leu	Tyr	Gln	Lys	Asn	Tyr	Ala	Leu	Ala	Lys
							65			70			75		80
Glu	Ile	Lys	Asn	Lys	Arg	Glu	Glu	Leu	Phe	Ile	Val	Gly	Gln	Lys	Ile
							85			90			95		
Arg	Gly	Leu	Glu	Ser	Leu	Ile	Glu	Ile	Lys	Lys	Gly	Ala	Asn	Gly	Gly

100	105	110
Gly His Leu Tyr Asp Glu Val Asp	Leu Glu Asn Leu Ser	Leu Asn Gln
115	120	125
Lys His Leu Ala Leu Met Leu Ile Pro Asn Gly	Met Pro Leu Lys Thr	
130	135	140
Tyr Ser Ala Ile Lys Pro Thr Lys Glu Arg Asn His	Pro Ile Lys Lys	
145	150	155
Ile Lys Gly Val Glu Ser Gly Ile Asp Phe Ile Ala Pro	Leu Asn Thr	
165	170	175
Pro Val Tyr Ala Ser Ala Asp Gly Ile Val Asp Phe Val	Lys Thr Arg	
180	185	190
Ser Asn Ala Gly Tyr Gly Asn Leu Val Arg Ile Glu His	Ala Phe Gly	
195	200	205
Phe Ser Ser Ile Tyr Thr His Leu Asp His Val Asn Val	Gln Pro Lys	
210	215	220
Ser Phe Ile Gln Lys Gly Gln Leu Ile Gly Tyr Ser Gly	Lys Ser Gly	
225	230	235
Asn Ser Gly Gly Glu Lys Leu His Tyr Glu Val Arg Phe	Leu Gly Lys	
245	250	255
Ile Leu Asp Ala Glu Lys Phe Leu Ala Trp Asp Leu Asp	His Phe Gln	
260	265	270
Ser Ala Leu Glu Glu Asn Lys Phe Ile Glu Trp Lys Asn	Leu Phe Trp	
275	280	285
Val Leu Glu Asp Ile Val Gln Leu Gln Glu His Val Asp	Lys Asp Thr	
290	295	300
Leu Lys Gly Gln		
305		

## (2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574

Met Ile Thr Gly Ser His Asn Pro Lys Glu Tyr Asn Gly	Phe Lys Ile
1 5 10 15	
Thr Leu Asn Gln Asn Pro Phe Tyr Gly Lys Asp Ile Gln Ala	Leu Lys
20 25 30	
Asn Thr Leu Leu Asn Ala Lys His Glu Ile Lys Pro Leu Lys	Glu Thr
35 40 45	
Pro Glu Lys Val Asn Ala Leu Glu Ala Tyr His Arg Tyr	Leu Ile Lys
50 55 60	
Asp Phe Lys His Leu Lys Asn Leu Lys Tyr Ile Ala Leu Asp	Phe
65 70 75 80	
Gly Asn Gly Val Gly Ala Leu Gly Leu Glu Pro Ile Leu Lys	Ala Leu
85 90 95	
Asn Ile Asp Phe Ser Ser Leu Tyr Ser Asp Pro Asp Gly Asp	Phe Pro
100 105 110	
Asn His His Pro Asp Pro Ser Glu Ala Lys Asn Leu Lys Asp	Leu Glu
115 120 125	

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Lys His Met Arg Glu Asn Ala Ile Leu Ile Gly Phe Ala Phe Asp Gly  
 130               135               140  
 Asp Ala Asp Arg Ile Ala Met Leu Ser Ser His His Ile Tyr Ala Gly  
 145               150               155               160  
 Asp Glu Leu Ala Ile Leu Phe Ala Lys Arg Leu His Ala Gln Gly Ile  
 165               170               175  
 Thr Pro Phe Val Ile Gly Glu Val Lys Cys Ser Gln Val Met Tyr Asn  
 180               185               190  
 Ala Ile Asn Thr Phe Gly Lys Thr Leu Met Tyr Lys Thr Gly His Ser  
 195               200               205  
 Asn Leu Lys Ile Lys Leu Lys Glu Thr Asn Ala His Phe Ala Ala Glu  
 210               215               220  
 Met Ser Gly His Ile Phe Phe Lys Glu Arg Tyr Phe Gly Tyr Asp Asp  
 225               230               235               240  
 Ala Leu Tyr Ala Cys Leu Arg Ala Leu Glu Leu Leu Glu Gln Ser  
 245               250               255  
 Pro Ser Asp Leu Glu Asn Thr Ile Lys Asn Leu Pro Tyr Ser Tyr Thr  
 260               265               270  
 Thr Pro Glu Glu Lys Ile Ala Val Ser Glu Glu Glu Lys Phe Glu Ile  
 275               280               285  
 Ile Arg Asn Leu Gln Glu Ala Leu Lys Asn Pro Pro Ser His Phe Pro  
 290               295               300  
 Thr Ile Lys Glu Ile Ile Ser Ile Asp Gly Val Arg Val Val Phe Glu  
 305               310               315               320  
 His Gly Phe Gly Leu Ile Arg Ala Ser Asn Thr His Pro Leu Phe Ser  
 325               330               335  
 Gln Pro Leu

## (2) INFORMATION FOR SEQ ID NO:575:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...207

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:575

Met Ser Lys Asn Leu Gln Lys Lys Asn Pro Lys Lys Ser Unk Pro Gln  
 1               5               10               15  
 Ala Gln Lys Ala Ile Arg Glu Met Lys Met Phe Glu Thr Ile Ala Phe  
 20               25               30  
 Tyr Phe Phe Ala Ile Leu Thr Leu Ser Met Ala Leu Val Val Ile Thr  
 35               40               45  
 Thr Thr Asn Ile Leu Tyr Ala Ile Thr Ala Leu Ala Ser Ser Met Val  
 50               55               60  
 Phe Ile Ser Ala Phe Phe Leu Leu Asp Ala Glu Phe Leu Gly Val  
 65               70               75               80  
 Val Gln Ile Thr Val Tyr Val Gly Ala Val Ile Val Met Tyr Ala Phe  
 85               90               95  
 Gly Met Met Phe Phe Asn Ser Ala Ala Glu Val Val Glu Arg Lys Gln  
 100              105              110  
 Ser Pro Lys Ile Leu Cys Val Leu Ser Phe Gly Val Ala Leu Leu

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115	120	125
Thr Leu Ile Leu Ser Ala Pro Ser Ile Unk Glu Asn Leu Ser Lys Gln		
130	135	140
Val Asn Ser Asn Ala Ile Asp Ala Gln Unk Pro Asn Ile Lys Ala Ile		
145	150	155
Gly Tyr Val Leu Phe Thr Asn Tyr Leu Ile Pro Phe Glu Ala Ala Ala		160
165	170	175
Leu Met Leu Leu Val Ala Met Val Gly Gly Ile Ala Thr Gly Ile Gln		
180	185	190
Lys Ile His Gly Lys Asn His Thr Gln Phe Ile Lys Glu Ser Leu		
195	200	205

## (2) INFORMATION FOR SEQ ID NO:576:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...251

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:576

Met Gly Ala Ile Leu Ser Ile Leu Lys Leu Glu Ile Lys Ser Tyr Leu		
1	5	10
Thr Asn Thr Ser Ala Leu Phe Trp Thr Phe Ile Tyr Pro Ile Leu Met		15
20	25	30
Leu Leu Leu Ile Phe Val Phe Ser Lys Asn Thr Thr Glu Ile Phe		
35	40	45
Tyr Phe Asn Asn Ile Ile Gly Leu Met Gly Leu Leu Ile Ile Ser Ser		
50	55	60
Ala Ile Phe Gly Leu Thr Gln Ala Ile Thr Ser Ser Arg Ser His Asn		
65	70	75
Ile Phe Leu Phe Tyr Met Leu Ser Pro Ala Thr Phe Lys Gln Ile Thr		80
85	90	95
Leu Ala Leu Ile Ala Ser Arg Leu Ile Val Val Ile Leu Tyr Ala Phe		
100	105	110
Ile Phe Ile Val Leu Ser Phe Tyr Ala Leu Asn Ile Ile Thr Ile Leu		
115	120	125
Asn Phe Lys Ala Leu Ile Leu Gly Phe Ile Ser Ile Phe Ser Ser Ala		
130	135	140
Leu Phe Cys Phe Cys Leu Ala Ile Phe Val Ala Arg Ile Phe Gln Asn		
145	150	155
Glu Gln Ser Ile Leu Gly Phe Cys Asn Ile Ile Asn Leu Tyr Ala Leu		160
165	170	175
Met Ser Cys Asn Val Phe Val Pro Leu Glu Tyr Leu Pro Asn Ile Gly		
180	185	190
Gln Leu Phe Ile Lys Thr Ser Ile Phe Tyr Tyr Leu Asn Gln Leu Leu		
195	200	205
Ile Lys Ala Phe Gln Gly Ile Asp Thr Ile Leu Val Leu Ala Thr Ser		
210	215	220
Thr Phe Phe Ile Ile Gly Gly Ile Ile Leu Phe Leu Leu Ser Ala Asn		
225	230	235
Arg Met Leu Leu Thr Pro Lys Glu Arg Met Arg		240
245	250	

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## (2) INFORMATION FOR SEQ ID NO:577:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 69 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...69
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:577

Met Ala Gly Thr Gln Ala Ile Tyr Glu Ser Ser Ser Ala Gly Phe Leu  
 1 5 10 15  
 Ser Gln Val Ser Ser Ile Ile Ser Ser Thr Ser Gly Val Ala Gly Pro  
 20 25 30  
 Phe Ala Gly Ile Val Ala Gly Ala Met Thr Ala Ala Ile Ile Pro Ile  
 35 40 45  
 Val Val Gly Phe Thr Asn Pro Gln Met Thr Asp Ile Ile Asn Pro Ile  
 50 55 60  
 Lys Ser Lys His Arg  
 65

## (2) INFORMATION FOR SEQ ID NO:578:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...112
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:578

Val Ser Arg Ile Leu Gly Leu Ser Asp Asp Leu Ala Met Thr Leu Cys  
 1 5 10 15  
 Ala Glu Ser Ile Arg Ile Gln Ala Pro Ile Lys Gly Lys Asp Val Val  
 20 25 30  
 Gly Ile Glu Ile Pro Asn Ser Gln Ser Gln Ile Ile Tyr Leu Arg Glu  
 35 40 45  
 Ile Leu Glu Ser Glu Leu Phe Gln Lys Ser Ser Ser Pro Leu Thr Leu  
 50 55 60  
 Ala Leu Gly Lys Asp Ile Val Gly Asn Pro Phe Ile Thr Asp Leu Lys  
 65 70 75 80  
 Lys Leu Pro His Leu Leu Ile Ala Gly Thr Thr Gly Ser Gly Lys Ser

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85	90	95
Val Gly Val Asn Ala Met Ile Leu Ser Leu Leu Tyr Lys Lys Pro Pro		
100	105	110

## (2) INFORMATION FOR SEQ ID NO:579:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579

Met Asp Glu Unk Leu Val Tyr Gly Val Ile Cys Met Pro Ser Gln Val			
1	5	10	15
Phe Ala Asn Thr Gly Thr Asn Val Ser Ile Ile Phe Phe Gln Lys Thr			
20	25	30	
Pro Ser Ala Lys Glu Val Ile Leu Ile Asp Ala Ser Lys Leu Gly Glu			
35	40	45	
Glu Tyr Thr Glu Asn Lys Asn Lys Thr Arg Leu Arg Pro Ser Asp			
50	55	60	
Met Asp Leu Ile Leu Glu Thr Phe Gln Asn Lys Ala Pro Lys Ser Asp			
65	70	75	80
Phe Cys Ala Leu Val Ser Phe Asp Glu Ile Thr Glu Lys Asn Tyr Ser			
85	90	95	
Leu Asn Pro Gly Gln Tyr Phe Thr Ile Glu Asp Thr Ser Glu Thr Ile			
100	105	110	
Ser Gln Ala Glu Phe Glu Asn Leu Met Gln Gln Tyr Ser Ser Glu Leu			
115	120	125	
Ala Ser Leu Phe Asp Glu Ser Gln Asn Leu Gln Gln Glu Ile Leu Glu			
130	135	140	
Thr Leu Lys Gly Val Arg Phe Glu			
145	150		

## (2) INFORMATION FOR SEQ ID NO:580:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...129

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:580

Met Arg Lys Gly Arg Val Met Leu Cys Val Phe Asp Ile Glu Thr Ile  
 1 5 10 15  
 Pro Asn Ile Ser Leu Cys Lys Glu His Phe Gln Leu Lys Glu Asp Asp  
 20 25 30  
 Ala Leu Lys Ile Cys Glu Trp Ser Phe Glu Lys Gln Lys Glu Lys Ser  
 35 40 45  
 Gly Ser Glu Phe Leu Pro Leu Tyr Leu His Glu Ile Ile Ser Ile Ala  
 50 55 60  
 Ala Val Ile Gly Asp Asp Tyr Gly Gln Phe Ile Lys Val Gly Asn Phe  
 65 70 75 80  
 Gly Gln Lys His Glu Asn Lys Glu Asp Phe Ala Ser Glu Lys Glu Leu  
 85 90 95  
 Leu Glu Asp Phe Phe Lys Tyr Phe Asn Glu Lys Gln Pro Arg Leu Ile  
 100 105 110  
 Ser Phe Unk Gly Arg Gly Phe Gly Tyr Ser Pro Thr His Ala Gln Ser  
 115 120 125  
 Pro

## (2) INFORMATION FOR SEQ ID NO:580:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 129 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...129

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:580

Met Arg Lys Gly Arg Val Met Leu Cys Val Phe Asp Ile Glu Thr Ile  
 1 5 10 15  
 Pro Asn Ile Ser Leu Cys Lys Glu His Phe Gln Leu Lys Glu Asp Asp  
 20 25 30  
 Ala Leu Lys Ile Cys Glu Trp Ser Phe Glu Lys Gln Lys Glu Lys Ser  
 35 40 45  
 Gly Ser Glu Phe Leu Pro Leu Tyr Leu His Glu Ile Ile Ser Ile Ala  
 50 55 60  
 Ala Val Ile Gly Asp Asp Tyr Gly Gln Phe Ile Lys Val Gly Asn Phe  
 65 70 75 80  
 Gly Gln Lys His Glu Asn Lys Glu Asp Phe Ala Ser Glu Lys Glu Leu  
 85 90 95  
 Leu Glu Asp Phe Phe Lys Tyr Phe Asn Glu Lys Gln Pro Arg Leu Ile  
 100 105 110  
 Ser Phe Unk Gly Arg Gly Phe Gly Tyr Ser Pro Thr His Ala Gln Ser  
 115 120 125  
 Pro

## (2) INFORMATION FOR SEQ ID NO:581:

- (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581

Met	Arg	Arg	Ile	Ile	Lys	Asn	Thr	Leu	Ser	Arg	Leu	Gly	Tyr	Glu	Asp
1															15
Val	Leu	Glu	Ala	Glu	His	Gly	Val	Glu	Ala	Trp	Glu	Lys	Leu	Asp	Ala
															30
Asn	Ala	Asp	Thr	Lys	Val	Leu	Ile	Thr	Asp	Trp	Asn	Met	Pro	Glu	Met
															45
Asn	Gly	Leu	Asp	Leu	Val	Lys	Lys	Val	Arg	Ala	Asp	Asn	Arg	Phe	Lys
															60
Glu	Ile	Pro	Ile	Ile	Met	Ile	Thr	Thr	Glu	Gly	Gly	Lys	Ala	Glu	Val
															80
Ile	Thr	Thr	Leu	Lys	Ala	Gly	Val	Asn	Asn	Tyr	Ile	Val	Lys	Pro	Phe
															95
Thr	Pro	Gln	Val	Leu	Lys	Glu	Lys	Leu	Glu	Val	Val	Leu	Gly	Thr	Asn
															110
Asp															

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 174 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582

Met	Ala	Glu	Glu	Gln	Glu	Asn	Thr	Ala	Gln	Gln	Pro	Gln	Lys	Lys	Ser
1															15
Lys	Ala	Leu	Leu	Phe	Val	Ile	Ile	Gly	Ser	Val	Leu	Val	Met	Leu	Leu
															30
Leu	Val	Gly	Val	Ile	Ile	Met	Leu	Leu	Met	Gly	Asn	Lys	Glu	Ser	
															45
Lys	Glu	Asn	Ala	Ser	Lys	Asn	Thr	Gln	Glu	Val	Gln	Ala	Asn	Pro	Met
															60
Ala	Asn	Lys	Asn	Gln	Glu	Ala	Lys	Glu	Gly	Ser	Asn	Ile	Gln	Gln	Tyr
															80

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Leu Val Leu Gly Pro Leu Tyr Ala Ile Asp Ala Pro Phe Ala Val Asn  
           85                 90                 95  
 Leu Val Ser Gln Asn Gly Arg Arg Tyr Leu Lys Ala Ser Ile Ser Leu  
           100             105             110  
 Glu Leu Ser Asn Glu Lys Leu Leu Asn Glu Val Lys Val Lys Asp Thr  
           115             120             125  
 Ala Ile Lys Asp Thr Ile Ile Glu Ile Leu Ser Ser Lys Ser Val Glu  
           130             135             140  
 Glu Val Val Thr Asn Lys Gly Lys Asn Lys Leu Lys Asp Glu Ile Lys  
           145             150             155             160  
 Ser His Leu Asn Ser Phe Leu Ile Asp Gly Phe Ile Lys Asn  
           165                         170

## (2) INFORMATION FOR SEQ ID NO:583:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...35
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:583

Met Gly Cys Phe Ser Thr Ile Cys Cys Lys Gly Leu Thr Leu Ser Val  
     1                 5                 10                 15  
 Gly Gly Phe Leu Val Met Met Arg Phe Leu Ile Phe Lys Asp Phe Cys  
     20                 25                         30  
 Lys Asp Phe  
     35

## (2) INFORMATION FOR SEQ ID NO:584:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 307 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...307
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:584

Met Ala Lys Lys Lys Ile Ala Ile Ser Cys Gly Asp Ile Gln Gly Val  
     1                 5                 10                 15  
 Gly Leu Glu Leu Ile Leu Lys Ser His Lys Glu Val Ser Ala Leu Cys

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Glu	Pro	Leu	Tyr	Leu	Val	His	Ser	Glu	Leu	Leu	Glu	Arg	Ala	Asn	Gln
20							25								30
35							40								45
Leu	Leu	Asp	Asn	Ala	Tyr	Glu	Thr	Lys	Thr	Leu	Asn	Ala	Ile	Ala	Ile
50							55								60
Asp	Ala	Pro	Leu	Pro	Leu	Leu	Asn	Ser	Ser	Thr	Ile	Gly	Lys	Val	Ser
65							70								80
Thr	Gln	Ser	Gly	Ala	Tyr	Ser	Phe	Glu	Ser	Phe	Lys	Lys	Ala	Cys	Glu
85							90								95
Leu	Ala	Asp	Ser	Lys	Glu	Val	Asp	Gly	Ile	Cys	Thr	Leu	Pro	Ile	Asn
100							105								110
Lys	Leu	Ala	Trp	Gln	Gln	Ala	Gln	Ile	Pro	Phe	Val	Gly	His	Thr	Asp
115							120								125
Phe	Leu	Lys	Gln	Arg	Tyr	Lys	Asp	His	Gln	Ile	Ile	Met	Met	Leu	Gly
130							135								140
Cys	Ser	Lys	Leu	Phe	Val	Gly	Leu	Phe	Ser	Asp	His	Val	Pro	Leu	Ser
145							150								160
Ala	Val	Ser	Gln	Leu	Ile	Gln	Val	Lys	Ala	Leu	Val	Lys	Phe	Leu	Leu
165							170								175
Ala	Phe	Gln	Lys	Ser	Thr	Gln	Ala	Lys	Ile	Val	Gln	Val	Cys	Gly	Phe
180							185								190
Asn	Pro	His	Ala	Gly	Glu	Glu	Gly	Leu	Phe	Gly	Glu	Glu	Asp	Glu	Lys
195							200								205
Ile	Leu	Lys	Ala	Ile	Gln	Glu	Ser	Asn	Gln	Thr	Leu	Gly	Phe	Glu	Cys
210							215								220
Phe	Leu	Gly	Pro	Leu	Pro	Ala	Asp	Ser	Ala	Phe	Ala	Pro	Asn	Lys	Arg
225							230								240
Lys	Ile	Thr	Pro	Phe	Tyr	Val	Ser	Met	Ser	His	Asp	Val	Gly	Leu	Ala
245							250								255
Pro	Leu	Lys	Ala	Leu	Tyr	Phe	Asp	Glu	Ser	Ile	Asn	Val	Ser	Leu	Asn
260							265								270
Ala	Pro	Ile	Leu	Arg	Ala	Ser	Thr	Asp	His	Gly	Thr	Ala	Phe	Asp	Ile
275							280								285
Ala	Tyr	Gln	Asn	Lys	Ala	Asn	His	Lys	Ser	Tyr	Leu	Asn	Ala	Ile	Lys
290							295								300
Tyr	Leu	Ala													
305															

## (2) INFORMATION FOR SEQ ID NO:584:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...307

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:584

Met	Ala	Lys	Lys	Ile	Ala	Ile	Ser	Cys	Gly	Asp	Ile	Gln	Gly	Val	
1								5						15	
Gly	Leu	Glu	Leu	Ile	Leu	Lys	Ser	His	Lys	Glu	Val	Ser	Ala	Leu	Cys
								20							30
Glu	Pro	Leu	Tyr	Leu	Val	His	Ser	Glu	Leu	Leu	Glu	Arg	Ala	Asn	Gln
								35							45

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Leu Leu Asp Asn Ala Tyr Glu Thr Lys Thr Leu Asn Ala Ile Ala Ile  
 50 55 60  
 Asp Ala Pro Leu Pro Leu Leu Asn Ser Ser Thr Ile Gly Lys Val Ser  
 65 70 75 80  
 Thr Gln Ser Gly Ala Tyr Ser Phe Glu Ser Phe Lys Lys Ala Cys Glu  
 85 90 95  
 Leu Ala Asp Ser Lys Glu Val Asp Gly Ile Cys Thr Leu Pro Ile Asn  
 100 105 110  
 Lys Leu Ala Trp Gln Gln Ala Gln Ile Pro Phe Val Gly His Thr Asp  
 115 120 125  
 Phe Leu Lys Gln Arg Tyr Lys Asp His Gln Ile Ile Met Met Leu Gly  
 130 135 140  
 Cys Ser Lys Leu Phe Val Gly Leu Phe Ser Asp His Val Pro Leu Ser  
 145 150 155 160  
 Ala Val Ser Gln Leu Ile Gln Val Lys Ala Leu Val Lys Phe Leu Leu  
 165 170 175  
 Ala Phe Gln Lys Ser Thr Gln Ala Lys Ile Val Gln Val Cys Gly Phe  
 180 185 190  
 Asn Pro His Ala Gly Glu Glu Gly Leu Phe Gly Glu Glu Asp Glu Lys  
 195 200 205  
 Ile Leu Lys Ala Ile Gln Glu Ser Asn Gln Thr Leu Gly Phe Glu Cys  
 210 215 220  
 Phe Leu Gly Pro Leu Pro Ala Asp Ser Ala Phe Ala Pro Asn Lys Arg  
 225 230 235 240  
 Lys Ile Thr Pro Phe Tyr Val Ser Met Ser His Asp Val Gly Leu Ala  
 245 250 255  
 Pro Leu Lys Ala Leu Tyr Phe Asp Glu Ser Ile Asn Val Ser Leu Asn  
 260 265 270  
 Ala Pro Ile Leu Arg Ala Ser Thr Asp His Gly Thr Ala Phe Asp Ile  
 275 280 285  
 Ala Tyr Gln Asn Lys Ala Asn His Lys Ser Tyr Leu Asn Ala Ile Lys  
 290 295 300  
 Tyr Leu Ala  
 305

## (2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 702 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585

Val Ala Arg Leu Val Val Lys Arg Arg Lys Ile Asp Tyr Lys Gln Ser  
 1 5 10 15  
 Ile Gln Ser Asp Ser Gln Tyr Leu Gln Ala Unk Leu Asn Gln Phe Glu  
 20 25 30  
 Asn Lys Glu Val Tyr Glu Asn Gln Tyr Phe Leu Val Leu Glu Ser Thr  
 35 40 45  
 His Ser Leu His Gly Val Leu Glu His Lys Lys Lys Ser Phe Met His  
 50 55 60  
 Ala Asn Arg Glu Asn Phe Lys Asp Ile Leu Ser Tyr Lys Ala His Phe

65	70	75	80
Leu Gln Glu Thr Leu Lys Ser Leu Glu Ile Gln Leu Lys Asn Tyr Ala			
85	90	95	
Pro Lys Leu Leu Asn Ser Lys Glu Val Leu Asn Phe Tyr Ala Glu Tyr			
100	105	110	
Ile Asn Gly Phe Glu Leu Pro Leu Lys Pro Leu Val Gly Gly Tyr Leu			
115	120	125	
Ser Asp Ser Tyr Ile Ala Ser Ser Ile Thr Phe Glu Lys Asp Tyr Phe			
130	135	140	
Ile Gln Glu Ser Phe Asn Gln Lys Thr Tyr Asn Arg Leu Ile Gly Ile			
145	150	155	160
Lys Ala Tyr Glu Ser Glu Arg Ile Thr Ser Ile Ala Val Gly Ala Leu			
165	170	175	
Leu Tyr Gln Glu Thr Pro Leu Asp Ile Ile Phe Ser Ile Glu Pro Met			
180	185	190	
Ser Val Asn Lys Thr Leu Ser Phe Leu Lys Glu Arg Ala Lys Phe Ser			
195	200	205	
Met Ser Asn Leu Val Lys Asn Glu Leu Leu Glu Tyr Gln Glu Leu Val			
210	215	220	
Lys Thr Lys Arg Leu Ser Met Gln Lys Phe Ala Leu Asn Val Leu Ile			
225	230	235	240
Lys Ala Pro Ser Leu Glu Asp Leu Asp Ala Gln Thr Ser Leu Ile Leu			
245	250	255	
Gly Leu Leu Phe Lys Glu Asn Leu Val Gly Val Ile Glu Thr Phe Gly			
260	265	270	
Leu Lys Gly Gly Tyr Phe Ser Phe Phe Pro Glu Arg Ile His Leu Asn			
275	280	285	
His Arg Leu Arg Phe Leu Thr Ser Lys Ala Leu Ala Cys Leu Met Val			
290	295	300	
Phe Glu Arg Gln Asn Leu Gly Phe Lys Ala Asn Ser Trp Gly Asn Ser			
305	310	315	320
Pro Leu Ser Val Phe Lys Asn Leu Asp Tyr Ser Pro Phe Leu Phe Asn			
325	330	335	
Phe His Asn Gln Glu Val Ser His Asn Asn Ala Lys Glu Ile Ala Arg			
340	345	350	
Val Asn Gly His Thr Leu Val Ile Gly Ala Thr Gly Ser Gly Lys Ser			
355	360	365	
Thr Leu Ile Ser Tyr Leu Met Met Ser Ala Leu Lys Tyr Gln Asn Met			
370	375	380	
Arg Leu Leu Ala Phe Asp Arg Met Gln Gly Leu Tyr Ser Phe Thr Glu			
385	390	395	400
Phe Phe Lys Gly His Tyr His Asp Gly Gln Ser Phe Ser Ile Asn Pro			
405	410	415	
Phe Cys Leu Glu Pro Asn Leu Gln Asn Leu Glu Phe Leu Gln Ser Phe			
420	425	430	
Phe Leu Ser Met Leu Asp Leu Ala Pro Ser Arg Asp Lys Glu Ala Leu			
435	440	445	
Glu Asp Met Asn Ala Ile Ser Gly Ala Ile Lys Ser Leu Tyr Glu Thr			
450	455	460	
Leu Tyr Pro Lys Asp Phe Ser Leu Leu Asp Phe Lys Glu Thr Leu Lys			
465	470	475	480
Arg Thr Ser Ser Asn Gln Leu Gly Leu Ser Leu Glu Pro Tyr Leu Asn			
485	490	495	
Asn Pro Leu Phe Asn Ala Leu Asn Asp Ala Phe Asn Ser Asn Ala Phe			
500	505	510	
Leu Asn Val Ile Asn Leu Asp Ala Ile Thr Gln Asn Pro Lys Asp Leu			
515	520	525	
Gly Leu Leu Ala Tyr Tyr Leu Phe Tyr Lys Ile Leu Glu Glu Ser Arg			
530	535	540	
Lys Asn Asp Ser Gly Phe Leu Val Phe Leu Asp Glu Phe Lys Ser Tyr			
545	550	555	560
Val Glu Asn Asp Leu Leu Asn Thr Lys Ile Asn Ala Leu Ile Thr Gln			
565	570	575	
Ala Arg Lys Ala Asn Gly Val Val Leu Ala Leu Gln Asp Ile Tyr			
580	585	590	

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Gln Leu Ser Gly Val Lys Asn Ala His Ser Phe Leu Ser Asn Met Gly  
 595 600 605  
 Thr Leu Ile Leu Tyr Pro Gln Lys Asn Ala Arg Glu Leu Lys His Asn  
 610 615 620  
 Phe Asn Val Pro Leu Ser Glu Thr Glu Ile Ser Phe Leu Glu Asn Thr  
 625 630 635 640  
 Pro Leu Tyr Ala Arg Gln Val Leu Val Lys Asn Leu Gly Asn Gly Ser  
 645 650 655  
 Ser Asn Met Ile Asp Val Ser Leu Glu Gly Leu Gly Cys Tyr Leu Lys  
 660 665 670  
 Ile Phe Asn Ser Asp Ser Ser His Val Asn Lys Val Lys Ala Leu Gln  
 675 680 685  
 Lys Asp Tyr Pro Thr Glu Trp Arg Glu Lys Leu Leu Lys Ser  
 690 695 700

## (2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 293 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586

Met Gln Glu Asp Trp Gln Ala Val Gln Asp Thr Ile Lys Val Val Ser  
 1 5 10 15  
 Asp Val Lys Ala Gly Asn Phe Ala Val Arg Ile Thr Ala Glu Pro Ala  
 20 25 30  
 Ser Pro Asp Leu Lys Glu Leu Arg Asp Ala Leu Asn Gly Ile Met Unk  
 35 40 45  
 Tyr Leu Gln Glu Ser Val Gly Thr His Met Pro Ser Ile Phe Lys Ile  
 50 55 60  
 Phe Glu Ser Tyr Ser Gly Leu Asp Phe Arg Gly Arg Ile Gln Asn Ala  
 65 70 75 80  
 Ser Gly Arg Val Glu Leu Val Thr Asn Ala Leu Gly Gln Glu Ile Gln  
 85 90 95  
 Lys Met Leu Glu Thr Ser Ser Asn Phe Ala Lys Asp Leu Ala Asn Asp  
 100 105 110  
 Ser Ala Asn Leu Lys Glu Cys Val Gln Asn Leu Glu Lys Ala Ser Asn  
 115 120 125  
 Ser Gln His Lys Ser Leu Met Glu Thr Ser Lys Thr Ile Glu Asn Ile  
 130 135 140  
 Thr Thr Ser Ile Gln Gly Val Ser Ser Gln Ser Glu Ala Met Ile Glu  
 145 150 155 160  
 Gln Gly Lys Asp Ile Lys Ser Ile Val Glu Ile Ile Arg Asp Ile Ala  
 165 170 175  
 Asp Gln Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile Glu Ala Ala Arg  
 180 185 190  
 Ala Gly Glu His Gly Arg Gly Phe Ala Val Val Ala Asp Glu Val Arg  
 195 200 205  
 Lys Leu Ala Glu Arg Thr Gln Lys Ser Leu Ser Glu Ile Glu Ala Asn  
 210 215 220  
 Ile Asn Ile Leu Val Gln Ser Ile Ser Asp Thr Ser Glu Ser Ile Lys

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225	230	235	240
Asn Gln Val Lys Glu Val Glu Glu Ile Asn Ala Ser Ile Glu Ala Leu			
245	250	255	
Arg Ser Val Thr Glu Gly Asn Leu Lys Ile Ala Ser Asp Ser Leu Glu			
260	265	270	
Ile Ser Gln Glu Ile Asp Lys Val Ser Asn Asp Ile Leu Glu Asp Val			
275	280	285	
Asn Lys Lys Gln Phe			
290			

## (2) INFORMATION FOR SEQ ID NO:587:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...52

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:587

Met Pro Lys Ser Phe Thr Leu Pro Thr Phe Val Trp Cys Leu Phe Val			
1	5	10	15
Gly Val Ile Leu Arg Asn Ala Leu Ser Phe Phe Lys Ile His Ser Val			
20	25	30	
Phe Asp Arg Glu Val Ser Val Ile Gly Asn Val Ser Leu Ser Leu Phe			
35	40	45	
Leu Ala Tyr Ala			
50			

## (2) INFORMATION FOR SEQ ID NO:588:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...182

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:588

Val Gly Leu Leu Asn Ser Lys Ala Phe Lys Pro Tyr Arg Lys Ile Leu			
1	5	10	15
Gln Met Val Phe Gln Asp Pro Tyr Ala Ser Leu Asn Pro Arg Leu Ser			
20	25	30	

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Ile Gln Ser Ile Leu Ile Glu Ala Leu Arg Phe Ala Tyr Pro Lys Ala  
 35                   40                   45  
 Ser Gln Gln Glu Trp His His Leu Ala Glu Leu Cys Leu Glu Glu Val  
 50                   55                   60  
 Cys Leu Asn Pro Glu Leu Leu Asn Phe Tyr Ala Tyr Glu Leu Ser Gly  
 65                   70                   75                   80  
 Gly Glu Arg Gln Arg Val Ala Ile Ala Arg Ala Ile Ala Leu Lys Pro  
 85                   90                   95  
 Arg Ile Ile Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Lys Ser Ile  
 100                  105                  110  
 Gln Lys Ser Val Leu Glu Leu Leu Asn Leu Gln Glu Lys Gln Asp  
 115                  120                  125  
 Leu Ser Tyr Leu Phe Ile Ser His Asp Leu Asp Val Ile Lys Ala Phe  
 130                  135                  140  
 Cys Asp Arg Val Leu Val Val Ser Glu Gly Lys Ile Val Glu Thr Gly  
 145                  150                  155                  160  
 Ala Ile Glu Glu Val Phe Asp Asn Pro Lys His Ala Tyr Thr Lys Arg  
 165                  170                  175  
 Leu Leu Glu Ser Arg Leu  
 180

## (2) INFORMATION FOR SEQ ID NO:589:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...251

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:589

Val Ser Leu Ile Lys Val Ser Gly Asp Lys Lys Val Ile Glu Val Ser  
 1                   5                   10                   15  
 Ile Pro Leu Thr Ser Ile Ser Gly Lys Ala Arg Val Lys Ile Arg His  
 20                  25                  30  
 Ala Phe Ser Asp Tyr Gly Ile Ser Thr Ala Thr Arg Lys Ile Pro Phe  
 35                  40                  45  
 Ser Leu Lys His Tyr Val Glu Trp Gln Ile Gly Tyr Asp Val Pro Ile  
 50                  55                  60  
 Lys Asp Lys Glu Lys Phe Glu Leu Thr Thr Leu Lys Asp Glu Lys Tyr  
 65                  70                  75                  80  
 His Phe Leu Gly Ala Asn Asn Lys Val Lys Thr Leu Tyr Glu Leu Ser  
 85                  90                  95  
 Glu Met Ile Tyr Tyr Ala Lys Arg Leu Gly Leu Ile Ser Leu Glu Asn  
 100                105                110  
 Leu Glu Asn Thr Leu Lys Phe Leu Glu Lys Gln Lys Gln Phe Ile Glu  
 115                120                125  
 Asp Asn Phe Met Ile Thr Arg Glu Arg Phe Arg Ser His Gln Phe Gly  
 130                135                140  
 Gly Met Asp Phe Glu Leu Ser Arg Ile Ser Tyr Pro Leu Leu Ile His  
 145                150                155                160  
 Ser Phe Asp Asp Asn Glu Leu Ser Glu Ile Val Ile Lys Glu Gln Gln  
 165                170                175  
 Tyr Gly Ser Lys Thr Gln Ala Met Leu Tyr Phe Cys Phe Ser Ile Leu

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180	185	190
Glu Leu Lys Thr Ala Thr Pro Leu	Leu Asn Arg Thr Ala Met Pro Lys	
195	200	205
Glu His Ala Leu Leu Ile Ile His	Glu Thr Asn Ala Leu Val Phe Leu	
210	215	220
Glu Met Leu Lys Ile Phe Gly Leu Leu Ser Gln Val His His Asn Asp		
225	230	235
Val Leu Lys Ile Leu Glu Lys Ile Leu Gln Asn		240
245	250	

## (2) INFORMATION FOR SEQ ID NO:590:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590

Val Ile Thr Ala Cys Phe Asn Arg Glu Lys Thr Ile Glu Asp Thr Ile			
1	5	10	15
Leu Ser Val Leu Asn Gln Thr Tyr Lys Asn Ile Glu Tyr Ile Ile Ile			
20	25	30	
Asp Gly Ala Ser Ala Ile Ala Leu			
35	40		

## (2) INFORMATION FOR SEQ ID NO:591:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591

Val Phe Val Gly Leu Tyr His Gly Ala Ser Ile Phe Asp Leu Lys Phe			
1	5	10	15
Glu Val Tyr Leu Thr Met Leu Ile Ser Leu Met Pro Phe Val Ala Thr			
20	25	30	
Ile Tyr Ile Asn Phe Pro Lys Thr Glu Thr Ser His Gly Tyr Ala			
35	40	45	

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Arg Trp Ala Asn Val Lys Asp Ile Glu Cys Phe Lys Ile Phe Ser Lys  
 50 55 60  
 Glu Gly Phe Cys Lys Val Val His Arg Leu Gly Val Gln Phe Asp Asn  
 65 70 75 80  
 Gly Phe Ile Leu Gly Lys Phe Gly Phe Pro Lys Leu Arg Asn Val Cys  
 85 90 95  
 Tyr Asp Lys Pro Leu Gly Thr Met Ile Val Ala Pro Pro Gly Ala Glu  
 100 105 110  
 Lys Leu His Val Trp Leu Cys Gln Ile Tyr  
 115 120

## (2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592

Met Lys Arg Leu Ala Val Ala Leu Ile Leu Val Leu Gly Val Val Trp  
 1 5 10 15  
 Gly Lys Ser Leu Pro Lys Trp Ala Lys Asp Cys Ser Lys Glu Met Arg  
 20 25 30  
 Ile Glu Lys Thr Gln Thr Lys Asp Glu Lys Ile Leu Val Cys Gly Met  
 35 40 45  
 Ser Asp Ile Leu Leu Ser Asp Met Asp Tyr Ser Leu Ser Ser Ala Arg  
 50 55 60  
 Gln Asn Ala Leu Glu Lys Val Met Glu Ala Phe Lys Gly Asp Arg Ile  
 65 70 75 80  
 Glu Ile Lys Ala Gly Glu Leu Lys Ala Thr Phe Ile Asp Thr Asp Lys  
 85 90 95  
 Val Tyr Val Leu Leu Arg Ile Thr Lys Lys His Val Ala Leu Met Asn  
 100 105 110  
 Glu

## (2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 437 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593

```

Met Asn Pro Gln Ile Gln Pro Ala Thr Lys Lys Pro Leu Lys Ser Leu
1          5           10          15
Leu Ala Ala Ser Ser Gly Asn Leu Val Glu Trp Tyr Asp Phe Tyr Ala
20         25           30
Tyr Ala Phe Leu Ala Pro Tyr Phe Ala Lys Glu Phe Thr His Thr Asn
35         40           45
Asp Pro Thr Leu Ala Leu Ile Ser Ala Phe Leu Val Phe Met Leu Gly
50         55           60
Phe Phe Met Arg Pro Leu Gly Ser Leu Phe Phe Gly Lys Leu Gly Asp
65         70           75           80
Lys Lys Gly Arg Lys Thr Ser Met Val Tyr Ser Ile Ile Leu Met Ala
85         90           95
Leu Gly Ser Phe Met Leu Ala Leu Leu Pro Thr Lys Glu Ile Val Gly
100        105          110
Glu Trp Ala Phe Leu Phe Leu Leu Ala Arg Leu Leu Gln Gly Phe
115        120          125
Ser Val Gly Gly Glu Tyr Gly Val Val Ala Thr Tyr Leu Ser Glu Leu
130        135          140
Gly Lys Asn Gly Lys Lys Gly Phe Tyr Gly Ser Phe Gln Tyr Val Thr
145        150          155          160
Leu Val Gly Gly Gln Leu Leu Ala Ile Phe Ser Leu Phe Ile Val Glu
165        170          175
Asn Val Tyr Thr His Glu Gln Ile Ser Ala Phe Ala Trp Arg Tyr Leu
180        185          190
Phe Ala Leu Glu Gly Ile Leu Ala Leu Leu Ser Leu Phe Leu Arg Asn
195        200          205
Ile Met Glu Glu Thr Met Asp Asn Glu Ala Thr Pro Gln Lys Lys Thr
210        215          220
Asn Val Asn Asn Thr Lys Glu Thr His Ile Lys Glu Thr Gln Arg Gly
225        230          235          240
Ser Leu Lys Glu Leu Leu Asn His Lys Lys Ala Leu Met Ile Val Phe
245        250          255
Gly Leu Thr Met Gly Gly Ser Leu Cys Phe Tyr Thr Phe Thr Val Tyr
260        265          270
Leu Lys Ile Phe Leu Thr Asn Ser Ser Phe Ser Pro Lys Glu Ser
275        280          285
Ser Phe Ile Met Leu Leu Ala Leu Ser Tyr Phe Ile Phe Leu Gln Pro
290        295          300
Leu Cys Gly Met Leu Ala Asp Lys Ile Lys Arg Thr Gln Met Leu Met
305        310          315          320
Val Phe Ala Ile Thr Gly Leu Ile Val Thr Pro Ile Val Phe Tyr Gly
325        330          335
Ile Lys His Ala Thr Ser Val Tyr Glu Ala Leu Phe Tyr Glu Ile Leu
340        345          350
Ala Leu Ser Ser Met Ser Phe Tyr Thr Cys Ile Ala Gly Val Ile Lys
355        360          365
Ala Glu Leu Phe Pro Glu His Val Arg Ala Leu Gly Val Gly Leu Ala
370        375          380
Tyr Ala Ile Ala Asn Ala Leu Phe Gly Gly Ser Ala Ser Tyr Ile Ala
385        390          395          400
Leu Glu Phe Lys Gln His Gly Phe Glu Glu Gly Phe Val Gly Tyr Val
405        410          415
Met Leu Ser Ile Val Ile Phe Met Val Met Val Ile Ile Phe Pro Lys
420        425          430
Lys Thr Tyr Leu Glu
435

```

(2) INFORMATION FOR SEQ ID NO:594:

**SUBSTITUTE SHEET (RULE 26)**

494

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 146 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594

```

Met Ser Ser Gly Leu Ile Tyr Ile Ser Leu Glu Val Leu Val Unk Cys
1           5          10          15
Leu Ile Thr Ala Leu Ile Met Tyr Tyr Val Met Lys Lys Ile Tyr Tyr
20          25          30
Ala Arg Gly Gln Ala Ile Leu Lys Gly Ala Ser Ala Lys Ala Lys Leu
35          40          45
Met Glu Phe Gln Ala Lys Ser Phe Val Glu Ala Glu Glu Met Arg Met
50          55          60
Lys Ser Gln Glu Cys Lys Leu Gln Gln Tyr Glu Asn Lys Asn Leu
65          70          75          80
Gln Leu Gln Thr His Phe Asp Lys Lys Glu Ala His Leu Lys His Leu
85          90          95
Glu Ala Gln His Lys Glu Phe Val Arg Asp Glu Lys Arg Tyr Leu Glu
100         105         110
Lys Glu Lys Lys Glu Leu Glu Lys Glu Arg Gln Ile Leu Glu Unk Glu
115         120         125
Arg Glu Asn Phe Unk Unk Gln Arg Ala Phe Val Unk Unk Unk Unk Ala
130         135         140
Lys Ala
145

```

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 146 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594

```

Met Ser Ser Gly Leu Ile Tyr Ile Ser Leu Glu Val Leu Val Unk Cys
1           5          10          15
Leu Ile Thr Ala Leu Ile Met Tyr Tyr Val Met Lys Lys Ile Tyr Tyr
20          25          30
Ala Arg Gly Gln Ala Ile Leu Lys Gly Ala Ser Ala Lys Ala Lys Leu

```

495

35	40	45
Met Glu Phe Gln Ala Lys Ser Phe Val Glu Ala Glu Glu		Met Arg Met
50	55	60
Lys Ser Gln Glu Cys Lys Leu Gln Gln Tyr Glu Asn Lys Asn Leu		
65	70	75
Gln Leu Gln Thr His Phe Asp Lys Lys Glu Ala His Leu Lys His Leu		80
85	90	95
Glu Ala Gln His Lys Glu Phe Val Arg Asp Glu Lys Arg Tyr Leu Glu		
100	105	110
Lys Glu Lys Lys Glu Leu Glu Lys Glu Arg Gln Ile Leu Glu Unk Glu		
115	120	125
Arg Glu Asn Phe Unk Unk Gln Arg Ala Phe Val Unk Unk Unk Unk Ala		
130	135	140
Lys Ala		
145		

## (2) INFORMATION FOR SEQ ID NO:595:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...127

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:595

Met Asn Ile Lys Ile Leu Lys Ile Leu Val Gly Gly Leu Phe Phe Leu		
1	5	10
Ser Leu Asn Ala His Leu Trp Gly Lys Gln Asp Asn Ser Phe Leu Gly		
20	25	30
Ile Gly Glu Arg Ala Tyr Lys Ser Gly Asn Tyr Ser Lys Ala Ala Ser		
35	40	45
Tyr Phe Lys Lys Ala Cys Asn Asp Gly Val Ser Glu Gly Cys Thr Gln		
50	55	60
Leu Gly Ile Ile Tyr Glu Asn Gly Gln Gly Thr Arg Ile Asp Tyr Lys		
65	70	75
Lys Ala Leu Glu Tyr Tyr Lys Thr Ala Cys Gln Ala Asp Asp Arg Glu		80
85	90	95
Gly Cys Phe Gly Leu Gly Gly Leu Tyr Asp Glu Gly Leu Gly Thr Ala		
100	105	110
Gln Asn Tyr Gln Glu Ala Unk Asp Ala Tyr Ala Arg His Ala Phe		
115	120	125

## (2) INFORMATION FOR SEQ ID NO:595:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

**SUBSTITUTE SHEET (RULE 26)**

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595

Met	Asn	Ile	Lys	Ile	Leu	Lys	Ile	Leu	Val	Gly	Gly	Leu	Phe	Phe	Leu
1				5				10				15			
Ser	Leu	Asn	Ala	His	Leu	Trp	Gly	Lys	Gln	Asp	Asn	Ser	Phe	Leu	Gly
					20			25				30			
Ile	Gly	Glu	Arg	Ala	Tyr	Lys	Ser	Gly	Asn	Tyr	Ser	Lys	Ala	Ala	Ser
	35					40			45						
Tyr	Phe	Lys	Lys	Ala	Cys	Asn	Asp	Gly	Val	Ser	Glu	Gly	Cys	Thr	Gln
	50				55			60							
Leu	Gly	Ile	Ile	Tyr	Glu	Asn	Gly	Gln	Gly	Thr	Arg	Ile	Asp	Tyr	Lys
65				70				75			80				
Lys	Ala	Leu	Glu	Tyr	Tyr	Lys	Thr	Ala	Cys	Gln	Ala	Asp	Asp	Arg	Glu
	85					90			95						
Gly	Cys	Phe	Gly	Leu	Gly	Gly	Leu	Tyr	Asp	Glu	Gly	Leu	Gly	Thr	Ala
	100			105			110								
Gln	Asn	Tyr	Gln	Glu	Ala	Unk	Asp	Ala	Tyr	Ala	Arg	His	Ala	Phe	
	115				120			125							

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 95 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596

Met	Asp	Ile	Ser	Ile	Phe	Arg	Glu	Tyr	Asp	Ile	Arg	Gly	Ile	Tyr	Pro
1				5			10				15				
Thr	Thr	Leu	Asp	Glu	Asn	Thr	Ala	Phe	Ser	Ile	Gly	Val	Glu	Leu	Gly
				20			25			30					
Lys	Ile	Met	Arg	Glu	Tyr	Asp	Lys	Ser	Val	Phe	Val	Gly	His	Asp	Ala
	35				40			45							
Arg	Val	His	Gly	Arg	Phe	Leu	Phe	Glu	Val	Leu	Ser	Ala	Gly	Leu	Gln
	50			55			60								
Ser	Ser	Gly	Leu	Lys	Val	Tyr	Asp	Leu	Gly	Leu	Ile	Pro	Thr	Pro	Val
65				70			75			80					
Ala	Tyr	Phe	Ala	Ala	Phe	Asn	Glu	Ile	Asp	Asn	Ile	Gln	Trp	Pro	
	85				90			95							

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

**SUBSTITUTE SHEET (RULE 26)**

(A) LENGTH: 102 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597

Val	Cys	Asp	Ile	Phe	Ser	Asp	Gly	Val	Leu	Leu	Asp	Ala	Leu	Val	
1								5		10			15		
Ile	Tyr	Phe	Lys	Ala	Pro	Tyr	Ser	Phe	Thr	Gly	Asp	Val	Cys	Glu	
								20		25			30		
Ile	Gln	Cys	His	Gly	Ser	Pro	Leu	Leu	Ala	Gln	Asn	Ile	Leu	Gln	Ala
							35		40		45				
Cys	Leu	Asn	Leu	Gly	Ala	Arg	Leu	Ala	Lys	Ala	Gly	Glu	Phe	Ser	Lys
						50		55		60					
Lys	Ala	Phe	Leu	Asn	His	Lys	Met	Asp	Leu	Ser	Glu	Ile	Glu	Ala	Ser
						65		70		75		80			
Val	Gln	Leu	Ile	Leu	Cys	Glu	Asp	Glu	Ser	Val	Leu	Asn	Ala	Leu	Ala
						85		90		95					
Arg	Gln	Leu	Gln	Gly	Gly										
					100										

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 127 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598

Met	Phe	Lys	Lys	Met	Cys	Leu	Ser	Leu	Leu	Met	Ile	Ser	Gly	Val	Cys
1						5				10			15		
Val	Gly	Ala	Lys	Asp	Leu	Asp	Phe	Lys	Leu	Asp	Tyr	Arg	Ala	Thr	Gly
							20		25		30				
Gly	Lys	Phe	Met	Gly	Lys	Met	Thr	Asp	Ser	Ser	Leu	Leu	Ser	Ile	Thr
						35		40		45					
Ser	Met	Asn	Asp	Glu	Pro	Val	Val	Ile	Lys	Asn	Leu	Ile	Val	Asn	Arg
						50		55		60					
Gly	Asn	Ser	Val	Glu	Ala	Thr	Lys	Lys	Val	Glu	Pro	Lys	Phe	Gly	Asp
						65		70		75		80			
Lys	Phe	Lys	Lys	Glu	Lys	Leu	Phe	Asp	His	Glu	Leu	Lys	Tyr	Ser	Gln
						85		90		95					

Gln	Ile	Phe	Tyr	Arg	Leu	Asp	Cys	Lys	Pro	Asn	Gln	Leu	Leu	Glu	Val
100							105							110	
Lys	Ile	Ile	Thr	Asp	Lys	Gly	Glu	Tyr	Tyr	His	Lys	Phe	Ser	Lys	
															125
115							120								

## (2) INFORMATION FOR SEQ ID NO:599:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...502

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:599

Met	Thr	Leu	Lys	Pro	Tyr	Pro	Thr	Lys	Glu	Thr	Gly	Leu	Ala	Ser	Gln
1								5	10						15
Leu	Ser	Gly	His	Trp	Phe	Phe	Gln	Leu	Ser	Leu	Phe	Asn	Lys	Thr	Asn
															20
Phe	Asn	Pro	Asn	Lys	Ile	Trp	Ile	Pro	Leu	Glu	Phe	Asn	Lys	Arg	Ser
															35
Lys	Ile	Lys	Phe	Asp	Lys	Asp	Leu	Glu	Ile	Tyr	Phe	Asp	Ser	His	Glu
															50
Ser	Phe	Asn	Ile	Ser	Lys	Lys	Tyr	Leu	Gln	Glu	Ile	Asp	Gln	Glu	Ser
															65
Leu	Lys	Lys	Ile	Lys	Gln	Ser	Lys	Asp	Phe	Phe	Ser	Ile	Gln	Lys	Ile
															85
Glu	Ser	Lys	His	Asp	Asn	Asn	Asp	Ile	Leu	Gln	Leu	Glu	Phe	Phe	Glu
															100
Asn	Asp	Thr	Ser	Phe	Leu	Phe	Ala	Lys	Gly	Ser	Phe	Ala	Glu	Ile	Leu
															115
Glu	Tyr	Asn	Met	Gln	Leu	Lys	Ile	Asp	Ser	Leu	Ile	Thr	Lys	Glu	Phe
															130
Asn	Lys	Leu	Leu	Ala	Ile	Val	Gln	Asp	Ser	Pro	Gln	Asp	Ser	Tyr	Gln
															145
Leu	Lys	Ile	Arg	Val	Arg	His	Asn	Asn	Lys	Leu	Pro	Arg	Glu	Lys	Tyr
															165
Thr	Glu	His	Ile	Lys	Leu	Glu	Val	Tyr	Asp	Cys	Arg	Lys	Ser	His	
															180
Asp	His	Asn	Glu	Pro	Ile	Ile	Leu	Ser	Gln	Gln	Ser	Thr	Gly	Phe	Gln
															195
Trp	Ala	Phe	Asn	Phe	Met	Phe	Gly	Phe	Leu	Tyr	Asn	Val	Gly	Ser	His
															210
Phe	Ser	Phe	Asn	His	Asn	Ile	Ile	Tyr	Val	Met	Asp	Glu	Pro	Ala	Thr
															225
His	Leu	Ser	Val	Pro	Ala	Arg	Lys	Glu	Phe	Arg	Lys	Phe	Leu	Lys	Glu
															245
Tyr	Ala	His	Lys	Asn	His	Val	Thr	Phe	Val	Leu	Ala	Thr	His	Asp	Pro
															260
Phe	Leu	Val	Asp	Thr	Asp	His	Leu	Asp	Glu	Ile	Arg	Ile	Val	Glu	Lys
															275
Glu	Thr	Glu	Gly	Ser	Val	Ile	Lys	Asn	His	Phe	Asn	Tyr	Pro	Leu	Asn
															290
Asn	Ala	Ser	Lys	Asp	Ser	Asp	Ala	Leu	Asp	Lys	Ile	Lys	Arg	Ser	Leu
															295
															300

499

305	310	315	320
Gly Val Gly Gln His Val Phe His Asn Pro Gln Lys His Arg Ile Ile			
325	330	335	
Phe Val Glu Gly Ile Thr Asp Tyr Cys Tyr Leu Ser Ala Phe Lys Leu			
340	345	350	
Tyr Leu Arg Tyr Lys Glu Tyr Lys Asp Asn Pro Ile Pro Phe Thr Phe			
355	360	365	
Leu Pro Ile Ser Gly Leu Lys Asn Asp Ser Asn Asp Met Lys Glu Thr			
370	375	380	
Ile Glu Lys Leu Cys Glu Leu Asp Asn His Pro Ile Val Leu Thr Asp			
385	390	395	400
Asp Asp Arg Lys Cys Val Phe Asn Gln Gln Ala Thr Ser Glu Arg Phe			
405	410	415	
Lys Arg Ala Asn Glu Glu Met His Asp Pro Ile Thr Ile Leu Gln Leu			
420	425	430	
Ser Asp Cys Asp Arg His Phe Lys Gln Ile Glu Asp Cys Phe Ser Ala			
435	440	445	
Asn Asp Arg Asn Lys Tyr Ala Lys Asn Lys Gln Met Glu Leu Ser Met			
450	455	460	
Ala Phe Lys Thr Arg Leu Leu Tyr Gly Gly Glu Asp Ala Ile Glu Lys			
465	470	475	480
Gln Thr Lys Arg Asn Phe Leu Lys Leu Phe Lys Trp Ile Ala Trp Ala			
485	490	495	
Thr Asn Leu Ile Lys Asn			
500			

## (2) INFORMATION FOR SEQ ID NO:600:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600

Val	Tyr	Phe	Phe	Leu	Ala	Leu	Ser	Gly	Glu	Lys	Val	Leu	Leu	Pro	Val				
1				5				10			15								
Ile					Gly	Gly	Leu	Glu	Lys	Asn	Ala	Leu	Glu	Ala	Gly	Leu	Leu	Lys	Gly
					20			25			30								
Asp	Arg	Ile	Leu	Leu	Ser	Thr	Ile	Lys	Lys										
					35			40											

## (2) INFORMATION FOR SEQ ID NO:601:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

**SUBSTITUTE SHEET (RULE 26)**

500

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601

```

Met Glu Asn Phe Lys Leu Ile Asn Phe Phe Thr Gly Gln Asn Asp Ala
1           5          10          15
Gly Lys Thr Asn Leu Leu Glu Ala Leu Tyr Thr Asn Thr Gly Leu Cys
20          25          30
Asp Pro Thr Ala Asn Gln Val Ser Leu Pro Pro Glu His Ala Val Asn
35          40          45
Ile Ser Glu Phe Arg Lys Ile Lys Leu Asp Ala Asp Asn Leu Lys Thr
50          55          60
Phe Phe Tyr Gln Gly Asn Thr Ala Asn Pro Ile Ser Ile Arg Thr Glu
65          70          75          80
Phe Glu His Ala Thr Ile Pro Leu Thr Ile Gln Tyr Pro Thr Gln Thr
85          90          95
Ser Tyr Ser Lys Asp Ile Asn Leu Asn Ser Asp Asp Ala His Met Thr
100         105         110
Asn Leu Ile Asn Thr Thr Ile Thr Lys Pro Gln Leu Gln Phe Ser Tyr
115         120         125
Asn Pro Ser Leu Ser Pro Met Thr Met Thr Tyr Glu Phe Glu Arg Gln
130         135         140
Asn Leu Gly Leu Ile His Ser Asn Leu Asp Lys Ile Ala Gln Thr Tyr
145         150         155         160
Lys Glu Asn Ala Met Phe Ile Pro Ile Glu Leu Ser Ile Val Asn Ser
165         170         175
Leu Lys Ala Leu Glu Asn Leu Gln Leu Ala Ser Lys Glu Lys Glu Leu
180         185         190
Ile Glu Ile Leu Gln Cys Phe Asn Pro Asn Ile Leu Asn Ala Asn Thr
195         200         205
Ile Arg Lys Ser Val Tyr Ile Gln Ile Lys Asp Glu Asn Thr Pro Leu
210         215         220
Glu Glu Ser Pro Lys Arg Leu Leu Asn Leu Phe Gly Trp Gly Phe Ile
225         230         235         240
Lys Phe Phe Ile Met Val Ser Ile Leu Ile Asp Asn Arg Val Lys Tyr
245         250         255
Leu Phe Ile Asp Glu Ile Glu Ser Gly Leu His His Thr Lys Met Gln
260         265         270
Glu Phe Leu Lys Ala Leu Phe Lys Leu Ala Gln Lys Leu Gln Ile Gln
275         280         285
Ile Phe Ala Thr Thr His Asn Lys Glu Phe Leu Leu Asn Ala Ile Asn
290         295         300
Thr Ile Ser Asp Asn Glu Thr Gly Val Phe Lys Asp Ile Ala Leu Phe
305         310         315         320
Glu Leu Glu Lys Glu Ser Ala Ser Asp Phe Ile Arg His Ser Tyr Ser
325         330         335
Met Leu Glu Lys Ala
340

```

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 465 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602

Met Asp Phe Lys Lys Cys Pro Asn Phe Glu Lys Lys Cys Ala Phe Leu  
 1 5 10 15  
 Cys Phe Ser Asn Leu Val Leu Leu Ile Glu Ile His Ser Lys Gly Leu  
 20 25 30  
 His Met Gln Lys Lys Lys Pro Lys Asn Pro Gln Pro Asn Leu Phe Ser  
 35 40 45  
 Ile Leu Asp Lys Gly Asp Val Ala Thr Asn Asn Pro Val Glu Glu Ser  
 50 55 60  
 Asp Lys Ala Asn Lys Ile Gln Glu Pro Leu Pro Tyr Val Val Lys Thr  
 65 70 75 80  
 Gln Ile Asn Lys Ala Ser Met Ile Ser Arg Asp Pro Ile Glu Trp Ala  
 85 90 95  
 Lys Tyr Leu Ser Phe Glu Lys Arg Val Tyr Lys Asp Asn Ser Lys Glu  
 100 105 110  
 Asp Val Asn Phe Phe Ala Asn Gly Glu Ile Lys Glu Ser Ser Arg Val  
 115 120 125  
 Tyr Glu Ala Asn Lys Glu Gly Phe Glu Arg Arg Ile Thr Lys Arg Tyr  
 130 135 140  
 Asp Leu Ile Asp Arg Asn Ile Asp Arg Asn Arg Glu Phe Phe Ile Lys  
 145 150 155 160  
 Glu Ile Glu Ile Leu Thr His Thr Asn Ser Leu Lys Glu Leu Lys Glu  
 165 170 175  
 Gln Gly Leu Glu Ile Gln Leu Thr His His Asn Glu Thr His Lys Lys  
 180 185 190  
 Ala Leu Glu Asn Gly Asn Glu Ile Val Lys Glu Tyr Asp His Leu Lys  
 195 200 205  
 Asp Ile Tyr Gln Glu Val Glu Arg Thr Lys Asp Gly Gly Leu Val Arg  
 210 215 220  
 Glu Ile Ile Pro Ser Ile Ser Ser Ala Glu Tyr Phe Lys Leu Tyr Asn  
 225 230 235 240  
 Lys Leu Pro Phe Glu Ser Ile Asn Asn Glu Asn Thr Lys Leu Asn Thr  
 245 250 255  
 Asn Asp Asn Glu Val Lys Lys Leu Glu Phe Glu Leu Ala Lys Glu  
 260 265 270  
 Val His Ile Leu Ile Leu Glu Gln Gln Leu Leu Ser Ala Thr Asn Tyr  
 275 280 285  
 Tyr Ser Trp Ile Asp Lys Asp Asp Asn Ala Asn Phe Ala Trp Lys Met  
 290 295 300  
 His Arg Leu Ile Asn Glu Asn Lys Leu Lys Glu Asn His Leu Ser Ala  
 305 310 315 320  
 Asn Asn Ala Asn Lys Ile Lys Gln Phe Phe Asn Asn Gly Ser Ile  
 325 330 335  
 Leu Gly Trp Thr Lys Glu Glu Gln Ser Ala Ile Gln Glu Asn Arg Asp  
 340 345 350  
 Tyr Ser Leu Arg Ser Ala Leu Leu Ser Leu Glu Glu Ile Ala Gln Ala  
 355 360 365  
 Lys Ile Glu Leu Gln Lys Tyr Tyr Glu Ser Val Tyr Val Asn Gly Asp  
 370 375 380  
 Gly Asn Lys Arg Glu Ile Lys Pro Phe Lys Glu Ile Leu Arg Asp Thr  
 385 390 395 400  
 Asn Asn Phe Glu Lys Ala Tyr Lys Glu Arg Tyr Asp Lys Leu Val Ser  
 405 410 415  
 Leu Ser Ala Ala Ile Ile Gln Ala Lys Glu Gly Gly Asn Glu Arg Gln  
 420 425 430

502

Asn	Ser	Ser	Ala	Asn	Asn	Asn	Pro	Ile	Lys	Asn	Thr	Ile	Glu	Thr
				435		440						445		
Asn	Thr	Ser	Asn	Asn	Ile	Ile	Gln	Asn	Asn	Asp	Asn	Ile	Ile	Ile
				450		455						460		
Ile														
465														

## (2) INFORMATION FOR SEQ ID NO:603:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...193

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:603

Met	Ala	Leu	Glu	Val	Val	Leu	Trp	Asp	Phe	Asp	Gly	Val	Ile	Phe	Asp
1				5					10				15		
Ser	Met	His	Leu	Lys	Tyr	Glu	Gly	Phe	Lys	Ala	Leu	Phe	Gln	Lys	His
					20				25				30		
Gly	Asn	Asp	Ser	Lys	Glu	Gly	Leu	Lys	Gln	Phe	Glu	Val	Tyr	His	Tyr
					35				40				45		
Gln	Ser	Gly	Gly	Ile	Ser	Arg	Asn	Glu	Lys	Ile	Gln	Tyr	Phe	Tyr	Asn
					50				55				60		
Glu	Ile	Leu	Lys	Thr	Pro	Ile	Ala	Gln	Glu	Ile	Asp	Ala	Leu	Ala	
					65				70				75		80
Leu	Glu	Phe	Gly	Ala	Ile	Ile	Glu	Gln	Lys	Leu	Phe	Asp	Arg	Gly	His
					85				90				95		
Leu	Asn	Ser	Glu	Val	Met	Ala	Phe	Ile	Asp	Lys	His	Tyr	Gln	Asn	Tyr
					100				105				110		
Ile	Phe	His	Ile	Ala	Ser	Ala	Ala	Leu	His	Ser	Glu	Leu	Gln	Val	Leu
					115				120				125		
Cys	Glu	Phe	Leu	Gly	Ile	Thr	Lys	Tyr	Phe	Lys	Ser	Val	Glu	Gly	Ser
					130				135				140		
Pro	Pro	Asp	Lys	Pro	Lys	Ile	Ile	Ala	Asn	Ile	Ile	Gln	Lys	Tyr	Ala
					145				150				155		160
Tyr	Asp	Pro	Ser	Arg	Met	Leu	Met	Ile	Ala	Ile	Ala	Ser	Met	Ile	Met
					165				170				175		
Lys	Ala	Leu	Arg	Leu	Ile	Lys	Trp	Arg	Phe	Trp	Ala	Ile	Thr	Ala	Arg
					180				185				190		
Phe															

## (2) INFORMATION FOR SEQ ID NO:604:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604

Met	Leu	Lys	Lys	Ile	Asp	Leu	His	Lys	Asp	Ser	Ile	Arg	Lys	Leu	
1				5				10				15			
Phe	Phe	Tyr	Tyr	Phe	Ile	Pro	Leu	Val	Phe	Ser	Met	Ile	Ser	Leu	
					20			25				30			
Thr	Tyr	Ser	Met	Val	Asp	Asp	Met	Phe	Val	Gly	Lys	Lys	Leu	Gly	Lys
					35			40			45				
Glu	Ala	Ile	Ala	Ala	Val	Asn	Ile	Ala	Trp	Pro	Ile	Phe	Pro	Gly	Leu
					50			55			60				
Ile	Ala	Tyr	Glu	Leu	Leu	Phe	Gly	Phe	Gly	Ala	Ala	Ser	Ile	Val	Gly
					65			70			75			80	
Tyr	Phe	Leu	Gly	Gln	Asn	Lys	Thr	His	Arg	Ala	Arg	Leu	Val	Phe	Ser
					85			90			95				
Ser	Val	Phe	Tyr	Phe	Val	Ala	Leu	Ser	Ala	Phe	Ile	Leu	Ser	Met	Ala
					100			105			110				
Leu	Leu	Pro	Phe	Ser	Glu	Asn	Ile	Ala	Gln	Phe	Phe	Gly	Ser	Asn	Asp
					115			120			125				
Ala	Leu	Leu	Asn	Met	Ser	Asn	Ala	Ile	Leu	Lys	Ser	Phe			
					130			135			140				

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids  
(B) TYPE: amino acid  
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605

Val	Lys	Cys	Leu	Leu	Ile	Lys	Ser	Leu	Leu	Phe	Ala	Leu	Lys	Pro	
1					5			10			15				
Leu	Pro	Asp	Leu	Lys	Thr	Thr	Thr	Pro	Ile	Leu	Ala	Pro	Met	Ser	Val
					20			25			30				
Val	Ala	Gly	Arg	Leu	Unk	Unk	His	Leu	Val	Gln	His	Tyr	Leu	Leu	Ala
					35			40			45				
Leu	Glu	His	Val	Lys	Gly	Phe	Met	Gly	Lys	Gly	Val	Ile	Leu	Gly	Gly
					50			55			60				
Leu	Ser	Gly	Ala	Gln	Arg	Ala	Lys	Ile	Val	Val	Ile	Gly	Gly	Gly	Val
					65			70			75			80	
Val	Gly	Met	Glu	Ser	Ala	Lys	Val	Leu	Unk	Gln	Met	Gly	Unk	Lys	Val
					85			90			95				
Thr	Ile	Leu	Glu	Leu	Asp	Tyr	Ala	Lys	Leu	Gln	Asn	His	Pro	Tyr	Tyr
					100			105			110				

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His	Leu	Tyr	Asp	Leu	Glu	Val	Leu	Ser	Val	Asn	Glu	Ala	Asn	Ile	Ile
115							120					125			
Gln	Ala	Leu	Asn	Gly	Unk	Val	Gly	Leu	Val	Gly	Ala	Val	Leu	Val	Thr
130							135					140			
Unk	Ser	Gln	Thr	Pro	Lys	Val	Unk	Leu	Arg	Arg	His	Leu	Lys	Tyr	
145							150					155			

## (2) INFORMATION FOR SEQ ID NO:606:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...376

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:606

Met	Leu	Ala	Lys	Ile	Val	Phe	Ser	Ser	Leu	Val	Ala	Phe	Gly	Val	Leu
1				5					10				15		
Ser	Ala	Asn	Val	Glu	Gln	Phe	Gly	Ser	Phe	Phe	Asn	Glu	Ile	Lys	Lys
				20				25				30			
Glu	Gln	Glu	Glu	Val	Ala	Ala	Lys	Glu	Asp	Ala	Leu	Lys	Ala	Arg	Lys
				35				40				45			
Lys	Leu	Leu	Asn	Asn	Thr	His	Asp	Phe	Leu	Glu	Asp	Leu	Val	Phe	Arg
				50				55				60			
Lys	Gln	Lys	Ile	Lys	Glu	Leu	Val	Asp	Tyr	Arg	Ala	Lys	Val	Leu	Leu
				65				70				75			80
Asp	Leu	Glu	Asn	Lys	Tyr	Lys	Glu	Lys	Glu	Ala	Leu	Glu	Lys	Glu	
				85				90				95			
Thr	Arg	Gly	Lys	Ile	Leu	Thr	Ala	Lys	Ser	Lys	Ala	Tyr	Gly	Asp	Leu
				100				105				110			
Glu	Gln	Ala	Leu	Lys	Asp	Asn	Pro	Leu	Tyr	Lys	Leu	Leu	Pro	Asn	
				115				120				125			
Pro	Tyr	Ala	Tyr	Val	Leu	Asn	Gln	Glu	Thr	Phe	Thr	Gln	Glu	Asp	Lys
				130				135				140			
Glu	Arg	Leu	Ser	Tyr	Tyr	Pro	Gln	Val	Lys	Thr	Ser	Ser	Ile	Phe	
				145				150				155			160
Lys	Lys	Thr	Thr	Ala	Thr	Thr	Lys	Asp	Lys	Ala	Gln	Ala	Leu	Gln	
				165				170				175			
Met	Gly	Val	Phe	Ser	Leu	Asp	Glu	Gln	Asn	Lys	Lys	Ala	Ser	Arg	
				180				185				190			
Leu	Ala	Leu	Ser	Tyr	Lys	Gln	Ala	Ile	Glu	Glu	Tyr	Ser	Asn	Asn	Ile
				195				200				205			
Ser	Asn	Leu	Leu	Ser	Arg	Lys	Glu	Leu	Asp	Asn	Ile	Asp	Tyr	Tyr	Leu
				210				215				220			
Gln	Leu	Glu	Arg	Asn	Lys	Phe	Asp	Ser	Lys	Ala	Lys	Asp	Ile	Ala	Gln
				225				230				235			240
Lys	Ala	Thr	Asn	Thr	Leu	Ile	Phe	Asn	Ser	Glu	Arg	Leu	Ala	Phe	Ser
				245				250				255			
Met	Ala	Ile	Asp	Lys	Ile	Asn	Glu	Lys	Tyr	Leu	Arg	Gly	Tyr	Glu	Ala
				260				265				270			
Phe	Ser	Asn	Leu	Leu	Lys	Asn	Val	Lys	Asp	Asp	Val	Glu	Leu	Asn	Thr
				275				280				285			
Leu	Thr	Lys	Asn	Phe	Thr	Asn	Gln	Lys	Leu	Ser	Phe	Ala	Gln	Lys	Gln

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290	295	300
Lys	Leu	Cys
Leu	Leu	Leu
Val	Leu	Asp
305	310	Ser
Lys	Lys	Phe
Ser	Ile	Asn
Ile	Leu	Asp
325	330	Thr
Lys	Lys	Glu
Asp	Thr	Tyr
Pro	Asn	Asn
Met	Met	Ile
340	345	Phe
Ser	Asp	Val
Asp	Asp	Asp
355	360	Val
Lys	Ile	Val
Ile	Phe	Ser
Phe	Phe	Ala
370	375	Tyr
Lys	Lys	Tyr
Asn	Asn	Arg
Asn	Pro	Asn
370	375	Asn
Val	Ala	Asn
Ala	Lys	Asn
Lys	Asn	Asn
Asn	Pro	Phe
Asn	Pro	Glu

## (2) INFORMATION FOR SEQ ID NO:607:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607

Met	Asp	Phe	Val	Gly	Phe	Glu	Asp	Leu	Lys	Cys	Lys	Asp	Lys	Glu	Asn
1								5			10				15
Ser	Gln	Lys	Val	Phe	Val	Ile	Arg	Asn	Asp	Lys	Leu	Gly	Asp	Phe	Ile
								20			25				30
Leu	Glu	Ile	Pro	Ala	Leu	Ile	Ala	Leu	Lys	His	Ala	Phe	Leu	Glu	Lys
								35			40				45
Gly	Val	Glu	Val	Tyr	Leu	Gly	Val	Val	Val	Pro	Ser	Tyr	Thr	Thr	Pro
								50			55				60
Ile	Ala	Leu	Glu	Phe	Pro	Phe	Ile	Asp	Glu	Val	Ile	Ile	Glu	Asp	Asn
								65			70				80
His	Leu	Ala	Thr	Thr	His	Lys	Asn	Arg	Ser	Ile	Asp	Ala	Leu	Ile	Phe
								85			90				95
Leu	Phe	Ser	Asn	Phe	Lys	Asn	Ala	Lys	Leu	Ala	Phe	Ser	Leu	Arg	Lys
								100			105				110
Ser	Ile	Pro	Tyr	Ile	Leu	Ala	Pro	Lys	Thr	Lys	Ile	Tyr	Ser	Trp	Leu
								115			120				125
Tyr	Gln	Lys	Arg	Val	Arg	Gln	Asn	Arg	Ser	Leu	Cys	Leu	Lys	Thr	Glu
								130			135				140
Tyr	Glu	Tyr	Asn	Leu	Asp	Leu	Ile	His	Ala	Phe	Cys	Lys	Asp	Tyr	Asp
								145			150				160
Leu	Pro	Asn	Ala	Gln	Leu	Lys	Lys	Ile	Ala	Trp	Lys	Leu	Lys	Asp	Lys
								165			170				175
Ser	Lys	Glu	Arg	Ser	Ile	Ile	Ala	Ser	Lys	Leu	Asn	Ala	Asn	Val	Asp
								180			185				190
Leu	Leu	Trp	Ile	Gly	Val	His	Met	His	Ser	Gly	Gly	Ser	Ser	Pro	Val
								195			200				205
Leu	Pro	Ala	Ser	His	Phe	Ile	Glu	Leu	Ile	Ala	Ile	Leu	His	Glu	Lys
								210			215				220
Leu	Ser	Cys	Glu	Ile	Ile	Leu	Ile	Cys	Gly	Pro	Gly	Glu	Arg	Lys	Ala
								225			230				240
Thr	Glu	Glu	Leu	Leu	Lys	Glu	Val	Pro	Phe	Ala	His	Leu	Tyr	Asp	Thr
								245			250				255

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Ser	His	Ser	Leu	Val	Asp	Leu	Ala	Lys	Leu	Cys	Ala	Asn	Leu	Ser	Val
260						265							270		
Cys	Ile	Gly	Asn	Ala	Ser	Gly	Pro	Leu	His	Val	Asn	Ala	Leu	Phe	Asp
275						280							285		
Asn	Gln	Ser	Ile	Gly	Phe	Tyr	Pro	Asn	Glu	Leu	Thr	Ala	Ser	Ile	Ala
290						295					300				
Arg	Trp	Arg	Pro	Phe	Asn	Gln	Phe	Leu	Gly	Ile	Thr	Pro	Pro	Asn	
305						310					315			320	
Gly	Ser	Asn	Asp	Met	Gly	Leu	Ile	Asp	Ile	Gln	Lys	Glu	Ser	Glu	Lys
325						330					335				
Ile	Met	Gly	Phe	Ile	Thr	Lys	Asn	Leu	Ser	His	His	Met	Gln	Glu	Arg
340						345					350				

## (2) INFORMATION FOR SEQ ID NO:608:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...88

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:608

Val	Gly	Val	Leu	Ser	Leu	Lys	Ile	Glu	Ala	Ile	Ser	Asn	Phe	Tyr	Gly
1							5					10			15
Leu	Cys	Val	Leu	Gly	Val	Leu	Leu	Cys	Phe	Tyr	Leu	Leu	Asp	Ala	
							20				25		30		
Tyr	Tyr	Leu	Met	Gln	Glu	Arg	Leu	Phe	Arg	Glu	Gln	Tyr	Gln	Trp	Leu
							35			40		45			
Ile	Lys	Asn	Arg	Leu	Lys	Thr	Asp	Glu	Arg	Leu	Phe	Glu	Val	Phe	Pro
	50						55			60					
Ile	His	Gln	Thr	Cys	Gln	Ser	Thr	Gln	Phe	Leu	Ser	Pro	Cys	Val	Arg
	65						70			75		80			
Leu	Val	Phe	Ser	Pro	Ile	Gly	Arg								
					85										

## (2) INFORMATION FOR SEQ ID NO:609:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...86

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:609

Met Ser Leu Gly Ala Val Val Ser Ser Leu Leu Cys His Lys Leu Glu  
 1 5 10 15  
 Gly Ala Ile Leu Asp Leu Arg Ala Tyr Arg Unk Unk Ala Tyr Tyr His  
 20 25 30  
 Glu Asn Lys Asp Thr Leu Leu Ile Lys Gly Lys Lys Arg Leu Leu Tyr  
 35 40 45  
 Asn Tyr Ile Lys Ala His Ile Unk Leu Asn Leu Leu Trp Thr Ile Arg  
 50 55 60  
 Asn Arg Thr Unk Ser Leu Gly Lys Phe Thr Gln Asn Pro Thr Glu Gln  
 65 70 75 80  
 Pro Pro Thr Asn Asn His  
 85

## (2) INFORMATION FOR SEQ ID NO:610:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...76

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:610

Met Lys Thr Thr Leu Phe Val Leu Gly Leu Leu Phe Asn Ser Ser  
 1 5 10 15  
 Leu Ser Ala Val Asp Gly Ile Ser Gln Thr Glu Pro Ser Ser Leu Asn  
 20 25 30  
 Leu Ala Glu Asp Ser Leu Pro Leu Asn His Ser Asn Ala Gln Lys Leu  
 35 40 45  
 Ser Leu Lys Asn Ala Trp Asn Arg Val Leu Ser Asn His Glu Gly Leu  
 50 55 60  
 His Ala Gln Asn Thr Pro Leu Ser Glu Arg Val Lys  
 65 70 75

## (2) INFORMATION FOR SEQ ID NO:611:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 98 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature

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## (B) LOCATION 1...98

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:611

Val	Lys	Lys	Val	Glu	Ser	Met	Asn	Val	Val	Pro	Phe	Ile	Asp	Ile	Met
1			5					10				15			
Leu	Val	Leu	Leu	Val	Ile	Val	Leu	Thr	Thr	Ala	Ser	Phe	Val	Gln	Thr
	20						25					30			
Ser	Lys	Leu	Pro	Ile	Ser	Ile	Pro	Gln	Val	Asp	Lys	Asp	Ser	Thr	Asp
	35						40				45				
Ser	Lys	Asp	Val	Leu	Asp	Lys	Lys	Gln	Val	Thr	Ile	Ala	Ile	Ser	Asn
	50					55			75		60				
Lys	Gly	Ser	Phe	Tyr	Phe	Asp	Asp	Lys	Glu	Ile	Ser	Phe	Glu	Asn	Leu
	65					70			80						
Lys	His	Lys	Val	Ser	Thr	Leu	Ala	Lys	Asp	Thr	Pro	Ile	Val	Phe	Ala
	85					90			95						
Arg	Arg														

## (2) INFORMATION FOR SEQ ID NO:612:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...162

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:612

Met	Gly	Ser	Tyr	Thr	Phe	Pro	Leu	Ile	Leu	Lys	Pro	Ile	Phe	Ile	Asn
1			5				10					15			
Lys	Val	Pro	Val	Thr	Ile	Asp	Phe	Tyr	Ala	Asn	Ala	Asn	Tyr	Phe	Leu
	20				25			30							
Ile	Tyr	Gly	Ala	Leu	Ala	Asn	Ala	Val	Val	Gly	Ser	Ile	Asn	Ala	Leu
	35				40			45							
Asn	Asp	Glu	Ile	Arg	Phe	Lys	Arg	Asn	Ala	Gln	Ile	Glu	Glu	Ala	Glu
	50				55			60							
Leu	Gly	Thr	Asp	Gly	Ile	Lys	Ile	Lys	Pro	Ile	Ala	Leu	Tyr	Asn	Pro
	65				70			75			80				
Ser	Glu	Gly	Tyr	Leu	Asn	Tyr	Ala	Leu	Ser	Ser	Val	Phe	Ile	Phe	Ile
	85				90			95							
Leu	His	Gln	Val	Met	Leu	Ile	Ala	Ser	Ser	Met	Phe	Thr	Ser	Ser	Arg
	100				105			110							
Arg	Leu	Glu	Leu	Ala	Leu	Leu	Asp	Lys	Lys	Gln	Ile	Ala	Leu	Arg	Leu
	115				120			125							
Cys	Ala	Arg	Leu	Leu	Val	Phe	Met	Gly	Ala	Phe	Ser	Val	Phe	Val	Leu
	130				135			140							
Trp	Tyr	Phe	Gly	Ala	Leu	Phe	Ser	Phe	Tyr	Gly	Ile	Glu	Arg	His	Gly
	145				150			155			160				
Ser	Ala														

## (2) INFORMATION FOR SEQ ID NO:613:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613

Val	Ile	Met	Thr	Lys	Leu	Asp	Gly	Thr	Ser	Lys	Gly	Gly	Ala	Ile	Leu
1				5				10					15		
Unk	Val	Leu	Tyr	Glu	Leu	Lys	Leu	Pro	Ile	Leu	Tyr	Leu	Gly	Met	Gly
			20					25				30			
Glu	Lys	Glu	Asp	Asp	Leu	Ile	Ala	Phe	Asp	Glu	Glu	Arg	Phe	Ile	Glu
	35				40				45						
Asp	Leu	Val	Asp	Ala	Val	Phe	Val	Glu	Gln						
	50				55										

## (2) INFORMATION FOR SEQ ID NO:614:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614

Val	Cys	Gly	Ala	His	Gly	Lys	Ser	Ser	Ile	Thr	Unk	Met	Leu	Ser	Ala
1					5				10			15			
Ile	Cys	Pro	Ala	Phe	Gly	Unk	Ile	Ile	Gly	Arg	His	Ser	Lys	Glu	Phe
				20				25			30				
Asp	Ser	Asn	Val	Unk	Glu	Ser	Ala	Asp	Met	Ser	Leu	Val	Phe	Glu	Unk
			35					40			45				
Asp	Glu	Ser	Asp	Ser	Ser	Phe	Phe	Ile	Phe	Gln	Pro	Phe	Leu	Arg	Asp
	50				55				60						
Cys	Ala														
	65														

## (2) INFORMATION FOR SEQ ID NO:615:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids

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(B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615

```

Met Ala Ile Ala Ile Lys Asp Leu Leu Ser Ala Tyr Lys Val Val Leu
1           5           10          15
Pro Leu Asp Lys Ile Ser Met Pro Ser Ser Ala Asp Leu Lys Leu Thr
20          25          30
Leu Gln Phe Leu Lys Asn Thr Ala Pro Leu Phe Ser Val Gln Gly Ser
35          40          45
Val Asn Leu Gln Glu Gly Thr Phe Ser Leu Tyr Asn Ile Pro Leu Tyr
50          55          60
Thr Gln Ser Ala Gln Ile Asn Leu Asp Ile Ala Gln Glu Tyr Gln Tyr
65          70          75          80
Ile Tyr Ile Asp Thr Ile His Thr Arg Tyr Ala Asn Met Unk Asp Leu
85          90          95
Asp Ala Lys Ile Ala Leu Asp Leu Gly Gln Lys Asn Leu Ser Unk Unk
100         105         110
Unk Leu Gly Pro
115

```

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 116 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615

```

Met Ala Ile Ala Ile Lys Asp Leu Leu Ser Ala Tyr Lys Val Val Leu
1           5           10          15
Pro Leu Asp Lys Ile Ser Met Pro Ser Ser Ala Asp Leu Lys Leu Thr
20          25          30
Leu Gln Phe Leu Lys Asn Thr Ala Pro Leu Phe Ser Val Gln Gly Ser
35          40          45
Val Asn Leu Gln Glu Gly Thr Phe Ser Leu Tyr Asn Ile Pro Leu Tyr
50          55          60
Thr Gln Ser Ala Gln Ile Asn Leu Asp Ile Ala Gln Glu Tyr Gln Tyr
65          70          75          80
Ile Tyr Ile Asp Thr Ile His Thr Arg Tyr Ala Asn Met Unk Asp Leu

```

511

Asp Ala Lys Ile Ala Leu Asp Leu Gly Gln Lys Asn Leu Ser Unk Unk	90	95
100	105	110
Unk Leu Gly Pro		
115		

## (2) INFORMATION FOR SEQ ID NO:616:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...82

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:616

Met Pro Asp Asn Leu His Leu His Thr Leu Leu Unk Lys Phe Leu Gln	1	5
10	15	
Gln Arg Ser Phe Asn Tyr Pro Asn Pro Leu Cys Ala Phe Ile Leu Ile		
20	25	30
Leu Cys Asn Leu Pro Phe Ile Leu Ile Ser Val Leu Phe Arg Leu Asp		
35	40	45
Ala Tyr Ala Leu Ile Val Ile Ser Leu Val Phe Ile Unk Cys Tyr Leu		
50	55	60
Ile Gly Unk Ala Tyr Leu Asn Arg Gln Val Cys Ala Leu Glu Lys Arg		
65	70	75
Ala Phe		80

## (2) INFORMATION FOR SEQ ID NO:616:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...82

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:616

Met Pro Asp Asn Leu His Leu His Thr Leu Leu Unk Lys Phe Leu Gln	1	5
10	15	
Gln Arg Ser Phe Asn Tyr Pro Asn Pro Leu Cys Ala Phe Ile Leu Ile		
20	25	30

**SUBSTITUTE SHEET (RULE 26)**

512

Leu Cys Asn Leu Pro Phe Ile Leu Ile Ser Val Leu Phe Arg Leu Asp  
 35 40 45  
 Ala Tyr Ala Leu Ile Val Ile Ser Leu Val Phe Ile Unk Cys Tyr Leu  
 50 55 60  
 Ile Gly Unk Ala Tyr Leu Asn Arg Gln Val Cys Ala Leu Glu Lys Arg  
 65 70 75 80  
 Ala Phe

## (2) INFORMATION FOR SEQ ID NO:617:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...77

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:617

Val Asn Glu Leu Lys Asn Ser Lys Gln Val Leu Gly Asn Gly Lys Ala  
 1 5 10 15  
 Asp Leu Ser Asn Glu Asn Thr Lys Val Arg Gln Thr Lys Thr Asn Leu  
 20 25 30  
 Thr Glu Lys Asn Gln Arg Leu Thr Thr Glu Lys Thr Glu Leu Asn Asn  
 35 40 45  
 Lys Ile Thr Gly Leu Ala Thr Glu Lys Glu Arg Leu Ala Ala Asp Lys  
 50 55 60  
 Glu Asn Leu Thr Lys Glu Ser Arg Gln Arg Lys Pro Asn  
 65 70 75

## (2) INFORMATION FOR SEQ ID NO:618:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...176

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:618

Met Asp Leu Gln Gln Ile Asp Glu Leu Glu Asn Lys Phe Glu Glu Gln  
 1 5 10 15  
 Glu Glu Gln Ala Gln Asp Thr Pro Leu Lys Gln Glu Pro Ser Thr Lys

**SUBSTITUTE SHEET (RULE 26)**

513

20	25	30
Glu Val Lys Ile Pro Lys Lys Arg Gly Arg Lys Ser Leu Leu Asp		
35	40	45
Glu Asp Lys Lys Lys Ser Phe Asn Ile Ala Phe Ser Pro Cys Val Ile		
50	55	60
Lys Glu Leu Asn Glu Phe Leu Leu Glu Phe Gly Ser Phe Lys Glu Thr		
65	70	75
Arg Ser Thr Phe Ile Glu Glu Ala Leu Ile Arg His Leu Lys His Arg		
85	90	95
Lys Asn Thr Gln Glu Gln Lys Leu Leu Lys Gln Leu Glu Arg Leu Gln		
100	105	110
Asn Lys Glu Lys Gly Ile Met Lys Thr Met Asn Leu Asn Glu Phe Phe		
115	120	125
Thr His Lys Ile Ile Tyr Lys Asp Thr Pro Leu Lys Phe Lys Asp Thr		
130	135	140
Leu Glu Gln Glu Ile Ser Gln Ala Ser Leu Val Glu Lys Leu Ile Leu		
145	150	155
Ala Asn Ile Leu Ala Asn Met Val Phe Ala Lys Ile Ser Asn Glu Asn		
165	170	175

## (2) INFORMATION FOR SEQ ID NO:619:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...144

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:619

Met Gly Cys Tyr Gly Ile Gly Ile Ser Arg Leu Leu Ser Val Ile Leu		
1	5	10
Glu Gln Lys Ser Asp Asp Leu Asp Cys Val Trp Thr Lys Asn Thr Ala		
20	25	30
Pro Phe Asp Val Val Ile Val Val Ser Asn Leu Lys Asp Glu Ala Gln		
35	40	45
Lys Lys Leu Ala Phe Glu Val Tyr Glu Arg Leu Leu Gln Lys Gly Val		
50	55	60
Asp Ala Leu Leu Asp Asp Arg Asp Ala Arg Phe Gly Ala Lys Met Arg		
65	70	75
Asp Phe Glu Leu Ile Gly Glu Arg Leu Ala Leu Ile Val Gly Lys Gln		
85	90	95
Thr Leu Glu Ser Lys Glu Phe Glu Cys Ile Lys Arg Ala Asn Leu Glu		
100	105	110
Lys Gln Thr Ile Lys Asp Ile Gly Ile Arg Arg Lys Asn Phe Arg Asn		
115	120	125
Val Ser Glu Arg Ile Arg Gly Gly Asn Gly Lys Asn Ser Asp Trp Leu		
130	135	140

## (2) INFORMATION FOR SEQ ID NO:620:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids

514

(B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620

Met	Glu	Ile	Gln	Gln	Thr	His	Arg	Lys	Ile	Asn	Arg	Pro	Leu	Val	Ser
1	5						10							15	
Leu	Val	Leu	Ala	Gly	Ala	Leu	Ile	Ser	Ala	Ile	Pro	Gln	Glu	Ser	His
	20						25						30		
Ala	Ala	Phe	Phe	Thr	Thr	Val	Ile	Ile	Pro	Ala	Ile	Val	Gly	Gly	Ile
	35						40					45			
Ala	Thr	Gly	Thr	Ala	Val	Gly	Thr	Val	Ser	Gly	Leu	Leu	Ser	Trp	Gly
	50					55			60						
Leu	Lys	Gln	Ala	Glu	Glu	Ala	Asn	Lys	Thr	Pro	Asp	Lys	Pro	Asp	Lys
	65					70		75				80			
Val	Trp	Arg	Ile	Gln	Ala	Gly	Lys	Gly	Leu						
	85					90									

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 268 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621

Met	Ser	Glu	Lys	Glu	Arg	Leu	Asn	Glu	Val	Ile	Leu	Glu	Glu	Asn	
1	5							10				15			
Asn	Gly	Ser	Gly	Thr	Lys	Lys	Val	Phe	Leu	Ile	Val	Ala	Ile	Ile	
	20						25					30			
Ile	Ile	Leu	Ala	Val	Leu	Leu	Met	Val	Phe	Trp	Lys	Ser	Thr	Arg	Val
	35						40				45				
Ala	Pro	Lys	Glu	Thr	Phe	Leu	Gln	Thr	Asp	Ser	Gly	Met	Gln	Lys	Ile
	50					55			60						
Gly	Asn	Thr	Lys	Asp	Glu	Lys	Lys	Asp	Asp	Glu	Phe	Glu	Ser	Leu	Asn
	65					70		75			80				
Met	Asp	Ser	Pro	Lys	Gln	Glu	Asp	Lys	Leu	Asp	Lys	Val	Val	Asp	Asn
	85					90					95				
Ile	Lys	Lys	Gln	Ser	Glu	Asn	Ser	Met	Pro	Ile	Gln	Thr	Asp	Gln	
	100					105				110					
Ala	Gln	Met	Glu	Met	Lys	Thr	Glu	Glu	Lys	Gln	Glu	Ser	Gln	Lys	

515

Glu	Leu	Lys	Ala	Val	Glu	Pro	Ile	Pro	Met	Ser	Thr	Gln	Lys	Glu	Ser
115					120							125			
130					135							140			
Gln	Ala	Val	Ala	Lys	Lys	Glu	Thr	Pro	His	Lys	Lys	Pro	Lys	Val	Ala
145						150				155				160	
Pro	Lys	Asp	Lys	Glu	Ala	His	Lys	Asp	Lys	Ala	Lys	His	Ala	Ala	Lys
165										170				175	
Glu	Pro	Lys	Val	Lys	Lys	Glu	Ala	Arg	Lys	Glu	Val	Ser	Lys	Lys	Ala
180									185				190		
Asn	Ser	Lys	Thr	Asn	Leu	Thr	Lys	Gly	His	Tyr	Leu	Gln	Val	Gly	Val
195									200			205			
Phe	Ala	His	Thr	Pro	Asn	Lys	Ala	Phe	Leu	Gln	Glu	Phe	Asn	Gln	Phe
210									215			220			
Pro	His	Lys	Ile	Glu	Asp	Arg	Gly	Ala	Thr	Lys	Arg	Tyr	Leu	Ile	Gly
225						230				235				240	
Pro	Tyr	Lys	Ser	Lys	Gln	Glu	Ala	Leu	Met	His	Ala	Asp	Glu	Val	Ser
245									250				255		
Lys	Lys	Met	Thr	Lys	Pro	Val	Val	Ile	Glu	Val	Arg				
260									265						

## (2) INFORMATION FOR SEQ ID NO:622:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...171

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:622

Val	Glu	Tyr	Tyr	Ala	Phe	Asn	Phe	Ser	Val	Leu	Asp	Phe	Val	Leu	Met
1						5			10				15		
Gly	Lys	Ala	Thr	His	Leu	Asn	Leu	Phe	Ala	Met	Pro	Lys	Ala	Lys	His
						20			25			30			
Ile	Lys	Glu	Ala	Thr	Ser	Val	Leu	Glu	Arg	Leu	Asp	Leu	Glu	Ser	Leu
						35			40			45			
Lys	Asp	Gln	Gly	Ile	Asn	Asp	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Met	Val
						50			55			60			
Leu	Leu	Ala	Arg	Ser	Leu	Leu	Gln	Arg	Thr	Pro	Leu	Leu	Leu	Asp	
						65			70			75			80
Glu	Pro	Thr	Ser	Ala	Leu	Asp	Leu	Lys	Asn	Gln	Ala	Leu	Phe	Phe	Asp
						85			90			95			
Ala	Ile	Lys	Asp	Glu	Met	Lys	Lys	Arg	Glu	Leu	Ser	Val	Leu	Val	Asn
						100			105			110			
Ile	His	Asp	Pro	Asn	Leu	Val	Ala	Arg	His	Ser	Thr	His	Val	Val	Met
						115			120			125			
Leu	Lys	Asp	Lys	Lys	Leu	Phe	Leu	Gln	Ala	Ser	Thr	Pro	Ile	Ala	Met
						130			135			140			
Thr	Ser	His	Asn	Leu	Ser	Ala	Leu	Tyr	Asp	Thr	Pro	Leu	Unk	Ala	Ile
						145			150			155			160
Trp	His	Asp	Asp	Lys	Leu	Val	Val	Tyr	Ala	Leu					
						165			170						

## (2) INFORMATION FOR SEQ ID NO:623:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...102

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:623

```

Met Met Ala His Ser Leu Ile Leu Val Ser Lys Thr Ser Leu Ser Asn
1           5          10          15
Leu Leu Ile Phe Val Val Gln Pro Asp Gly Lys Leu Ser Met Thr Asp
20          25          30
Ala Ala Ile Asp Pro Asn Met Thr Asn Ser Gly Leu Arg Trp Tyr Arg
35          40          45
Val Asn Glu Ile Ala Glu Lys Phe Lys Leu Ile Lys Asp Lys Ala Leu
50          55          60
Val Thr Val Ile Asn Lys Gly Tyr Gly Lys Asn Pro Leu Thr Lys Asn
65          70          75          80
Tyr Asn Ile Lys Asn Tyr Gly Glu Leu Glu Arg Val Ile Lys Lys Leu
85          90          95
Pro Leu Val Arg Asp Lys
100

```

## (2) INFORMATION FOR SEQ ID NO:624:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...116

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:624

```

Leu Lys Val Thr Asn Pro His Leu Leu Val Val Ile Gln Asp Leu Asn
1           5          10          15
Ala Arg Ile Ala Leu Met Lys Leu Leu Phe Gln Asn Val Lys Ser Ala
20          25          30
Asn Lys Glu Leu Val Phe Cys Asn Lys Glu Lys Arg Leu Ile Arg Ser
35          40          45
Phe Asp Ala Gln Lys Glu Tyr Gly Ile Thr Pro Val Glu Asn Ile Leu
50          55          60
Ser Val Leu Asp Thr Ala Met Asn Pro Asn Ser Ala Leu Val Ile Asp

```

517

65	70	75	80
Asn Leu Asn Glu Ala Lys Glu Leu His Asp Lys Val Gly Ala Glu Lys			
85	90	95	
Leu Lys Ser Phe Leu Glu Lys Ala Unk Arg Gln Arg Ala Val Leu Arg			
100	105	110	
His Phe Cys Ala			
115			

## (2) INFORMATION FOR SEQ ID NO:624:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...116

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:624

Leu Lys Val Thr Asn Pro His Leu Leu Val Val Ile Gln Asp Leu Asn			
1	5	10	15
Ala Arg Ile Ala Leu Met Lys Leu Leu Phe Gln Asn Val Lys Ser Ala			
20	25	30	
Asn Lys Glu Leu Val Phe Cys Asn Lys Glu Lys Arg Leu Ile Arg Ser			
35	40	45	
Phe Asp Ala Gln Lys Glu Tyr Gly Ile Thr Pro Val Glu Asn Ile Leu			
50	55	60	
Ser Val Leu Asp Thr Ala Met Asn Pro Asn Ser Ala Leu Val Ile Asp			
65	70	75	80
Asn Leu Asn Glu Ala Lys Glu Leu His Asp Lys Val Gly Ala Glu Lys			
85	90	95	
Leu Lys Ser Phe Leu Glu Lys Ala Unk Arg Gln Arg Ala Val Leu Arg			
100	105	110	
His Phe Cys Ala			
115			

## (2) INFORMATION FOR SEQ ID NO:625:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...237

518

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:625

Val Leu Asn Glu Glu Gln Asn Ser Leu Glu Glu Lys Gly Gly Glu Asn  
 1 5 10 15  
 Lys Asn Glu Lys Glu Thr Pro Leu Lys Gly Ile His Ser Lys Ile Pro  
 20 25 30  
 Ser Leu Lys Gln Ala Leu Glu Gln Thr Ile Ser Lys Ile Lys Ser Ser  
 35 40 45  
 Lys Glu Phe Phe Lys Gln Leu Leu His Asn Lys Lys Lys Leu Tyr Ile  
 50 55 60  
 Ala Leu Gly Ile Leu Leu Ser Leu Ile Ala Leu Ile Val Ala Leu Ser  
 65 70 75 80  
 Leu Leu Leu Gly His Lys Lys Glu Asn Lys Gln Thr Ser Leu Gln Thr  
 85 90 95  
 Asn Thr Ala Thr Thr Asn Asn Glu Thr Pro Asn Asp Thr Asn Asn Ala  
 100 105 110  
 Glu Ala Glu Gly Gln Ile Glu Asn Leu Asp Leu Pro Asp Leu Ile Gly  
 115 120 125  
 Lys Asp Ser Leu Lys Arg Asn Asp Glu Ser Gln Val Asp Ala Met Met  
 130 135 140  
 Gln Lys Ala Ser Leu Leu Tyr Glu Gln Gly Gln Lys Asp Glu Ala Leu  
 145 150 155 160  
 His Leu Phe Asp Lys Ile Ala Ser Phe Ser Gln Gly Ile Ala Ser His  
 165 170 175  
 Asn Leu Gly Val Ile Lys Phe Lys Glu Lys Asp Phe Asn Gly Ala Leu  
 180 185 190  
 Asp Leu Phe Asp Ser Ser Ile Ala Ser Lys Glu Asn Ala Ser Val Ser  
 195 200 205  
 Ala Ile Asp Ala Leu Val Thr Ala Tyr His Leu Gln Asp Ala Asp Leu  
 210 215 220  
 Tyr Tyr His Tyr Leu Lys Ile Val Lys Arg His Phe Val  
 225 230 235

## (2) INFORMATION FOR SEQ ID NO:626:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...198

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:626

Met Lys Glu Ser Phe Tyr Ile Glu Gly Met Thr Cys Thr Ala Cys Ser  
 1 5 10 15  
 Ser Gly Ile Glu Arg Ser Leu Gly Arg Lys Ser Phe Val Lys Lys Ile  
 20 25 30  
 Glu Val Ser Leu Leu Asn Lys Ser Ala Asn Ile Glu Phe Asn Glu Asn  
 35 40 45  
 Glu Thr Asn Leu Asp Glu Ile Phe Lys Leu Ile Glu Lys Leu Gly Tyr  
 50 55 60  
 Ser Pro Lys Lys Thr Leu Ala Glu Glu Lys Lys Glu Phe Phe Ser Pro  
 65 70 75 80  
 Asn Val Lys Leu Ala Leu Ala Val Ile Phe Thr Leu Phe Val Val Tyr

519

85	90	95
Leu Ser Met Gly Ala Met Leu Ser Pro Ser Leu Leu Pro Glu Ser Leu		
100	105	110
Leu Thr Ile Asn His His Ser Asn Phe Leu Asn Ala Cys Leu Gln Leu		
115	120	125
Ile Gly Ala Leu Ile Val Met His Leu Gly Arg Asp Phe Tyr Ile Gln		
130	135	140
Gly Phe Lys Ala Leu Trp His Arg Gln Pro Asn Met Ser Ser Leu Ile		
145	150	155
Ala Ile Gly Thr Ser Ala Ala Leu Ile Ser Ala Cys Gly Asn Cys Ile		
165	170	175
Trp Phe Ile Pro Ile Ile Pro Ile Ser Gly Leu Met Gly Ile Ile		
180	185	190
Ile Leu Lys Ala Cys Ala		
195		

## (2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 198 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626

Met Lys Glu Ser Phe Tyr Ile Glu Gly Met Thr Cys Thr Ala Cys Ser		
1	5	10
Ser Gly Ile Glu Arg Ser Leu Gly Arg Lys Ser Phe Val Lys Lys Ile		
20	25	30
Glu Val Ser Leu Leu Asn Lys Ser Ala Asn Ile Glu Phe Asn Glu Asn		
35	40	45
Glu Thr Asn Leu Asp Glu Ile Phe Lys Leu Ile Glu Lys Leu Gly Tyr		
50	55	60
Ser Pro Lys Lys Thr Leu Ala Glu Glu Lys Lys Glu Phe Phe Ser Pro		
65	70	75
Asn Val Lys Leu Ala Leu Ala Val Ile Phe Thr Leu Phe Val Val Tyr		
85	90	95
Leu Ser Met Gly Ala Met Leu Ser Pro Ser Leu Leu Pro Glu Ser Leu		
100	105	110
Leu Thr Ile Asn His His Ser Asn Phe Leu Asn Ala Cys Leu Gln Leu		
115	120	125
Ile Gly Ala Leu Ile Val Met His Leu Gly Arg Asp Phe Tyr Ile Gln		
130	135	140
Gly Phe Lys Ala Leu Trp His Arg Gln Pro Asn Met Ser Ser Leu Ile		
145	150	155
Ala Ile Gly Thr Ser Ala Ala Leu Ile Ser Ala Cys Gly Asn Cys Ile		
165	170	175
Trp Phe Ile Pro Ile Ile Pro Ile Ser Gly Leu Met Gly Ile Ile		
180	185	190
Ile Leu Lys Ala Cys Ala		
195		

## (2) INFORMATION FOR SEQ ID NO:627:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...225

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:627

```

Met Asn Thr Ser Leu Leu Thr Gln Ala Gln Val Leu Ser Ser Lys Glu
1           5          10          15
Asn Gln Ile His Arg Leu Leu Leu Glu Leu Leu Glu Ala Lys Leu
20          25          30
His Phe Glu Pro Lys Leu Tyr Ile Ile Asn Ala Pro Tyr Met Asn Ala
35          40          45
Phe Ala Ser Gly Trp Asp Glu Ser Asn Ser Leu Ile Ala Leu Thr Ser
50          55          60
Ala Leu Ile Glu Arg Leu Asp Arg Asp Glu Leu Lys Ala Val Ile Ala
65          70          75          80
His Glu Leu Ser His Ile Arg His Asn Asp Ile Arg Leu Thr Met Cys
85          90          95
Val Gly Ile Leu Ser Asn Ile Met Leu Leu Val Ala Asn Phe Ser Val
100         105         110
Tyr Phe Met Gly Asn Arg Lys Asn Ser Gly Ala Asn Leu Ala Arg
115         120         125
Met Ile Leu Trp Val Leu Gln Ile Ile Leu Pro Phe Leu Thr Leu Leu
130         135         140
Leu Gln Met Tyr Leu Ser Arg Thr Arg Glu Tyr Met Ala Asp Ser Gly
145         150         155         160
Ala Ala Phe Leu Met His Asp Asn Lys Pro Met Ile Arg Ala Leu Gln
165         170         175
Lys Ile Ser Asn Asp Tyr Thr Asn Asn Asp Tyr Lys Glu Ile Asp Lys
180         185         190
Asn Ser Thr Arg Ser Ala Ala Tyr Leu Phe Asn Ala Glu Met Phe Ser
195         200         205
Thr His Pro Ser Ile Lys Asn Arg Ile Gln Ser Leu Arg Lys Arg Val
210         215         220
Ile
225

```

## (2) INFORMATION FOR SEQ ID NO:628:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...85

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:628

Val Gly Ile Val Pro Asp Asn Leu Trp Lys Leu Lys Arg Phe Asn Gln  
 1               5                   10                   15  
 Asp Trp Arg Val Gly Asp Thr Leu Ile Thr Ala Ile Gly Gln Gly Ser  
 20              25                   30  
 Phe Leu Ala Thr Pro Leu Gln Val Leu Ala Tyr Thr Gly Leu Ile Ala  
 35              40                   45  
 Thr Gly Lys Leu Ala Thr Pro His Phe Ala Ile His Asn Gln Gln Pro  
 50              55                   60  
 Leu Lys Asp Pro Leu Asn Arg Phe Ser Lys Lys Glu Ala Pro Ser Leu  
 65              70                   75                   80  
 Ala Arg Gly His Val  
 85

## (2) INFORMATION FOR SEQ ID NO:628:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...85

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:628

Val Gly Ile Val Pro Asp Asn Leu Trp Lys Leu Lys Arg Phe Asn Gln  
 1               5                   10                   15  
 Asp Trp Arg Val Gly Asp Thr Leu Ile Thr Ala Ile Gly Gln Gly Ser  
 20              25                   30  
 Phe Leu Ala Thr Pro Leu Gln Val Leu Ala Tyr Thr Gly Leu Ile Ala  
 35              40                   45  
 Thr Gly Lys Leu Ala Thr Pro His Phe Ala Ile His Asn Gln Gln Pro  
 50              55                   60  
 Leu Lys Asp Pro Leu Asn Arg Phe Ser Lys Lys Glu Ala Pro Ser Leu  
 65              70                   75                   80  
 Ala Arg Gly His Val  
 85

## (2) INFORMATION FOR SEQ ID NO:629:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:  
    (A) NAME/KEY: misc\_feature  
    (B) LOCATION 1...496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629

Met Phe Asn Ile Lys Arg Thr Phe Leu Ile Thr Ile Ile Ser Phe Phe  
 1 5 10 15  
 Leu Ile Val Pro Asn Trp Leu Lys Ala Ile Asp Leu Pro Ile Val Ser  
 20 25 30  
 Asn Leu Lys Ile Tyr Gln Thr Val Tyr Cys Met Leu Ile Pro Ser Tyr  
 35 40 45  
 Val Leu Thr Asn Lys Ser Phe Ala Asp Ile Leu Thr Gly Tyr Thr Ser  
 50 55 60  
 Ile Gly Ala Ser Gly Ser Gly Lys Ser Ser Gly Gln Gly Val Ile Glu  
 65 70 75 80  
 Ala Leu Ser Thr Pro Leu Ala Thr Ser Leu Ala Ala Ser Asn Leu Val  
 85 90 95  
 Lys Tyr Leu Asn Thr Leu Gly Pro Leu Trp Gly Ser Ala Trp Ala Ser  
 100 105 110  
 Val Ala Thr Ala Ile Gln Gly Phe Ala Leu Thr Pro Ser Ser Gly Cys  
 115 120 125  
 Asn Phe Gly Trp Asn Ala Leu Ile Asn Lys Asn Ile Asp Val Ser Met  
 130 135 140  
 Asp Ser Val Leu Asp Asn Leu Ser Asn Lys Ile Gln Asn Phe Thr Lys  
 145 150 155 160  
 Gly Gly Val Glu Asp Asn Val Lys Gly Asn Ile Leu Leu Gln Ile Ile  
 165 170 175  
 Gly Ser Ile Thr Ala Gln Ala Ser Thr Asn Ile Thr Ala Asp Gly Leu  
 180 185 190  
 Ile Trp Leu Ile Gly Lys Glu Phe Thr Ala Asn Lys Leu Gln Asn Asn  
 195 200 205  
 Thr Ile Ala Met Leu Ala Phe Ala Ala Leu Glu Ser Val Val Lys Gly  
 210 215 220  
 Ala Asp Ala Ala Val Leu Pro Ala Tyr Gly Val Val Asn Leu Pro Asp  
 225 230 235 240  
 Ile Ile Ile Gly Gln Gly Ser Tyr Leu Asp Phe Val Ser Tyr Leu Ile  
 245 250 255  
 Tyr Ile Val Phe Gly Ile Phe Val Phe Ile Ser Phe Met Lys Leu Arg  
 260 265 270  
 Asp Ile Ser Asn Gly Ile Gln Ile Asn Ile Gly Phe Glu Tyr Met Arg  
 275 280 285  
 Phe Val Gly Gly Thr Leu Phe Lys Met Ala Met Val Ser Phe Ile Ala  
 290 295 300  
 Tyr Ala Gly Phe Gly Tyr Leu Tyr Lys Ile Ser Tyr Ser Ile Tyr Phe  
 305 310 315 320  
 Gly Leu Ala Gly Ala Phe Gly Leu Asn Gln Val Leu Phe Trp Ala Leu  
 325 330 335  
 Asp Leu Val Leu Asn Tyr Thr Val Asn Ser Ile Leu Pro Ala Val Arg  
 340 345 350  
 Ala Val Phe Ser Asn Val Gly Asn Asn Ala Pro Ser Leu Leu Gln Gly  
 355 360 365  
 Leu Gln Val Ala Gly Ile Ser Leu Phe Ala Ile Phe Met Gln Val Thr  
 370 375 380  
 Ile Ile Met Arg Ile Ser Thr Val Val Val Lys Pro Leu Ile Ala Gly  
 385 390 395 400  
 Ala Phe Ser Gly Ile Val Phe Pro Ile Ala Val Cys Leu Ile Val Leu  
 405 410 415  
 Asp Trp Phe Lys Asp Ser Met Lys Asn Ile Leu Ile Trp Phe Ile Asn  
 420 425 430  
 Asn Leu Phe Ile Leu Val Leu Ala Ile Pro Ile Leu Leu Phe Gly Val

523

435	440	445
Leu Ala Leu Leu Ala Phe Asn Leu Thr Ile Thr Pro Ser Val Ala Ile		
450	455	460
Gln Asn Ile Asn Gln Gly Gly Leu Gly Ile Asp Ser Thr Ile Ala Ser		
465	470	475
Leu Ile Thr Leu Phe Ile Leu Lys Gly Phe Ile Glu Thr Ile Ile Glu		480
485	490	495

## (2) INFORMATION FOR SEQ ID NO:630:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...142

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:630

Met Ala Phe Trp Gln Ala Ile Arg Trp Trp Ile Leu Lys Leu Pro Phe		
1	5	10
Met Met Gly Ala Thr Met Met Trp Ile Leu Ser Glu Met Ala Phe Lys		15
20	25	30
Ile Ala Gly Unk Met Ala Phe Lys Glu Ala Ser Arg Ala Ala Asn Pro		
35	40	45
Val Leu Leu Glu Pro Met Met Lys Val Glu Val Val Pro Glu Glu		
50	55	60
Tyr Met Gly Asp Val Ile Gly Asp Leu Asn Arg Arg Arg Gly Gln Ile		
65	70	75
Asn Ser Met Asp Asp Arg Leu Gly Leu Lys Ile Val Asn Ala Phe Val		80
85	90	95
Pro Leu Val Glu Met Phe Gly Tyr Ser Thr Asp Leu Arg Ser Ala Thr		
100	105	110
Gln Gly Arg Gly Thr Tyr Ser Met Glu Phe Asp His Tyr Gly Glu Val		
115	120	125
Pro Ser Asn Ile Ala Lys Glu Ile Val Glu Lys Arg Lys Gly		
130	135	140

## (2) INFORMATION FOR SEQ ID NO:631:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature

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## (B) LOCATION 1...153

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:631

Met Gln Asn Leu Pro Gly Met Ala Arg Ala Ala Met Leu Thr Thr Ser  
 1           5                   10                   15  
 Ser Ala Pro Ala Pro Glu Gly Glu Gly Ala Phe Arg Ala Met Lys Met  
 20           25                   30  
 Ala Ser Glu Met Ala Lys Val Glu Val Gly Tyr Val Asn Ala His Gly  
 35           40                   45  
 Thr Ser Thr His Tyr Asn Asp Trp Tyr Glu Ser Ile Ala Leu Lys Asn  
 50           55                   60  
 Val Leu Ala Leu Lys Lys Ser Leu Leu Leu Ala Pro Leu Lys Gly  
 65           70                   75                   80  
 Arg Leu Gly Leu Leu Gly Cys Cys Gly Val Arg Ser Arg Tyr Ser Ile  
 85           90                   95  
 Met Ala Met Unk Gln Gly Ile Leu Pro Pro Thr Ile Asn Gln Glu Thr  
 100           105                   110  
 Pro Asp Pro Glu Cys Unk Leu Asp Tyr Ile Pro Asn Thr Ala Arg Glu  
 115           120                   125  
 Lys Gln Val Asn Ala Val Met Ser Asn Ser Phe Gly Phe Gly Gly Thr  
 130           135                   140  
 Asn Gly Val Val Ile Phe Lys Lys Ala  
 145           150

## (2) INFORMATION FOR SEQ ID NO:632:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...343

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:632

Met Gln Asn Leu Leu Ile Gln Ala Glu Asn Ala Ile Ala Leu Leu Phe  
 1           5                   10                   15  
 Leu Leu Asn Asp Lys Asn Leu Lys Gly Lys Ile Asp Leu Ile Tyr Ile  
 20           25                   30  
 Asp Pro Pro Phe Ala Thr Asn Asn His Phe Thr Ile Thr Asn Gly Arg  
 35           40                   45  
 Ala Thr Thr Ile Ser Asn Ser Lys Asn Gly Asp Ile Ala Tyr Ser Asp  
 50           55                   60  
 Lys Val Val Gly Met Asp Phe Met Glu Phe Leu Lys Gln Arg Leu Val  
 65           70                   75                   80  
 Leu Leu Lys Glu Leu Leu Ser Glu Gln Gly Ser Ile Tyr Val His Thr  
 85           90                   95  
 Asp Tyr Lys Ile Gly His Tyr Val Lys Val Met Leu Asp Glu Ile Phe  
 100           105                   110  
 Gly Ile Gln Asn Phe Arg Asn Glu Ile Thr Arg Ile Lys Cys Asn Pro  
 115           120                   125  
 Lys Asn Phe Lys Arg Ile Gly Tyr Gly Asn Ile Lys Asp Met Ile Leu  
 130           135                   140  
 Phe Tyr Ser Lys Gly Lys Asn Pro Ile Phe Asn Glu Pro Lys Ile Pro

145	150	155	160
Tyr	Thr	Pro	Gln
Asp	Leu	Glu	Lys
Arg	Phe	Pro	Lys
Ile	Asp	Lys	Asp
165	170	175	
Lys	Arg	Arg	Tyr
Tyr	Thr	Thr	Val
Pro	Ile	His	Ala
Ala	Pro	Gly	Glu
Glu			
180	185	190	
Ser	Gly	Cys	Ser
Lys	Ala	Phe	Lys
Gly			
195	200	205	
Arg	His	Trp	Arg
Thr	Asp	Ile	Ala
Ala	Thr	Leu	Glu
Glu			
210	215	220	
Gly	Leu	Ile	Glu
Tyr	Ser	Asn	Asn
Asn			
225	230	235	240
Ala	Leu	Glu	Gln
Gln	Val	Gly	Lys
Arg	Val	Arg	Val
Gln	Asp	Ile	Trp
			Glu
245	250	255	
Asp	Pro	Gln	Tyr
Pro	Ser	Tyr	Pro
Thr	Glu	Lys	Asn
Ala	Gln	Leu	Leu
260	265	270	
Asp	Leu	Ile	Ile
Lys	Thr	Ser	Ser
Ser	Asn	Lys	Asp
			Ser
275	280	285	
Cys	Phe	Cys	Gly
Ser	Gly	Thr	Thr
Leu	Lys	Leu	Lys
Ser	Ala	Phe	Leu
			Gln
290	295	300	
Arg	Lys	Phe	Ile
Ile	Gly	Ile	Asp
Asp	Asn	Ser	Asp
			Leu
305	310	315	320
Lys	Asn	Lys	Leu
Glu	Thr	Ile	Thr
Lys	Asp	Leu	Phe
			Val
325	330	335	
Phe	Tyr	Asp	Phe
			Leu
			Val
			Phe
340			

## (2) INFORMATION FOR SEQ ID NO:632:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...343

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:632

Met	Gln	Asn	Leu	Leu	Ile	Gln	Ala	Glu	Asn	Ala	Ile	Ala	Leu	Leu	Phe	
1						5			10				15			
Leu	Leu	Asn	Asp	Lys	Asn	Leu	Lys	Gly	Lys	Ile	Asp	Leu	Ile	Tyr	Ile	
						20			25				30			
Asp	Pro	Pro	Phe	Ala	Thr	Asn	Asn	His	Phe	Thr	Ile	Thr	Asn	Gly	Arg	
						35			40				45			
Ala	Thr	Thr	Ile	Ser	Asn	Ser	Lys	Asn	Gly	Asp	Ile	Ala	Tyr	Ser	Asp	
						50			55				60			
Lys	Val	Val	Gly	Met	Asp	Phe	Met	Glu	Phe	Leu	Lys	Gln	Arg	Leu	Val	
						65			70				75		80	
Leu	Leu	Lys	Glu	Leu	Leu	Ser	Glu	Gln	Gly	Ser	Ile	Tyr	Val	His	Thr	
						85			90				95			
Asp	Tyr	Lys	Ile	Gly	His	Tyr	Val	Lys	Val	Met	Leu	Asp	Glu	Ile	Phe	
						100			105				110			
Gly	Ile	Gln	Asn	Phe	Arg	Asn	Glu	Ile	Thr	Arg	Ile	Lys	Cys	Asn	Pro	
						115			120				125			
Lys	Asn	Phe	Lys	Arg	Ile	Gly	Tyr	Gly	Asn	Ile	Lys	Asp	Met	Ile	Leu	
						130			135				140			

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Phe Tyr Ser Lys Gly Lys Asn Pro Ile Phe Asn Glu Pro Lys Ile Pro  
 145 150 155 160  
 Tyr Thr Pro Gln Asp Leu Glu Lys Arg Phe Pro Lys Ile Asp Lys Asp  
 165 170 175  
 Lys Arg Arg Tyr Thr Thr Val Pro Ile His Ala Pro Gly Glu Val Glu  
 180 185 190  
 Ser Gly Glu Cys Ser Lys Ala Phe Lys Gly Met Leu Pro Pro Lys Gly  
 195 200 205  
 Arg His Trp Arg Thr Asp Ile Ala Thr Leu Glu Arg Trp Asp Lys Glu  
 210 215 220  
 Gly Leu Ile Glu Tyr Ser Asn Asn Asn Pro Arg Lys Lys Ile Tyr  
 225 230 235 240  
 Ala Leu Glu Gln Val Gly Lys Arg Val Gln Asp Ile Trp Glu Phe Lys  
 245 250 255  
 Asp Pro Gln Tyr Pro Ser Tyr Pro Thr Glu Lys Asn Ala Gln Leu Leu  
 260 265 270  
 Asp Leu Ile Ile Lys Thr Ser Ser Asn Lys Asp Ser Ile Val Leu Asp  
 275 280 285  
 Cys Phe Cys Gly Ser Gly Thr Thr Leu Lys Ser Ala Phe Leu Leu Gln  
 290 295 300  
 Arg Lys Phe Ile Gly Ile Asp Asn Ser Asp Leu Ala Ile Gln Ala Cys  
 305 310 315 320  
 Lys Asn Lys Leu Glu Thr Ile Thr Lys Asp Leu Phe Val Ser Gln Asn  
 325 330 335  
 Phe Tyr Asp Phe Leu Val Phe  
 340

## (2) INFORMATION FOR SEQ ID NO:633:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...93

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:633

Met Ile Leu Lys Asn Leu Ile Leu Leu Phe Leu Ala Lys Arg Lys Leu  
 1 5 10 15  
 Ile Phe Ile Glu Ala Asn Phe Tyr Thr Ile Ser Gly Ser Lys Leu Asn  
 20 25 30  
 Glu Val Ala Arg Ser Tyr Gln Asp Leu Ala Leu Lys Phe Glu Ala Phe  
 35 40 45  
 Pro Asn Tyr Glu Phe Ile Trp Ile Thr Asp Gly Ile Gly Trp Leu Asp  
 50 55 60  
 Ala Lys Ser Lys Leu Gln Glu Ala Tyr Lys Ser Val Glu Ile Tyr Asn  
 65 70 75 80  
 Leu Ser Tyr Val Asn Asp Phe Ile Ser Lys Val Gln Lys  
 85 90

## (2) INFORMATION FOR SEQ ID NO:634:

## (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 176 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634

Met	Thr	Ser	Val	Val	Ile	Lys	Pro	His	Ala	Tyr	Gly	Glu	Gln	Val	Gln	
1																
														15		
Glu	Ile	Glu	Glu	Glu	Ser	Asp	Ser	Asp	Tyr	Glu	Lys	Asn	Asn	Asp	Gln	
														30		
Glu	Ala	Ile	Asn	Phe	Gly	Ile	Ala	Leu	His	Lys	Gly	Leu	Glu	Tyr	Gln	
														45		
Tyr	Ala	Tyr	Asn	Ile	Pro	Lys	Gln	Ser	Val	Leu	Glu	Tyr	Leu	Asn	Tyr	
														55	60	
His	Tyr	Gly	Phe	Tyr	Gly	Leu	Asp	Tyr	Gln	Ala	Leu	Glu	Glu	Ser	Leu	
														80		
Glu	Leu	Phe	Glu	Asn	Asp	Ala	Gly	Ile	Gln	Ala	Leu	Phe	Lys	Asn	His	
														95		
Ala	Leu	Lys	Gly	Glu	Ala	Ala	Ala	Phe	Leu	Phe	Gln	Gly	Val	Val	Ser	Arg
														100	110	
Ile	Asp	Val	Leu	Leu	Trp	Asp	Arg	Gly	Gln	Asn	Leu	Tyr	Val	Leu	Asp	
														115	125	
Tyr	Lys	Ser	Ser	Gln	Asn	Tyr	Gln	Gln	Ser	His	Lys	Ala	Gln	Val	Ser	
														130	140	
His	Tyr	Ala	Glu	Phe	Leu	Arg	Thr	Gln	Unk	Pro	His	Phe	Lys	Ile	Gln	
														145	160	
Ala	Gly	Ile	Ile	Tyr	Ala	His	Lys	Arg	Leu	Leu	Glu	Lys	Unk	Trp	Unk	
														165	175	

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 176 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634

Met	Thr	Ser	Val	Val	Ile	Lys	Pro	His	Ala	Tyr	Gly	Glu	Gln	Val	Gln	
1																
														15		
Glu	Ile	Glu	Glu	Glu	Ser	Asp	Ser	Asp	Tyr	Glu	Lys	Asn	Asn	Asp	Gln	
														30		

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Glu Ala Ile Asn Phe Gly Ile Ala Leu His Lys Gly Leu Glu Tyr Gln  
 35 40 45  
 Tyr Ala Tyr Asn Ile Pro Lys Gln Ser Val Leu Glu Tyr Leu Asn Tyr  
 50 55 60  
 His Tyr Gly Phe Tyr Gly Leu Asp Tyr Gln Ala Leu Glu Glu Ser Leu  
 65 70 75 80  
 Glu Leu Phe Glu Asn Asp Ala Gly Ile Gln Ala Leu Phe Lys Asn His  
 85 90 95  
 Ala Leu Lys Gly Glu Ala Ala Phe Leu Phe Gln Gly Val Val Ser Arg  
 100 105 110  
 Ile Asp Val Leu Leu Trp Asp Arg Gly Gln Asn Leu Tyr Val Leu Asp  
 115 120 125  
 Tyr Lys Ser Ser Gln Asn Tyr Gln Gln Ser His Lys Ala Gln Val Ser  
 130 135 140  
 His Tyr Ala Glu Phe Leu Arg Thr Gln Unk Pro His Phe Lys Ile Gln  
 145 150 155 160  
 Ala Gly Ile Ile Tyr Ala His Lys Arg Leu Leu Glu Lys Unk Trp Unk  
 165 170 175

## (2) INFORMATION FOR SEQ ID NO:635:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...88

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:635

Met Glu Ser Gln Leu Met Lys Leu Ala Ile Glu Thr Tyr Lys Ile Thr  
 1 5 10 15  
 Leu Met Ile Ser Leu Pro Val Leu Leu Ala Gly Leu Val Val Gly Leu  
 20 25 30  
 Leu Val Ser Ile Phe Gln Ala Thr Thr Gln Ile Asn Glu Met Thr Leu  
 35 40 45  
 Ser Phe Val Pro Lys Ile Leu Ala Val Ile Gly Val Leu Ile Leu Thr  
 50 55 60  
 Met Pro Trp Met Thr Asn Met Leu Leu Asp Tyr Thr Lys Thr Leu Ile  
 65 70 75 80  
 Lys Leu Ile Pro Lys Ile Ile Gly  
 85

## (2) INFORMATION FOR SEQ ID NO:636:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

**SUBSTITUTE SHEET (RULE 26)**

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636

```

Met Lys Phe Phe Thr Arg Ile Thr Asp Ser Tyr Lys Lys Val Val Val
1      5          10          15
Thr Leu Gly Leu Val Val Thr Thr Asn Pro Leu Met Ala Val Thr Ser
20     25          30
Pro Ala Thr Gly Val Thr Glu Thr Lys Ser Leu Val Ile Gln Ile Ile
35     40          45
Ser Val Leu Ala Ile Val Gly Gly Cys Ala Leu Gly Val Lys Gly Ile
50     55          60
Ala Asp Ile Trp Lys Ile Ser Asp Asp Ile Lys Arg Gly Gln Ala Thr
65     70          75          80
Val Phe Ala Tyr Ala Gln Pro Ile Ala Met Leu Ala Val Ala Gly Gly
85     90          95
Ile Ile Tyr Leu Ser Thr Lys Phe Gly Phe Asn Ile Gly Glu Ser Gly
100    105         110
Gly Ala Ser
115

```

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 260 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637

```

Met Ser Glu Asp Leu Pro Phe Ala Ser Asp Ser Gln Phe Thr Tyr Asn
1      5          10          15
Gly Val Ser Ile Thr Arg Pro Thr Asn Glu Val Asn Asp Val Ile Ser
20     25          30
Gly Val Asn Ile Thr Leu Glu Gln Thr Thr Glu Pro Asn Lys Pro Ala
35     40          45
Ile Ile Ser Val Ser Arg Asp Asn Gln Ala Ile Ile Asp Ser Leu Lys
50     55          60
Glu Phe Val Lys Ala Tyr Asn Glu Leu Ile Pro Lys Leu Asp Glu Asp
65     70          75          80
Thr Arg Tyr Asp Ala Asp Thr Lys Ile Ala Gly Ile Phe Asn Gly Val
85     90          95
Gly Asp Ile Arg Ala Ile Arg Ser Ser Leu Asn Asn Val Phe Ser Tyr
100    105         110
Ser Val His Thr Asp Asn Gly Val Glu Ser Leu Met Lys Tyr Gly Leu
115    120         125
Ser Leu Asp Asp Lys Gly Val Met Ser Leu Asp Glu Ala Lys Leu Ser
130    135         140

```

530

Ser Ala Leu Asn Ser Asn Pro Lys Ala Thr Gln Asp Phe Phe Tyr Gly  
 145               150               155               160  
 Ser Asp Ser Lys Asp Met Gly Gly Arg Glu Ile His Gln Glu Gly Ile  
 165               170               175  
 Phe Ser Lys Phe Asn Gln Val Ile Ala Asn Leu Ile Asp Gly Gly Asn  
 180               185               190  
 Ala Lys Leu Lys Ile Tyr Glu Asp Ser Leu Asp Arg Asp Ala Lys Ser  
 195               200               205  
 Leu Thr Lys Asp Lys Glu Asn Ala Gln Glu Leu Leu Lys Thr Arg Tyr  
 210               215               220  
 Asn Ile Met Ala Glu Arg Phe Ala Ala Tyr Asp Ser Gln Ile Ser Lys  
 225               230               235               240  
 Ala Asn Gln Lys Phe Asn Ser Val Gln Met Met Ile Asp Gln Ala Ala  
 245               250               255  
 Ala Lys Lys Asn  
 260

## (2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 260 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637

Met Ser Glu Asp Leu Pro Phe Ala Ser Asp Ser Gln Phe Thr Tyr Asn  
 1               5               10               15  
 Gly Val Ser Ile Thr Arg Pro Thr Asn Glu Val Asn Asp Val Ile Ser  
 20               25               30  
 Gly Val Asn Ile Thr Leu Glu Gln Thr Thr Glu Pro Asn Lys Pro Ala  
 35               40               45  
 Ile Ile Ser Val Ser Arg Asp Asn Gln Ala Ile Ile Asp Ser Leu Lys  
 50               55               60  
 Glu Phe Val Lys Ala Tyr Asn Glu Leu Ile Pro Lys Leu Asp Glu Asp  
 65               70               75               80  
 Thr Arg Tyr Asp Ala Asp Thr Lys Ile Ala Gly Ile Phe Asn Gly Val  
 85               90               95  
 Gly Asp Ile Arg Ala Ile Arg Ser Ser Leu Asn Asn Val Phe Ser Tyr  
 100              105              110  
 Ser Val His Thr Asp Asn Gly Val Glu Ser Leu Met Lys Tyr Gly Leu  
 115              120              125  
 Ser Leu Asp Asp Lys Gly Val Met Ser Leu Asp Glu Ala Lys Leu Ser  
 130              135              140  
 Ser Ala Leu Asn Ser Asn Pro Lys Ala Thr Gln Asp Phe Phe Tyr Gly  
 145              150              155              160  
 Ser Asp Ser Lys Asp Met Gly Gly Arg Glu Ile His Gln Glu Gly Ile  
 165              170              175  
 Phe Ser Lys Phe Asn Gln Val Ile Ala Asn Leu Ile Asp Gly Gly Asn  
 180              185              190  
 Ala Lys Leu Lys Ile Tyr Glu Asp Ser Leu Asp Arg Asp Ala Lys Ser  
 195              200              205  
 Leu Thr Lys Asp Lys Glu Asn Ala Gln Glu Leu Leu Lys Thr Arg Tyr

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210	215	220
Asn Ile Met Ala Glu Arg Phe Ala Ala Tyr Asp Ser Gln Ile Ser Lys		
225	230	235
Ala Asn Gln Lys Phe Asn Ser Val Gln Met Met Ile Asp Gln Ala Ala		240
245	250	255
Ala Lys Lys Asn		
260		

## (2) INFORMATION FOR SEQ ID NO:638:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...191

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:638

Met Lys Asn Pro Gln Ala Asn Val Leu Lys Leu Phe Leu Asn Gln Val		
1	5	10
		15
Ala Asp Gln Lys Tyr Ile Asp Met Asn Asp Glu Lys Asn Tyr Asp Pro		
20	25	30
Arg Glu Pro Glu Pro Pro Tyr Gly Thr Lys Gly Ala Leu Asp Glu Ile		
35	40	45
Ile Arg Thr Asp Ala Arg Ser Trp Ala Asn Thr Pro Asp Asp Glu Phe		
50	55	60
Gly Ser Ile Met Ser Ser Phe Lys Arg Phe Met Tyr Val Tyr Lys Asp		
65	70	75
		80
Pro Lys Val Arg Glu Ala Thr Ser Lys Met Ser Phe Asp Tyr Glu Glu		
85	90	95
Leu Arg Thr Gly Asn Ile Ser Ile Tyr Ile Val Ile Ala Gln Ile Asp		
100	105	110
Ile Gly Thr Leu Ser Ser Leu Val Arg Ala Phe Leu Glu Ser Ile Ala		
115	120	125
Lys Asn Leu Met Val Lys Glu Ser Ser Lys Pro Glu Glu Arg Ile Phe		
130	135	140
Ile Ile Ala Asp Glu Phe Val Arg Phe Gly Lys Leu Pro Phe Leu Leu		
145	150	155
		160
Glu Met Pro Ala Leu Cys Arg Ser Tyr Asn Val Val Pro Leu Phe Ile		
165	170	175
Thr Gln Asp Tyr Ala Met Ile Arg Asn Thr Ile Ala Met Met Ile		
180	185	190

## (2) INFORMATION FOR SEQ ID NO:639:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639

```

Met Ile Ser Glu Ile Ile Lys Phe Gln Leu Lys Gly Ile Lys Met Ile
1      5          10        15
Arg Leu Lys Gly Leu Asn Lys Thr Leu Lys Thr Ser Leu Leu Ala Gly
20     25          30
Val Leu Leu Gly Ala Thr Ala Pro Leu Met Ala Lys Pro Leu Leu Ser
35     40          45
Asp Glu Asp Leu Leu Lys Arg Val Lys Leu His Asn Ile Lys Glu Asp
50     55          60
Thr Leu Thr Ser Cys Asn Ala Lys Val Asp Gly Ser Gln Tyr Leu Asn
65     70          75        80
Ser Gly Trp Asn Leu Ser Lys Glu Phe Pro Gln Glu Tyr Arg Glu Lys
85     90          95
Ile Phe Glu Cys Val Glu Glu Lys His Lys Gln Ala Leu Asn Leu
100    105         110
Ile Asn Lys Glu Asp Thr Glu Asp Lys Glu Glu Leu Ala Lys Lys Ile
115    120         125
Lys Glu Ile Lys Glu Lys Ala Lys Val Leu Arg Gln Lys Phe Met Ala
130    135         140
Phe Glu Met Lys Glu His Ser Lys Glu Phe Pro Asn Lys Lys Gln Leu
145    150         155        160
Gln Thr Met Leu Glu Asn Ala Phe Asp Asn Gly Ala Glu Ser Phe Ile
165    170         175
Asp Asp Trp His Glu Arg Phe Gly Gly Ile Ser Arg Glu Asn Thr Tyr
180    185         190
Lys Ala Leu Gly Ile Lys Glu Tyr Ser Asp Glu Gly Lys Ile Leu Ala
195    200         205
Phe Gly Glu Arg Ser Tyr Ile Arg Gln Tyr Lys Lys Asp Phe Glu Glu
210    215         220
Ser Thr Tyr Asp Thr Arg Gln Thr Leu Ser Ala Met Ala Asn Met Ser
225    230         235        240
Gly Glu Asn Asp Tyr Lys Ile Thr Trp Leu Lys Pro Lys Tyr Gln Leu
245    250         255
His Ser Ser Asn Asn Ile Lys Pro Leu Met Ser Asn Thr Glu Leu Leu
260    265         270
Asn Met Ile Glu Leu Thr Asn Ile Lys Lys Glu Tyr Val Met Gly Cys
275    280         285
Asn Met Glu Ile Asp Gly Ser Lys Tyr Pro Ile His Lys Asp Trp Gly
290    295         300
Phe Phe Gly Lys Ala Lys Val Pro Glu Thr Trp Arg Asn Lys Ile Trp
305    310         315        320
Glu Cys Ile Lys Asn Lys Val Lys Ser Tyr Asp Asn Thr Thr Ala Glu
325    330         335
Ile Gly Ile Val Trp Lys Lys Asn Thr Tyr Ser Ile Ser His His
340    345         350

```

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 351 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640

Met Ala Asp Ile Leu Ser Gln Glu Glu Ile Asp Ala Leu Leu Glu Val  
 1 5 10 15  
 Val Asp Glu Asn Val Asp Ile Gln Asn Val Gln Lys Lys Asp Ile Ile  
 20 25 30  
 Pro Gln Arg Ser Val Thr Leu Tyr Asp Phe Lys Arg Pro Asn Arg Val  
 35 40 45  
 Ser Lys Glu Gln Leu Arg Ser Phe Arg Ser Ile His Asp Lys Met Ala  
 50 55 60  
 Arg Asn Leu Ser Ser Gln Val Ser Ser Ile Met Arg Ser Ile Val Glu  
 65 70 75 80  
 Ile Gln Leu His Ser Val Asp Gln Met Thr Tyr Gly Glu Phe Leu Met  
 85 90 95  
 Ser Leu Pro Ser Pro Thr Ser Phe Asn Val Phe Ser Met Lys Pro Met  
 100 105 110  
 Gly Gly Thr Gly Val Leu Glu Ile Asn Pro Ser Ile Ala Phe Pro Met  
 115 120 125  
 Ile Asp Arg Leu Leu Gly Gly Lys Gly Ser Ala Tyr Asp Gln Asn Arg  
 130 135 140  
 Glu Phe Ser Asp Ile Glu Leu Asn Leu Leu Asp Thr Ile Leu Arg Gln  
 145 150 155 160  
 Val Met Gin Ile Leu Lys Glu Val Trp Ser Pro Val Val Glu Met Tyr  
 165 170 175  
 Pro Thr Ile Asp Ala Lys Glu Ser Ser Ala Asn Val Val Gln Ile Val  
 180 185 190  
 Ala Gln Asn Glu Ile Ser Ile Met Val Val Leu Glu Ile Ile Ile Gly  
 195 200 205  
 His Ser Arg Gly Met Met Asn Ile Cys Tyr Pro Val Ile Ser Ile Glu  
 210 215 220  
 Ser Ile Leu Ser Lys Met Gly Ser Arg Asp Phe Met Leu Ser Glu Thr  
 225 230 235 240  
 Asn Ser Lys Lys Ser Arg Asn Lys Glu Leu Gln Ala Leu Leu Ser Gly  
 245 250 255  
 Val Ser Val Asp Met Met Val Phe Leu Gly Ala Val Glu Leu Ser Leu  
 260 265 270  
 Lys Glu Met Leu Asp Leu Asp Val Gly Asp Thr Ile Arg Leu Asn Lys  
 275 280 285  
 Val Ala Asn Asp Glu Val Ser Val Tyr Val His Lys Lys Lys Arg Tyr  
 290 295 300  
 Leu Ala Ser Val Gly Phe Gln Gly Tyr Arg Lys Thr Ile Gln Ile Lys  
 305 310 315 320  
 Glu Val Val Tyr Ser Glu Lys Glu Arg Thr Lys Glu Ile Leu Glu Met  
 325 330 335  
 Leu Glu Glu Gln Arg Arg Arg Gln Ser Trp Ala Met Leu Trp Ser  
 340 345 350

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

534

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641

Met	Arg	Ile	Val	Phe	Met	Gly	Thr	Pro	Ser	Phe	Ala	Glu	Val	Ile	Leu
1					5						10			15	
Arg	Ala	Leu	Val	Glu	Asn	Glu	Asp	Lys	Lys	Ile	Glu	Val	Val	Gly	Leu
					20			25				30			
Phe	Thr	Gln	Arg	Asp	Lys	Pro	Phe	Gly	Arg	Lys	Glu	Leu	Lys	Ala	
					35			40			45				
Pro	Glu	Thr	Lys	Thr	Tyr	Ile	Leu	Glu	Asn	His	Leu	Asn	Ile	Pro	Ile
					50			55			60				
Phe	Gln	Pro	Gln	Ser	Leu	Lys	Glu	Pro	Glu	Val	Gln	Ile	Leu	Gly	
					65			70			75			80	
Leu	Lys	Pro	Asp	Phe	Ile	Val	Val	Ala	Tyr	Gly	Lys	Ile	Leu	Pro	
					85			90			95				
Lys	Glu	Val	Leu	Thr	Ile	Ala	Pro	Cys	Ile	Asn	Leu	His	Ala	Ser	Leu
					100			105			110				
Leu	Pro	Lys	Tyr	Arg	Gly	Ala	Ser	Pro	Ile	His	Glu	Met	Ile	Leu	Asn
					115			120			125				
Asp	Asp	Arg	Ile	Tyr	Gly	Ile	Ser	Thr	Met	Leu	Met	Unk	Phe	Gly	Ile
					130			135			140				
Gly															
	145														

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641

Met	Arg	Ile	Val	Phe	Met	Gly	Thr	Pro	Ser	Phe	Ala	Glu	Val	Ile	Leu
1					5						10			15	
Arg	Ala	Leu	Val	Glu	Asn	Glu	Asp	Lys	Lys	Ile	Glu	Val	Val	Gly	Leu
					20			25			30				
Phe	Thr	Gln	Arg	Asp	Lys	Pro	Phe	Gly	Arg	Lys	Glu	Leu	Lys	Ala	
					35			40			45				
Pro	Glu	Thr	Lys	Thr	Tyr	Ile	Leu	Glu	Asn	His	Leu	Asn	Ile	Pro	Ile
					50			55			60				
Phe	Gln	Pro	Gln	Ser	Leu	Lys	Glu	Pro	Glu	Val	Gln	Ile	Leu	Gly	
					65			70			75			80	
Leu	Lys	Pro	Asp	Phe	Ile	Val	Val	Ala	Tyr	Gly	Ile	Leu	Pro		

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85	90	95
Lys Glu Val Leu Thr Ile Ala Pro Cys Ile Asn Leu His Ala Ser Leu		
100	105	110
Leu Pro Lys Tyr Arg Gly Ala Ser Pro Ile His Glu Met Ile Leu Asn		
115	120	125
Asp Asp Arg Ile Tyr Gly Ile Ser Thr Met Leu Met Unk Phe Gly Ile		
130	135	140
Gly		
145		

## (2) INFORMATION FOR SEQ ID NO:642:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...190

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:642

Met Pro Thr Met Leu Ala Val Gly Phe Trp Val Leu Val Phe Leu Ser			
1	5	10	15
Thr Ser Asn Ala Val Asn Leu Thr Asp Gly Leu Asp Gly Leu Ala Ser			
20	25	30	
Val Pro Ser Ile Phe Thr Leu Leu Ser Leu Ser Ile Phe Val Tyr Val			
35	40	45	
Ala Gly Asn Ala Glu Phe Ser Lys Tyr Leu Leu Tyr Pro Lys Val Ile			
50	55	60	
Asp Val Gly Glu Leu Phe Val Ile Ser Leu Ala Leu Val Gly Ser Leu			
65	70	75	80
Phe Gly Phe Leu Trp Tyr Asn Cys Asn Pro Ala Ser Val Phe Met Gly			
85	90	95	
Asp Ser Gly Ser Leu Ala Ile Gly Gly Phe Ile Ala Tyr Asn Ala Ile			
100	105	110	
Val Ser His Asn Glu Ile Leu Leu Val Leu Met Gly Ser Ile Phe Val			
115	120	125	
Ile Glu Thr Leu Ser Val Ile Leu Gln Val Gly Ser Tyr Lys Thr Arg			
130	135	140	
Lys Lys Arg Leu Phe Leu Met Ala Pro Ile His His His Phe Glu Gln			
145	150	155	160
Lys Gly Trp Ala Glu Asn Lys Val Ile Val Arg Phe Trp Ile Ile Ser			
165	170	175	
Met Leu Ser Asn Leu Val Ala Leu Leu Ser Leu Lys Val Cys			
180	185	190	

## (2) INFORMATION FOR SEQ ID NO:643:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643

Val Arg Phe Glu Asn Phe Ile Asn Arg Leu Ala Phe Tyr Met Ala Thr  
 1               5                   10                   15  
 Gly Ser Gly Lys Thr Ile Val Ile Ile Lys Leu Val Glu Leu Leu Ser  
 20               25                   30  
 Val Ala Met Gly Met Gly Leu Ile Pro Lys Lys Asn Ile Met Phe Phe  
 35               40                   45  
 Ser Ala Asn Glu His Leu Ile Lys Gln Phe Glu Lys Glu Ile Glu Lys  
 50               55                   60  
 Tyr Asn Arg Asn Lys Asp Tyr Ser Lys Gln Ile Asp Phe Lys Asn Leu  
 65               70                   75                   80  
 Lys Ser Val Lys Asn Lys Asp Phe Tyr Arg Ala Pro Lys Asp Ser Leu  
 85               90                   95  
 Met Lys Glu Ile Ala Leu Phe Tyr Tyr Arg Ala Asp Leu Met Ser Asp  
 100              105                   110  
 Glu Glu Ser Lys Glu Asn Leu Leu Asn Tyr Lys Asp Cys Trp Asp Asn  
 115              120                   125  
 Gly Glu Asn Tyr Val Ile Leu Asp Glu Ala His Lys Gly Asn Lys Thr  
 130              135                   140  
 Glu Ser Lys Arg Gln Ala Ile Phe Ser Leu Leu Ser Leu Lys Gly Phe  
 145              150                   155                   160  
 Leu Phe Asn Phe Ser Ala Thr Phe Thr Glu Glu Ser Asp Leu Ile Thr  
 165              170                   175  
 Ala Val Tyr Asn Leu Ser Val Gly Glu Trp Val Lys Leu Gly Tyr Gly  
 180              185                   190  
 Lys Glu Ser Val Leu Leu Lys Lys Asn Asn Leu Asn Ala Phe Lys Glu  
 195              200                   205  
 Leu Lys Asp Leu Asn Asp Arg Glu Lys Glu Ile Ala Leu Leu Lys Ala  
 210              215                   220  
 Leu Leu Leu Leu Gly Met Gln Lys Arg Tyr Lys Val Glu Gly Tyr Phe  
 225              230                   235                   240  
 His Asp Pro Leu Met Leu Val Phe Thr His Ser Val Asn Met Glu Asn  
 245              250                   255  
 Ser Asp Ala Unk Ile Phe Phe Lys Thr Leu Ala Arg Val Ile Glu Asn  
 260              265                   270  
 Asp Asp Glu Ser Asp Phe Ser Lys Ala Lys Asp Asp Leu Leu Glu Glu  
 275              280                   285  
 Leu Lys Asn Pro Glu Phe Leu Phe Ser Asp Gly Lys Asp Lys Glu Lys  
 290              295                   300  
 Asp Tyr Lys Ile Glu Val Phe Lys Glu Ser Leu Lys Gly Met Asp Phe  
 305              310                   315                   320  
 Lys Gly Leu Lys Glu Ala Val Phe Tyr Ala Ser Asn Gly His Ile Glu  
 325              330                   335  
 Val Ile Ile Asn Pro Lys Asn Asn Gln Glu Ile Ala Phe Lys Leu Asn  
 340              345                   350  
 Thr Ser Asp Lys Val Phe Cys Leu Ile Arg Ile Gly Asp Ile Thr Glu  
 355              360                   365  
 Trp Ile Arg Glu Lys Leu Lys Ser Val Lys Val Val Ser Lys Asn Leu  
 370              375                   380  
 Ser Phe Lys Glu Glu Ser Tyr Phe Ser Gln Ile Asp Lys Ser Ser Ile  
 385              390                   395                   400  
 Asn Ile Leu Val Gly Ser Arg Ala Phe Asp Thr Gly Trp Asp Ser Thr  
 405              410                   415  
 Arg Pro Ser Val Ile Leu Phe Leu Asn Ile Gly Leu Asp Asp Ala

537

420	425	430
Lys Lys Leu Val Lys Gln Ser Phe Gly Arg Gly Val Arg Ile Glu Ser		
435	440	445
Val Lys Asn Gln Arg Gln Arg Leu Ala Tyr Leu Glu Ile Asp Glu Ala		
450	455	460
Ile Lys Glu Gln Ala Glu Thr Lys Arg Cys Asn Ala Gly Asn Ala Phe		
465	470	475
Cys Asp Thr Tyr Gln Pro Cys Lys Pro		480
485		

## (2) INFORMATION FOR SEQ ID NO:644:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644

Met Arg Phe Tyr Phe Lys Phe Leu Trp Leu Leu Gly Ile Phe Leu Ile		
1	5	10
Phe Tyr Phe Leu Asp Ile Lys Gly Ser Ser Ser Tyr Ile Ser Asp Arg		15
20	25	30
Val Lys Ser Ala Leu Met Ser Ala Lys Asn Ser Leu Leu Asp Asn Val		
35	40	45
Gln Ala Tyr Phe Phe Gln Ala Gln Asn Ile Lys Glu Phe Gln Lys Glu		
50	55	60
Arg Leu Ile Leu Glu Ala Leu Lys Leu Glu Asn Ala Asp Leu Lys Glu		
65	70	75
Arg Leu Asn Ser Ile Tyr Pro Leu Glu Asn Pro Lys Met Thr Tyr Thr		80
85	90	95
Pro Thr Phe Met Thr Ser Phe Ile Asn Leu Glu Asp Thr His Ser Val		
100	105	110
Ser Leu Asn Pro Ile Val Asn Leu Glu Asn Lys Ile Tyr Gly Leu		
115	120	125
Val Ser His Asn Gln Ala Ile Gly Ile Ala Val Leu Glu Lys Gly Arg		
130	135	140
Leu Asn Gly Phe Leu Asn Ala His Lys Arg Cys Ala Tyr Ser Val Met		
145	150	155
Ile Gly Gln Asn Gln Val Leu Gly Phe Ile Gly Thr Asn Phe Lys Gln		160
165	170	175
Glu Leu Val Val Asp Phe Ile Val Pro Ser Ala Glu Ile Asn Ile Gly		
180	185	190
Asp Gln Val Leu Thr Ser Gly Leu Asp Gly Ile Phe Gly Ala Gly Val		
195	200	205
Phe Val Gly Glu Val Ser Ser Val Glu Asp His Tyr Thr Tyr Lys Ser		
210	215	220
Ala Val Leu Lys Asn Ala Phe Leu Ser Glu Ala Lys Leu Leu Arg His		
225	230	235
Val Phe Leu Ser Gly Val Lys Asn		240
245		

## (2) INFORMATION FOR SEQ ID NO:644:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 248 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...248
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:644

```

Met Arg Phe Tyr Phe Lys Phe Leu Trp Leu Leu Gly Ile Phe Leu Ile
1           5           10          15
Phe Tyr Phe Leu Asp Ile Lys Gly Ser Ser Ser Tyr Ile Ser Asp Arg
20          25          30
Val Lys Ser Ala Leu Met Ser Ala Lys Asn Ser Leu Leu Asp Asn Val
35          40          45
Gln Ala Tyr Phe Phe Gln Ala Gln Asn Ile Lys Glu Phe Gln Lys Glu
50          55          60
Arg Leu Ile Leu Glu Ala Leu Lys Leu Glu Asn Ala Asp Leu Lys Glu
65          70          75          80
Arg Leu Asn Ser Ile Tyr Pro Leu Glu Asn Pro Lys Met Thr Tyr Thr
85          90          95
Pro Thr Phe Met Thr Ser Phe Ile Asn Leu Glu Asp Thr His Ser Val
100         105         110
Ser Leu Asn Pro Ile Val Asn Leu Glu Asn Lys Ile Tyr Gly Leu
115         120         125
Val Ser His Asn Gln Ala Ile Gly Ile Ala Val Leu Glu Lys Gly Arg
130         135         140
Leu Asn Gly Phe Leu Asn Ala His Lys Arg Cys Ala Tyr Ser Val Met
145         150         155         160
Ile Gly Gln Asn Gln Val Leu Gly Phe Ile Gly Thr Asn Phe Lys Gln
165         170         175
Glu Leu Val Val Asp Phe Ile Val Pro Ser Ala Glu Ile Asn Ile Gly
180         185         190
Asp Gln Val Leu Thr Ser Gly Leu Asp Gly Ile Phe Gly Ala Gly Val
195         200         205
Phe Val Gly Glu Val Ser Ser Val Glu Asp His Tyr Thr Tyr Lys Ser
210         215         220
Ala Val Leu Lys Asn Ala Phe Leu Ser Glu Ala Lys Leu Leu Arg His
225         230         235         240
Val Phe Leu Ser Gly Val Lys Asn
245

```

## (2) INFORMATION FOR SEQ ID NO:645:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 119 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645

```

Leu Ala Leu Arg Leu Pro Phe Leu Ile Ala His Val Ile Asn Met Phe
1      5          10          15
Leu Phe Tyr Leu Ile Gly Arg Lys Ile Leu Lys Lys Pro Lys Asp Ala
20     25          30
Leu Tyr Val Val Leu Thr Tyr Ala Leu Leu Pro Gly Val Asn Leu Phe
35     40          45
Ala Ile Leu Leu Ala Lys Ser Val Leu Val Leu Ser Leu Gly Leu Leu
50     55          60
Ile Ser Tyr Leu Tyr Ile Lys Thr Gln Lys Ile Pro Tyr Leu Thr Leu
65     70          75          80
Ser Ala Cys Ala Phe Leu Asp Gly Ala Phe Ile Pro Leu Leu Leu Gly
85     90          95
Val Phe Ala Tyr Ala Leu Arg Lys Thr Ala Ile Leu Arg Ala Arg Ser
100    105         110
Leu Leu Trp Trp Phe Unk Leu
115

```

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 119 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645

```

Leu Ala Leu Arg Leu Pro Phe Leu Ile Ala His Val Ile Asn Met Phe
1      5          10          15
Leu Phe Tyr Leu Ile Gly Arg Lys Ile Leu Lys Lys Pro Lys Asp Ala
20     25          30
Leu Tyr Val Val Leu Thr Tyr Ala Leu Leu Pro Gly Val Asn Leu Phe
35     40          45
Ala Ile Leu Leu Ala Lys Ser Val Leu Val Leu Ser Leu Gly Leu Leu
50     55          60
Ile Ser Tyr Leu Tyr Ile Lys Thr Gln Lys Ile Pro Tyr Leu Thr Leu
65     70          75          80
Ser Ala Cys Ala Phe Leu Asp Gly Ala Phe Ile Pro Leu Leu Leu Gly
85     90          95
Val Phe Ala Tyr Ala Leu Arg Lys Thr Ala Ile Leu Arg Ala Arg Ser
100    105         110
Leu Leu Trp Trp Phe Unk Leu
115

```

540

## (2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646

Val	Asn	Leu	Met	Asp	Tyr	Phe	Ser	Lys	Ser	Leu	Phe	Leu	Asn	Ser	Leu
1								5					10		15
Asn	Thr	Gln	Arg	Leu	Ile	Val	Ser	Asn	Lys	Leu	Ala	Ile	Asp	Val	Gln
								20				25		30	
Tyr	Gly	Met	Leu	Gln	Ser	Val	Arg	Lys	Asn	Tyr	Pro	Asp	Val	Val	Asp
							35			40		45			
Gly	Gly	Val	Arg	Glu	Gly	Pro	Phe	Trp	Val	Leu	Ala	Gly	Ala	Leu	Met
							50			55		60			
Pro	Ser	Ile	Leu	Ile	Glu	Ile	Gly	Tyr	Asn	Ser	His	Ala	Ile	Glu	Ser
							65			70		75		80	
Lys	Arg	Ile	Gln	Ser	Lys	Pro	Tyr	Gln	Lys	Ile	Leu	Ala	Lys	Gly	Ile
							85			90		95			
Ala	Asp	Gly	Ile	Asp	Ser	Phe	Phe	Ser	Lys	Asn	Asp				
							100			105					

## (2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646

Val	Asn	Leu	Met	Asp	Tyr	Phe	Ser	Lys	Ser	Leu	Phe	Leu	Asn	Ser	Leu
1								5				10		15	
Asn	Thr	Gln	Arg	Leu	Ile	Val	Ser	Asn	Lys	Leu	Ala	Ile	Asp	Val	Gln
								20			25		30		
Tyr	Gly	Met	Leu	Gln	Ser	Val	Arg	Lys	Asn	Tyr	Pro	Asp	Val	Val	Asp
							35			40		45			
Gly	Gly	Val	Arg	Glu	Gly	Pro	Phe	Trp	Val	Leu	Ala	Gly	Ala	Leu	Met
							50			55		60			
Pro	Ser	Ile	Leu	Ile	Glu	Ile	Gly	Tyr	Asn	Ser	His	Ala	Ile	Glu	Ser

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65	70	75	80
Lys Arg Ile Gln Ser	Lys Pro Tyr Gln Lys	Ile Leu Ala Lys	Gly Ile
85	90		95
Ala Asp Gly Ile Asp Ser Phe	Phe Ser Lys Asn Asp		
100	105		

## (2) INFORMATION FOR SEQ ID NO:647:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...213

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:647

Val Phe Lys Asn Ser Leu Phe Gly Ile Ser Ile Met Leu Ile Thr  
 1               5   10   15  
 Trp Val Leu Thr Ala Cys Ile Leu Ile Phe Ile Leu Phe Val Pro Asn  
 20               25   30  
 Phe Thr Leu Thr His Pro Asn Phe His Phe Thr Pro Phe Glu Lys Thr  
 35               40   45  
 Tyr Phe Gln Ile Leu Gly Leu Val Gly Ile Val Ser Ser Ile Ile Phe  
 50               55   60  
 Thr Gly Phe Leu Ala Asp Lys Ile Lys Pro His Lys Val Cys Met Ala  
 65               70   75   80  
 Phe Ser Thr Thr Phe Gly Phe Gly Phe Leu Phe Phe Lys Glu Phe  
 85               90   95  
 Tyr Ser Asn Ala Pro Ser Leu Val Asn Thr Ile Ile Leu Tyr Phe Leu  
 100              105   110  
 Ala Cys Phe Cys Ala Gly Ile Met Asn Phe Cys Pro Ile Phe Met Ser  
 115              120   125  
 Asp Val Phe Ser Ala Lys Ile Arg Phe Ser Gly Ile Ser Phe Ala Tyr  
 130              135   140  
 Asn Ile Ala Tyr Ala Ile Thr Ala Gly Phe Thr Pro Gln Leu Ser Ser  
 145              150   155   160  
 Trp Leu Asn Ala Lys Ala Ile Ala Val Pro Glu Ser Leu Gln Ser Tyr  
 165              170   175  
 Gly Leu Ser Phe Tyr Ile Leu Ile Val Ser Leu Ile Ala Phe Ile Thr  
 180              185   190  
 Ser Leu Leu Met Ala Pro Ile Tyr His Lys Ser Asn Thr Gln His Glu  
 195              200   205  
 Val Ser Pro Thr Ala  
 210

## (2) INFORMATION FOR SEQ ID NO:648:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648

Leu	Ala	Ser	Arg	Tyr	Ser	Val	Ala	Val	Gly	Asn	Leu	Phe	Ser	Glu	His
1				5					10					15	
Leu	Tyr	Asp	Leu	Arg	Asn	Glu	Thr	Met	Thr	Asn	Leu	Ile	Gly	Phe	Leu
	20							25					30		
Leu	Val	Leu	Ala	Ser	Ile	Trp	Val	Phe	Phe	Leu	Ala	Leu	Gly	Val	Leu
	35						40					45			
Leu	Gly	Lys	Met	Leu	Val	Phe	Ser	Gly	Leu	Gly	Ile	Ile	Asp	Lys	Ala
	50						55				60				
Leu	Gly	Phe	Ile	Phe	Ser	Cys	Leu	Lys	Thr	Phe	Leu	Val	Leu	Ser	Phe
	65						70			75			80		
Ile	Leu	Tyr	Ala	Leu	Ser	Lys	Met	Asp	Leu	Met	Lys	Asp	Ala	Asn	Ala
	85							90				95			
Tyr	Leu	Gln	Glu	Lys	Unk	Unk	Ile	Phe	Pro	Thr	Unk	Lys	Unk	Unk	Unk
		100						105			110				
Ser	Lys	Ile	Met	Arg	Leu	Asp	Gly	Val	Lys	His	Val	Glu	Lys	Asn	Leu
		115					120				125				
Lys	Asp	Asn	Leu	Glu	Glu	Met	Ser	Asp	Glu	Val	Lys	Asn	Lys	Gly	Ser
	130					135				140					
Ile	Asp	Asn	Ala	Lys	Glu	Ser	Phe	Asn	Lys	Gly	Tyr	Gly			
	145					150				155					

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648

Leu	Ala	Ser	Arg	Tyr	Ser	Val	Ala	Val	Gly	Asn	Leu	Phe	Ser	Glu	His
1				5					10					15	
Leu	Tyr	Asp	Leu	Arg	Asn	Glu	Thr	Met	Thr	Asn	Leu	Ile	Gly	Phe	Leu
	20							25				30			
Leu	Val	Leu	Ala	Ser	Ile	Trp	Val	Phe	Phe	Leu	Ala	Leu	Gly	Val	Leu
	35						40				45				
Leu	Gly	Lys	Met	Leu	Val	Phe	Ser	Gly	Leu	Gly	Ile	Ile	Asp	Lys	Ala
	50						55			60					
Leu	Gly	Phe	Ile	Phe	Ser	Cys	Leu	Lys	Thr	Phe	Leu	Val	Leu	Ser	Phe
	65						70			75			80		
Ile	Leu	Tyr	Ala	Leu	Ser	Lys	Met	Asp	Leu	Met	Lys	Asp	Ala	Asn	Ala

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85	90	95
Tyr Leu Gln Glu Lys Unk Unk Ile Phe Pro Thr Unk Lys Unk Unk Unk		
100	105	110
Ser Lys Ile Met Arg Leu Asp Gly Val Lys His Val Glu Lys Asn Leu		
115	120	125
Lys Asp Asn Leu Glu Glu Met Ser Asp Glu Val Lys Asn Lys Gly Ser		
130	135	140
Ile Asp Asn Ala Lys Glu Ser Phe Asn Lys Gly Tyr Gly		
145	150	155

## (2) INFORMATION FOR SEQ ID NO:649:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649

Met Lys Ser Asp Lys Pro Phe Leu Glu Arg Tyr Phe Tyr Asp Pro Thr			
1	5	10	15
Leu Leu Gln Lys Gly Leu Ile Phe Ala Leu Tyr Pro Phe Ser Leu Ile			
20	25	30	
Tyr Gln Cys Ile Ala Thr Ile Lys Arg Lys Thr Ala Lys Lys His Asp			
35	40	45	
Phe Lys Ile Pro Ile Ile Ser Ile Gly Asn Leu Ile Ala Gly Gly Ser			
50	55	60	
Gly Lys Thr Pro Phe Ile Leu Glu Ile Ala Pro Arg Tyr Gln Glu Val			
65	70	75	80
Ala Val Val Ser Arg Gly Tyr Gln Arg Asp Ser Lys Gly Leu Val Val			
85	90	95	
Val Ser Val Lys Gly Asn Ile Leu Val Pro Gln Lys Thr Ala Gly Asp			
100	105	110	
Glu Ala Tyr Leu Leu Ala Leu Asn Leu Lys Gln Ala Ser Val Ile Val			
115	120	125	
Ser Glu Lys Arg Glu Leu Gly Val Leu Lys Ala Leu Glu Leu Gly Ser			
130	135	140	
Lys Ile Val Phe Leu Asp Asp Gly Phe Arg Phe Asn Phe Asn Gln Phe			
145	150	155	160
Asn Ala Leu Leu Lys Pro Lys Val Pro Pro Tyr Tyr Pro Phe Cys Leu			
165	170	175	
Pro Ser Gly Leu Tyr Arg Glu Asn Ile Lys Ser Tyr Lys Glu Ala His			
180	185	190	
Leu Val Ile Thr Glu Asp Lys Asp Tyr Gln Arg Ile Thr Ser Ile Thr			
195	200	205	
Asn Pro Thr Lys Arg Met Leu Leu Val Thr Ala Ile Ala Asn Pro Ser			
210	215	220	
Arg Leu Asp Ala Phe Leu Pro Lys Glu Val Val Lys Lys Leu Tyr Phe			
225	230	235	240
Arg Asp His Ala Pro Phe Asp Leu Lys Leu Leu Glu Lys Glu Phe Tyr			
245	250	255	
Gln Asn Asn Ala Thr Ser Leu Leu Val Thr Ser Lys Asp Leu Val Lys			
260	265	270	

544

Leu	Gln	Asp	Cys	Lys	Leu	Pro	Leu	Ser	Val	Leu	Asp	Leu	Lys	Leu	Glu
															285
275															280
Ile	Cys	Pro	Lys	Val	Leu	Glu	Glu	Ile	Asp	Arg	Tyr	Ile	Leu	Ser	Tyr
															290
290															295
Pro	Cys	Asn	Ile	Lys	Glu	His	Leu								300
															305
															310

## (2) INFORMATION FOR SEQ ID NO:650:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...56

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:650

Met	Ser	Leu	Gly	Ala	Val	Ile	Arg	Leu	Ile	Phe	Cys	Tyr	Lys	Leu	Glu
															15
1															5
Gly	Val	Ile	Leu	Asp	Leu	Lys	Arg	Ile	Asn	Phe	Lys	Ser	Tyr	Tyr	Pro
															20
															25
Asn	Asn	Lys	Asn	Ala	Leu	Phe	Ile	Asn	Asn	Lys	Lys	Asn	Pro	Leu	Ser
															35
Ser	Thr	Ser	Lys	Phe	Ile	Leu	Leu								40
															45
															50
															55

## (2) INFORMATION FOR SEQ ID NO:651:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...199

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:651

Met	Leu	Glu	Thr	Thr	Ile	Asp	Phe	Ser	Arg	Tyr	Ser	Ser	Val	Lys	Ile
															15
1															5
Gly	Ala	Pro	Leu	Lys	Val	Ser	Val	Leu	Glu	Asn	Asp	Asn	Glu	Ile	Ser
															20
															25
Gln	Glu	His	Gln	Ile	Ile	Gly	Leu	Ala	Asn	Asn	Leu	Ile	Ala	Pro	
															35
Asp	Val	Lys	Asn	Leu	Ala	Leu	Leu	Gly	Lys	Asn	Tyr	Asp	Tyr	Ile	Cys
															40
															45

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50	55	60
Asp Lys Gly Glu Trp Val	Glu Val Gly Gly Ala Ala Asn Ala Ser Lys	
65	70	75
Ile Phe Asn Tyr Phe Arg Ala Asn Asp Leu	Glu Gly Leu Glu Phe Leu	80
85	90	95
Gly Gln Leu Pro Gly Thr Leu Gly Ala Leu Val Lys Met Asn Ala Gly		
100	105	110
Met Lys Glu Phe Glu Ile Lys Asn Val Leu Glu Ser Ala Cys Val Asn		
115	120	125
Gly Glu Trp Leu Glu Lys Glu Ala Leu Gly Leu Asp Tyr Arg Ser Ser		
130	135	140
Gly Phe Asn Gly Val Val Leu Arg Ala Arg Phe Lys Lys Thr His Gly		
145	150	155
Phe Arg Glu Gly Val Leu Lys Ala Cys Lys Ser Met Arg Lys Ser His		160
165	170	175
Pro Lys Leu Pro Asn Phe Gly Ser Cys Phe Lys Asn Pro Pro Asn Asp		
180	185	190
Tyr Ala Gly Arg Leu Leu Glu		
195		

## (2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 81 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652

Leu Ser Lys Gln Ser Ala Asp Ile Val	Ile Thr Asn Asp Ser Leu Ser	
1	5	10
Ser Leu Val Lys Val Leu Ala Ile Ala	Lys Lys Thr Lys Ser Ile Thr	15
20	25	30
Trp Gln Asn Ile Leu Phe Ala Leu Gly	Ile Lys Ala Val Phe Ile Val	
35	40	45
Leu Gly Leu Met Gly Val Ala Ser Leu	Trp Glu Ala Val Phe Gly Asp	
50	55	60
Val Gly Val Thr Leu Leu Ala Leu Ala	Asn Ser Unk Arg Thr Met Arg	
65	70	75
Ala		80

## (2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 81 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652

```

Leu Ser Lys Gln Ser Ala Asp Ile Val Ile Thr Asn Asp Ser Leu Ser
1           5          10          15
Ser Leu Val Lys Val Leu Ala Ile Ala Lys Lys Thr Lys Ser Ile Thr
20          25          30
Trp Gln Asn Ile Leu Phe Ala Leu Gly Ile Lys Ala Val Phe Ile Val
35          40          45
Leu Gly Leu Met Gly Val Ala Ser Leu Trp Glu Ala Val Phe Gly Asp
50          55          60
Val Gly Val Thr Leu Leu Ala Leu Asn Ser Unk Arg Thr Met Arg
65          70          75          80
Ala

```

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 89 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653

```

Met Leu Lys Asn Gly Asp Lys Ile Pro Asp Ala Ile Leu Val Asp Ile
1           5          10          15
Glu Met Pro Lys Met Asp Gly Tyr Thr Phe Ala Ser Glu Val Arg Lys
20          25          30
Tyr Asn Lys Phe Lys Asn Leu Pro Leu Ile Ala Val Thr Ser Arg Val
35          40          45
Thr Lys Thr Asp Arg Met Arg Gly Val Glu Ser Gly Met Thr Glu Tyr
50          55          60
Ile Thr Lys Pro Tyr Ser Gly Glu Tyr Leu Thr Thr Val Val Lys Arg
65          70          75          80
Ser Ile Lys Leu Glu Gly Asp Gln Ser
85

```

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654

Val	Phe	Glu	Pro	Val	Ile	Ala	Tyr	Lys	Leu	Phe	His	Ser	Phe	Val	Ile
1				5					10					15	
Leu	Gly	Cys	Ala	Ile	Glu	Thr	Leu	Thr	Thr	Lys	Cys	Val	Glu	Gly	Ile
					20			25					30		
Thr	Ala	Asn	Glu	Lys	Ile	Cys	His	Asp	Tyr	Val	Phe	Asn	Ser	Ile	Gly
					35			40				45			
Ile	Val	Thr	Ala	Leu	Asn	Pro	His	Ile	Gly	Tyr	Glu	Lys	Ser	Ala	Met
					50			55				60			
Ile	Ala	Lys	Glu	Ala	Leu	Lys	Ser	Asp	Arg	Ser	Ile	Tyr	Asp	Ile	Ala
65					70			75				80			
Leu	Glu	Lys	Ile	Leu	Thr	Lys	Glu	Gln	Leu	Asp	Asp	Ile	Phe	Lys	
					85			90				95			
Pro	Glu	Asn	Met	Leu	Arg	Thr	His	Ala	Phe	Lys	Lys	His	Lys	Asp	
					100			105				110			

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655

Met	Leu	Arg	Leu	Leu	Ala	Gln	Ser	Ala	Ile	Lys	Leu	Ile	Leu	Ile	
1					5				10				15		
Pro	Pro	Ser	Ala	Asn	Ala	Leu	Gly	Ile	Ala	Ser	Ile	Cys	Glu	Leu	Ser
						20			25				30		
Glu	Glu	Val	Phe	Glu	His	Glu	Ile	Val	Gly	Ile	Arg	Ala	Gln	Gly	
					35			40				45			
Asp	Phe	Thr	Ile	Asn	Ser	Asp	Asp	Arg	Gly	Phe	Trp	Glu	Arg	Arg	Cys
					50			55				60			
Gln															
65															

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 amino acids

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(B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656

Met	Lys	Lys	Leu	Leu	Leu	Leu	Glu	His	Lys	Ile	Val	Lys	Ile	Gly
1								10				15		
Leu	Ile	Ile	Val	Ile	Val	Leu	Val	Gly	Phe	Phe	Leu	Phe	Tyr	Glu
								20			25		30	
Glu	Ile	Lys	Glu	Lys	Ala	Val	Asn	Val	Ser	Gln	Gly	Lys	Phe	Pro
								35			40		45	
Ser	Ser	Tyr	Leu	Phe	Gln	Ala	Tyr	Glu	Gly	Ile	Lys	Asn	Lys	Ile
								50			55		60	Asp
Thr	Ile	Asn	Gln	Val	Lys	Pro	Asn	Asp	Glu	Thr	Lys	Ser	Val	Asn
								65			70		75	80
Asn	Ile	Glu	Lys	Thr	Gln	Lys	Asp	Leu	Asp	Asp	Phe	Asn	Ala	Leu
								85			90		95	Val
Gln	Lys	Leu	Pro	Asn	Leu	Pro	Lys	Asp	Phe	Asn	Lys	Thr	Leu	Ile
								100			105		110	Lys
Pro	Gln	Ser	Pro	Phe	Phe	Asn	Tyr	Asn	Thr	Ala	Asn	Glu	Asp	Glu
								115			120		125	Lys
Asn	Arg	Leu	Val	Ile	Leu	Ala	Ser	Arg	Ile	Ser	Ser	Gln	Lys	Glu
								130			135		140	Thr
Gln	Pro	Pro	Ile	Ser	Ile	Lys	Asn	Ser	Val	Ser	His	Ile	Lys	Ser
								145			150		155	lys
Glu	Lys	Arg	Glu	Leu	Glu	Lys	Glu	Trp	Ala	Lys	Pro	Ser	Val	Ser
								165			170		175	Phe
Gly	Ser	Phe	Ser	Leu	Leu	Ser	Ser	Ser	Ser	Phe	Ser	Ser	Phe	Glu
								180			185		190	
Val	Ser	Phe	Leu	Ser	Arg	Gly	Ile	Gly	Leu	Asp	Cys	Glu	Lys	Leu
								195			200		205	Lys
Ser	Phe	Leu	Lys	Ala	Phe	Ser	Ser	Leu	Phe	Ser	Leu	Leu	Ser	Ser
								210			215		220	
Leu	Phe	Cys	His	Pro	Leu	Ser	Leu	Phe	Cys	Ser	Leu	Ile	Gly	Leu
								225			230		235	Ile
Phe	Cys	Phe	Ser	Lys	Phe	Ser	Arg	Glu	Leu	Val	Asn	Ala	Ser	Asn
								245			250		255	Asn
Ser	Leu	Glu	Phe	Ser	Ser	Leu	Ser	Arg	Leu	Gly	Ser			
								260			265			

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 100 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...100

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:657

Met Gly Ala Ile Ala Ser Cys Tyr Ala His Gln Ile Ile Leu Thr Ser  
 1 5 10 15  
 Asp Asn Pro Arg Ser Glu Asn Glu Glu Asp Ile Ile Lys Asp Ile Leu  
 20 25 30  
 Lys Gly Ile Asn Asn Ser Ser Lys Val Ile Val Glu Lys Asp Arg Lys  
 35 40 45  
 Lys Ala Ile Leu Asn Ala Leu Glu Asn Leu Lys Asp Asp Glu Val Leu  
 50 55 60  
 Leu Ile Leu Gly Lys Gly Asp Glu Asn Ile Gln Ile Phe Lys Asp Lys  
 65 70 75 80  
 Thr Ile Phe Phe Ser Asp Gln Glu Val Val Lys Asp Tyr Tyr Leu Asn  
 85 90 95  
 Leu Lys Gln Gly  
 100

## (2) INFORMATION FOR SEQ ID NO:658:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...80

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:658

Val Met Asp Lys Leu Thr Lys Ser Leu Gln Thr Gln Lys Asn Phe Ala  
 1 5 10 15  
 Tyr Leu Gly Lys Ile Lys Pro Gln Gln Leu Ala Asp Phe Ile Ile Asn  
 20 25 30  
 Glu His Pro Gln Thr Ile Ala Leu Ile Leu Ala His Met Glu Unk Pro  
 35 40 45  
 Asn Ala Ala Glu Thr Leu Ser Tyr Phe Pro Asp Glu Met Lys Ala Glu  
 50 55 60  
 Ile Ser Ile Arg Met Ala Asn Phe Arg Arg Asn Ile Ala Pro Ser Gly  
 65 70 75 80

## (2) INFORMATION FOR SEQ ID NO:659:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

550

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659

Met Arg Tyr Phe Arg Ser Ala Phe Leu Leu Phe Met Thr Leu Phe  
 1 5 10 15  
 Phe Val Ser Cys Ser Lys His Pro Phe Ser Lys Gln Thr Pro Lys Thr  
 20 25 30  
 Lys Glu Arg Ile Arg Gln Glu Ala Asn Lys Lys Arg Glu Glu Thr  
 35 40 45  
 Leu Asn Ala Leu Arg Gln Phe Arg Leu Ile Tyr Ile Asn Thr Pro Val  
 50 55 60  
 Phe Arg Phe Tyr Asp Tyr Gly Thr Ile Lys Thr Asp Lys Asp His Asn  
 65 70 75 80  
 Thr Glu Val Thr Leu Tyr Lys Leu Ser Gln Lys Val Gly Asp Ile Tyr  
 85 90 95  
 Met Thr Lys Arg Ser Ile Cys Phe Ser Gln Lys Cys Ser Ala Lys Trp  
 100 105 110  
 Ile Ala Ala Arg Asp Leu Phe Gly Lys Val Ser Tyr Gly Asp Leu Phe  
 115 120 125  
 Asp Asp Ile Val Leu Gly Arg Asp Ile Phe Lys Gly Leu Gly Lys Arg  
 130 135 140  
 His Leu Thr Pro Glu Tyr Val Ile Gln Arg Phe Gln Lys Ser Gly Glu  
 145 150 155 160  
 Ile Ile Leu Tyr Glu Arg Lys Asn Gly Leu Ile Ser Phe Gln Asn Leu  
 165 170 175  
 Thr Gln Lys Ile Ala Ile Arg Ile Glu Pro Tyr Glu Pro Ser Leu Gln  
 180 185 190  
 Asp Leu Glu Asp Asn Glu Asn Ala Asp Ser Glu Leu Gln  
 195 200 205

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 124 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660

Met Arg Ile Glu Glu Asn Gly Val Ile Ser Leu Ala Phe Ser Asn Gly  
 1 5 10 15  
 Val Val Glu Pro Val Ala Arg Ile Gly Ile Unk Ala Phe Thr Asn Asp  
 20 25 30  
 Gln Gly Leu Arg Lys Ile Gly Gly Asn Leu Tyr Glu Met Gln Glu Gly  
 35 40 45  
 Thr Ile Asn Gly Glu Asn Arg Pro Leu Unk Gly Asn Pro Ile Leu Gly

**SUBSTITUTE SHEET (RULE 26)**

551

50	55	60
Trp Asp Glu Glu Gly Lys Leu Lys Phe Gly Lys Ile Arg His Lys Tyr		
65	70	75
Leu Glu Thr Ser Asn Val Asn Ala Gly Asn Ala Leu Thr Asn Leu Ile		80
85	90	95
Leu Met Gln Arg Gly Tyr Ser Met Asn Ala Arg Ala Phe Gly Ala Gly		
100	105	110
Asp Asp Met Ile Lys Glu Ala Ile Ser Leu Lys Lys		
115	120	

## (2) INFORMATION FOR SEQ ID NO:661:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...93

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:661

Val Glu Ala Arg Tyr Tyr Gly Asp Thr Ser Tyr Phe Tyr Leu His		
1	5	10
Val Gly Val Leu Gln Glu Phe Ala His Phe Gly Ser Asn Asp Val Ala		15
20	25	30
Ser Leu Asn Thr Phe Lys Ile Asn Ala Ala Arg Ser Pro Leu Ser Thr		
35	40	45
Tyr Ala Arg Ala Met Met Gly Gly Glu Leu Gln Leu Ala Lys Glu Val		
50	55	60
Phe Leu Asn Leu Gly Val Val Tyr Leu His Asn Leu Ile Ser Asn Ala		
65	70	75
Ser His Phe Ala Ser Asn Leu Gly Met Arg Tyr Ser Phe		80
85	90	

## (2) INFORMATION FOR SEQ ID NO:662:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...80

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:662

**SUBSTITUTE SHEET (RULE 26)**

552

Met Lys Asn Leu Arg His Phe Arg Lys Leu Ile Ala Phe Leu Gly Phe  
 1 5 10 15  
 Ser Pro Leu Leu Leu Gln Ala Asp Met Thr Thr Phe Phe Asn Ser Ile  
 20 25 30  
 Glu Gln Gln Leu Thr Ser Pro Thr Ala Lys Gly Ile Leu Met Val Ile  
 35 40 45  
 Phe Leu Gly Leu Ala Ile Phe Ile Trp Lys Asn Leu Asp Arg Trp Lys  
 50 55 60  
 Glu Ile Leu Met Thr Val Leu Ala Leu Lys Unk Val Val Pro Met Gln Unk  
 65 70 75 80

## (2) INFORMATION FOR SEQ ID NO:662:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (iii) MOLECULE TYPE: protein

## (viii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...80

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:662

Met Lys Asn Leu Arg His Phe Arg Lys Leu Ile Ala Phe Leu Gly Phe  
 1 5 10 15  
 Ser Pro Leu Leu Leu Gln Ala Asp Met Thr Thr Phe Phe Asn Ser Ile  
 20 25 30  
 Glu Gln Gln Leu Thr Ser Pro Thr Ala Lys Gly Ile Leu Met Val Ile  
 35 40 45  
 Phe Leu Gly Leu Ala Ile Phe Ile Trp Lys Asn Leu Asp Arg Trp Lys  
 50 55 60  
 Glu Ile Leu Met Thr Val Leu Ala Leu Lys Unk Val Val Pro Met Gln Unk  
 65 70 75 80

## (2) INFORMATION FOR SEQ ID NO:663:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (iii) MOLECULE TYPE: protein

## (viii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...214

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:663

Val Glu Glu Leu Ala Lys Leu Ile Asn Asn Asn Asn Asn Lys

**SUBSTITUTE SHEET (RULE 26)**

1	5	10	15												
Leu	Arg	Gly	Phe	Phe	Leu	Lys	Val	Leu	Ser	Leu	Val	Val	Phe	Ser	
			20		25								30		
Ser	Tyr	Gly	Ser	Ala	Asn	Asp	Asp	Lys	Glu	Ala	Lys	Lys	Glu	Ala	Leu
			35		40								45		
Glu	Lys	Glu	Lys	Asn	Thr	Pro	Asn	Gly	Leu	Val	Tyr	Thr	Asn	Leu	Asp
			50		55						60				
Phe	Asp	Ser	Phe	Lys	Ala	Thr	Ile	Lys	Asn	Leu	Lys	Asp	Lys	Lys	Val
			65		70					75			80		
Thr	Phe	Lys	Glu	Val	Asn	Pro	Asp	Ile	Ile	Lys	Asp	Glu	Val	Phe	Asp
			85							90			95		
Phe	Val	Ile	Val	Asn	Arg	Val	Leu	Lys	Lys	Ile	Lys	Asp	Leu	Lys	His
			100					105					110		
Tyr	Asp	Pro	Val	Ile	Glu	Lys	Ile	Phe	Asp	Glu	Lys	Gly	Lys	Glu	Met
			115				120					125			
Gly	Leu	Asn	Val	Glu	Leu	Gln	Ile	Asn	Pro	Glu	Val	Lys	Asp	Phe	Phe
			130			135					140				
Thr	Phe	Lys	Ser	Ile	Ser	Thr	Thr	Asn	Lys	Gln	Arg	Cys	Phe	Leu	Ser
			145			150				155			160		
Leu	His	Gly	Glu	Thr	Arg	Glu	Ile	Leu	Cys	Asp	Asp	Lys	Leu	Tyr	Asn
			165				170					175			
Val	Leu	Leu	Ala	Val	Phe	Asn	Ser	Tyr	Asp	Pro	Asn	Asp	Leu	Leu	Lys
			180				185					190			
His	Ile	Ser	Thr	Ile	Glu	Ser	Leu	Lys	Lys	Ile	Phe	Tyr	Thr	Ile	Thr
			195				200					205			
Cys	Glu	Ala	Val	Tyr	Leu										
			210												

## (2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 78 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(iv) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664

Val	Gly	Gly	Ile	Val	Ala	Asn	Met	Asn	Asp	Leu	Ser	Thr	Tyr	Met	Val
1			5				10						15		
Glu	Asn	Leu	Leu	Met	Gly	Leu	Tyr	Leu	Phe	Ser	Ser	Ala	Leu	Asp	Leu
				20			25					30			
Gly	Val	Lys	Lys	Ala	Ile	Asn	Leu	Ala	Ser	Ser	Cys	Ala	Tyr	Pro	Lys
			35			40					45				
Tyr	Ala	Pro	Asn	Pro	Leu	Lys	Glu	Ser	Asp	Leu	Leu	Asn	Gly	Ser	Leu
			50			55					60				
Glu	Pro	Thr	Asn	Glu	Gly	Tyr	Ala	Leu	Pro	Asn	Ser	Leu	Unk		
			65			70					75				

## (2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 177 amino acids

(B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665

Met	Lys	Lys	Arg	Lys	His	Val	Ser	Lys	Lys	Val	Phe	Asn	Val	Ile	Ile
1						5			10					15	
Leu	Phe	Val	Ala	Val	Phe	Thr	Leu	Leu	Val	Val	Ile	His	Lys	Thr	Leu
						20			25				30		
Ser	Asn	Gly	Ile	His	Ile	Gln	Asn	Leu	Lys	Ile	Gly	Lys	Leu	Gly	Ile
						35			40			45			
Ser	Glu	Leu	Tyr	Leu	Lys	Leu	Asn	Asn	Lys	Leu	Ser	Leu	Glu	Val	Glu
						50			55			60			
Arg	Val	Asp	Leu	Ser	Ser	Phe	Phe	His	Gln	Lys	Pro	Thr	Lys	Lys	Arg
65						70			75			80			
Leu	Glu	Val	Ser	Asp	Leu	Ile	Lys	Asn	Ile	Arg	Tyr	Gly	Ile	Trp	Ala
						85			90			95			
Val	Ser	Tyr	Phe	Glu	Lys	Leu	Lys	Val	Lys	Glu	Ile	Ile	Leu	Asp	Asp
						100			105			110			
Lys	Asn	Lys	Ala	Asn	Ile	Phe	Phe	Asp	Gly	Asn	Lys	Tyr	Glu	Unk	Arg
						115			120			125			
Ile	Ser	Arg	Asn	Gln	Arg	Gly	Ile	Phe	Pro	Arg	Arg	Arg	Leu	Lys	Ile
						130			135			140			
Ser	Ser	Leu	Lys	Ser	Ser	Ile	Cys	Phe	Leu	Lys	Met	Leu	Lys	Ser	Lys
145						150			155			160			
Trp	Met	Ala	Thr	Pro	Thr	Ile	Unk	Pro	Lys	Pro	Gly	Lys	Trp	Arg	Ser
						165			170			175			
Ile															

(2) INFORMATION FOR SEQ ID NO:666:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 258 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666

Val	Ser	Cys	Trp	Gly	Ala	Ser	Lys	Lys	Arg	Phe	Leu	Gly	Phe	Cys	Val
1						5			10			15			
Trp	Gly	Arg	Cys	Val	Tyr	Ala	Gly	Gly	Leu	Met	Ala	Glu	Gln	Asp	Pro

555

Lys	Glu	Leu	Ile	Phe	Ser	Gly	Ile	Thr	Ile	Tyr	Thr	Asp	Lys	Asn	Phe
20							25					30			
35							40					45			
Thr	Arg	Ala	Lys	Lys	Tyr	Phe	Glu	Lys	Ala	Cys	Lys	Ser	Asn	Asp	Ala
50							55					60			
Asp	Gly	Cys	Ala	Ile	Leu	Arg	Glu	Val	Tyr	Ser	Ser	Gly	Lys	Ala	Ile
65							70					75			80
Ala	Arg	Glu	Asn	Ala	Arg	Glu	Ser	Ile	Glu	Lys	Ala	Leu	Glu	His	Thr
							85					90			95
Ala	Thr	Ala	Lys	Val	Cys	Lys	Leu	Asn	Asp	Ala	Glu	Lys	Cys	Lys	Asp
							100					105			110
Leu	Ala	Glu	Phe	Tyr	Phe	Asn	Val	Asn	Asp	Leu	Lys	Asn	Ala	Leu	Glu
							115					120			125
Tyr	Tyr	Ser	Lys	Ser	Cys	Lys	Leu	Asn	Asn	Val	Glu	Gly	Cys	Met	Leu
							130					135			140
Ser	Ala	Thr	Phe	Tyr	Asn	Asp	Met	Ile	Lys	Gly	Leu	Lys	Lys	Asp	Lys
							145					150			160
Lys	Asp	Leu	Glu	Tyr	Tyr	Ser	Lys	Ala	Cys	Glu	Leu	Asn	Asn	Gly	Gly
							165					170			175
Gly	Cys	Ser	Lys	Leu	Gly	Gly	Asp	Tyr	Phe	Phe	Gly	Glu	Gly	Val	Thr
							180					185			190
Lys	Asp	Phe	Lys	Lys	Ala	Phe	Glu	Tyr	Ser	Ala	Lys	Ala	Cys	Glu	Leu
							195					200			205
Asn	Asp	Ala	Lys	Gly	Cys	Tyr	Ala	Leu	Ala	Ala	Phe	Tyr	Asn	Glu	Gly
							210					215			220
Lys	Gly	Val	Ala	Lys	Asp	Glu	Lys	Gln	Thr	Thr	Glu	Asn	Leu	Glu	Lys
							225					230			240
Ser	Cys	Lys	Leu	Gly	Leu	Lys	Glu	Ala	Cys	Asp	Ile	Leu	Lys	Glu	Gln
							245					250			255
Lys	Gln														

## (2) INFORMATION FOR SEQ ID NO:667:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...75

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:667

Val	Ala	Leu	Thr	Leu	Gly	Ala	Arg	Gly	Gly	Val	Tyr	Leu	Cys	Gly	Gly
1						5				10			15		
Ile	Ile	Pro	Arg	Phe	Ile	Asp	Tyr	Phe	Lys	Thr	Ser	Pro	Phe	Arg	Ala
							20			25			30		
Arg	Phe	Glu	Thr	Lys	Gly	Arg	Met	Gly	Ala	Phe	Leu	Ala	Ser	Ile	Pro
							35			40			45		
Val	His	Val	Val	Met	Lys	Lys	Thr	Pro	Gly	Leu	Asp	Gly	Ala	Gly	Ile
							50			55			60		
Ala	Leu	Glu	Asn	Tyr	Leu	Leu	His	Asp	Arg	Ile					
							65			70			75		

## (2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 421 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668

Met	Lys	Gly	Leu	Thr	Met	Lys	Lys	Leu	Val	Phe	Ser	Met	Leu	Leu	Cys
1															15
Cys	Lys	Ser	Val	Phe	Ala	Glu	Gly	Glu	Thr	Pro	Leu	Ile	Val	Asn	Asp
															30
Pro	Glu	Thr	His	Val	Ser	Gln	Ala	Thr	Ile	Ile	Gly	Lys	Met	Val	Asp
															45
Ser	Ile	Lys	Arg	Tyr	Glu	Glu	Ile	Ile	Ser	Lys	Ala	Gln	Ala	Gln	Val
															50
															60
Asn	Gln	Leu	Gln	Lys	Val	Asn	Asn	Met	Ile	Asn	Thr	Thr	Asn	Ser	Leu
															65
															80
Ile	Ser	Ser	Ser	Ala	Ile	Thr	Leu	Ala	Asn	Pro	Met	Gln	Val	Leu	Gln
															85
															95
Asn	Ala	Gln	Tyr	Gln	Ile	Glu	Ile	Ile	Ser	Lys	Ala	Gln	Ala	Gln	Val
															100
															110
Lys	Gln	Ser	Ile	Glu	Asn	Trp	Asn	Ala	Gln	Asn	Leu	Leu	Arg	Asn	Lys
															115
															125
Tyr	Leu	Gln	Gln	Cys	Pro	Trp	Leu	Asn	Val	Asn	Ala	Leu	Thr	Asn	
															130
															140
Asn	Lys	Ile	Val	Asn	Leu	Lys	Asp	Leu	Asn	Asn	Ile	Thr	Lys	Asn	
															145
															155
Gly	Glu	Gln	Thr	Gln	Thr	Ala	Arg	Asp	Val	Gln	Asn	Leu	Ile	Gln	Ser
															160
															165
Ile	Ser	Gly	Ser	Gly	Tyr	Gly	Asn	Met	Gln	Ser	Leu	Ala	Gly	Glu	Leu
															180
															185
Ser	Gly	Arg	Ala	Trp	Gly	Glu	Met	Leu	Cys	Lys	Met	Val	Asn	Asp	Ser
															195
															205
Asn	Tyr	Glu	Ser	Glu	Gln	Ala	Leu	Leu	Ala	Thr	Gly	Asn	Asn	Pro	Glu
															210
															215
															220
Glu	Gln	Lys	Arg	Arg	Phe	Leu	Leu	Arg	Val	Lys	Lys	Lys	Val	Asn	Asp
															225
															230
Asn	Lys	Gln	Leu	Lys	Asp	Lys	Leu	Asp	Pro	Phe	Leu	Lys	Arg	Leu	Asp
															245
															250
Val	Leu	Gln	Thr	Glu	Phe	Gly	Val	Thr	Asp	Pro	Thr	Ala	Asn	His	Asn
															260
															265
Lys	Gln	Gly	Ile	His	Tyr	Cys	Thr	Glu	Asn	Lys	Glu	Thr	Gly	Lys	Cys
															275
															280
Asp	Pro	Ile	Lys	Asn	Val	Phe	Arg	Thr	Arg	Leu	Asp	Asn	Glu	Leu	
															290
															295
Glu	Gln	Glu	Ile	Gln	Thr	Leu	Thr	Leu	Asp	Leu	Ile	Lys	Ala	Ser	Asn
															305
															310
Lys	Asp	Ala	Gln	Ser	Gln	Ala	Tyr	Ala	Asn	Phe	Asn	Gln	Arg	Ile	Lys
															325
															330
Leu	Leu	Thr	Leu	Lys	Tyr	Leu	Lys	Glu	Ile	Thr	Asn	Gln	Met	Leu	Phe
															340
															345
Leu	Asn	Gln	Thr	Met	Ala	Met	Gln	Ser	Glu	Ile	Met	Thr	Asp	Asp	Tyr
															350

557

355	360	365
Phe Arg Gln Asn Asn Asp Gly	Phe Gly Glu Lys Glu Asn His Ile Asp	
370	375	380
Glu Gln Leu Thr Gln Lys Arg Ile Asn Glu Arg Glu Arg Ala Arg Ile		
385	390	395
Tyr Phe Gln Asn Pro Asn Val Lys Phe Asp Gln Phe Gly Phe Pro Ile		400
405	410	415
Phe Ser Ile Trp Asp		
420		

## (2) INFORMATION FOR SEQ ID NO:669:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669

Met Ser Val Asn Leu Leu Glu Leu Leu Lys Leu Ala Val Pro Leu Ala			
1	5	10	15
Val Ile Leu Ser Val Gln Val Ala Val Met Ile Leu Tyr Val Val Leu			
20	25	30	
Val Thr Phe Arg Val Cys Gly Lys Asp Tyr Asp Ala Ala Val Leu Cys			
35	40	45	
Ala Gly His Cys Gly Phe Gly Leu Gly Ala Thr Pro Thr Ala Met Val			
50	55	60	
Asn Met Gln Thr Ile Thr Asn His Tyr Gly Pro Ser His Val Ala Phe			
65	70	75	80
Ile			

## (2) INFORMATION FOR SEQ ID NO:670:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670

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Met Gln Leu Ser Pro Leu Gln Ser Ala Leu Leu Tyr Phe Arg Tyr Phe		
1	5	10
Ile Tyr Pro Glu Lys Lys Thr Arg Ser Phe Asp Leu Ser Asp Leu Ile		15
20	25	30
Phe Ile Val Met Val Phe Leu Val Leu Ala Leu Gly Leu Leu Met Ser		
35	40	45
Glu Glu Ile Ser Ile Ser Tyr Asn Glu Ala Lys Asp Phe Phe Tyr Ser		
50	55	60
Asp Ala Trp Phe Val Lys Ile Ala Gln Lys Ser Val Ala Ile Leu Arg		
65	70	75
Pro Lys Arg Phe Gly Phe Lys Ile Ala Phe Phe Asp Arg Ser Arg His		80
85	90	95
Gln His Val Phe Ile Leu Pro His Arg Ala Lys Asp Phe Lys Lys Ala		
100	105	110

## (2) INFORMATION FOR SEQ ID NO:671:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...325

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:671

Leu Ala Gly Leu Unk Val Gly Cys Unk Arg Met Lys Gln Thr Phe Trp		
1	5	10
Unk Leu Ser Trp Gly Glu Lys Ser Gln Lys Val Cys Val His Arg Pro		15
20	25	30
Trp Tyr Ala Ile Trp Ser Cys Asp Lys Trp Glu Glu Lys Thr Gln Gln		
35	40	45
Phe Thr Gly Asn Gln Leu Ile Thr Lys Thr Trp Ala Gly Gly Asn Ala		
50	55	60
Ala Asn Tyr Tyr His Ser Gln Asn Asn Gln Asp Ile Thr Ala Asn Leu		
65	70	75
Lys Asn Asp Asn Gly Thr Tyr Phe Leu Ser Gly Leu Tyr Asn Tyr Thr		80
85	90	95
Gly Gly Glu Tyr Asn Gly Gly Asn Leu Asp Ile Glu Leu Gly Ser Asn		
100	105	110
Ala Thr Phe Asn Leu Gly Ala Ser Ser Gly Asn Ser Phe Thr Ser Trp		
115	120	125
Tyr Pro Asn Gly His Thr Asp Val Thr Phe Ser Ala Gly Thr Ile Asn		
130	135	140
Val Asn Asn Ser Val Glu Val Gly Asn Arg Val Gly Ser Gly Ala Gly		
145	150	155
Thr His Thr Gly Thr Ala Thr Leu Asn Leu Asn Ala Asn Lys Val Thr		160
165	170	175
Ile Asn Ser Asn Ile Ser Ala Tyr Lys Thr Ser Gln Val Asn Val Gly		
180	185	190
Asn Ala Asn Ser Val Ile Thr Ile Asn Ser Val Ser Leu Asn Gly Glu		
195	200	205
Thr Cys Unk Ser Leu Ala Arg Val Gly Val Gly Ala Asn Cys Ser Thr		
210	215	220
Ser Gly Pro Ser Tyr Ser Phe Lys Gly Thr Thr Asn Ala Thr Asn Thr		

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225	230	235	240
Thr Phe Ser Unk Ser Ser Gly Ser Phe Thr Phe Glu Glu Asn Ala Thr			
245	250	255	
Phe Ser Gly Ala Lys Leu Asn Gly Gly Ala Phe Thr Phe Asn Lys Lys			
260	265	270	
Phe Asn Ala Thr Asn Asn Thr Ala Phe Asn Ser Gly Ser Phe Thr Phe			
275	280	285	
Lys Gly Thr Ser Ser Phe Asn Gly Ala Asn Phe Ser Asn Ala Ser Tyr			
290	295	300	
Thr Phe Asn Asn Gln Ala Thr Phe Gln Asn Ser Ser Phe Asn Gly Gly			
305	310	315	320
Thr Phe Thr Phe Asn			
	325		

## (2) INFORMATION FOR SEQ ID NO:671:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671

Leu Ala Gly Leu Unk Val Gly Cys Unk Arg Met Lys Gln Thr Phe Trp			
1	5	10	15
Unk Leu Ser Trp Gly Glu Lys Ser Gln Lys Val Cys Val His Arg Pro			
20	25	30	
Trp Tyr Ala Ile Trp Ser Cys Asp Lys Trp Glu Glu Lys Thr Gln Gln			
35	40	45	
Phe Thr Gly Asn Gln Leu Ile Thr Lys Thr Trp Ala Gly Gly Asn Ala			
50	55	60	
Ala Asn Tyr Tyr His Ser Gln Asn Asn Gln Asp Ile Thr Ala Asn Leu			
65	70	75	80
Lys Asn Asp Asn Gly Thr Tyr Phe Leu Ser Gly Leu Tyr Asn Tyr Thr			
85	90	95	
Gly Gly Glu Tyr Asn Gly Gly Asn Leu Asp Ile Glu Leu Gly Ser Asn			
100	105	110	
Ala Thr Phe Asn Leu Gly Ala Ser Ser Gly Asn Ser Phe Thr Ser Trp			
115	120	125	
Tyr Pro Asn Gly His Thr Asp Val Thr Phe Ser Ala Gly Thr Ile Asn			
130	135	140	
Val Asn Asn Ser Val Glu Val Gly Asn Arg Val Gly Ser Gly Ala Gly			
145	150	155	160
Thr His Thr Gly Thr Ala Thr Leu Asn Leu Asn Ala Asn Lys Val Thr			
165	170	175	
Ile Asn Ser Asn Ile Ser Ala Tyr Lys Thr Ser Gln Val Asn Val Gly			
180	185	190	
Asn Ala Asn Ser Val Ile Thr Ile Asn Ser Val Ser Leu Asn Gly Glu			
195	200	205	
Thr Cys Unk Ser Leu Ala Arg Val Gly Val Gly Ala Asn Cys Ser Thr			
210	215	220	
Ser Gly Pro Ser Tyr Ser Phe Lys Gly Thr Thr Asn Ala Thr Asn Thr			
225	230	235	240

560

Thr Phe Ser Unk Ser Ser Gly Ser Phe Thr Phe Glu Glu Asn Ala Thr  
 245 250 255  
 Phe Ser Gly Ala Lys Leu Asn Gly Gly Ala Phe Thr Phe Asn Lys Lys  
 260 265 270  
 Phe Asn Ala Thr Asn Asn Thr Ala Phe Asn Ser Gly Ser Phe Thr Phe  
 275 280 285  
 Lys Gly Thr Ser Ser Phe Asn Gly Ala Asn Phe Ser Asn Ala Ser Tyr  
 290 295 300  
 Thr Phe Asn Asn Gln Ala Thr Phe Gln Asn Ser Ser Phe Asn Gly Gly  
 305 310 315 320  
 Thr Phe Thr Phe Asn  
 325

## (2) INFORMATION FOR SEQ ID NO:672:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...271

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:672

Leu Leu Ser Leu Val Lys Gly Lys Thr Met Leu Arg Ser Leu Tyr Ser  
 1 5 10 15  
 Ala Thr Ser Gly Met Leu Ala Gln Gln Thr His Ile Asp Thr Thr Ser  
 20 25 30  
 Asn Asn Ile Ala Asn Val Asn Thr Thr Gly Phe Lys Lys Ser Arg Ala  
 35 40 45  
 Asp Phe Asn Asp Leu Phe Tyr Gln Ala Met Gln Tyr Ala Gly Thr Asn  
 50 55 60  
 Thr Ser Asn Thr Thr Leu Ser Pro Asp Gly Met Glu Val Gly Leu Gly  
 65 70 75 80  
 Val Arg Pro Ser Ala Ile Thr Lys Met Phe Ser Gln Gly Ser Pro Lys  
 85 90 95  
 Glu Thr Glu Asn Asn Leu Asp Ile Ala Ile Thr Gly Lys Gly Phe Phe  
 100 105 110  
 Gln Val Gln Leu Pro Asp Gly Thr Thr Ala Tyr Thr Arg Ser Gly Asn  
 115 120 125  
 Phe Lys Leu Asp Glu Gln Gly Asn Leu Val Thr Ser Glu Gly Tyr Leu  
 130 135 140  
 Leu Ile Pro Gln Ile Thr Leu Pro Glu Asp Thr Thr Gln Val Asn Ile  
 145 150 155 160  
 Gly Val Asp Gly Thr Val Ser Val Thr Gln Gly Leu Gln Thr Thr Ser  
 165 170 175  
 Asn Val Ile Gly Gln Ile Thr Leu Ala Asn Phe Val Asn Pro Ala Gly  
 180 185 190  
 Leu His Ser Met Gly Asp Asn Leu Phe Ser Ile Thr Asn Ala Ser Gly  
 195 200 205  
 Asp Ala Ile Val Gly Asn Pro Asp Ser Gln Gly Leu Gly Lys Leu Arg  
 210 215 220  
 Gln Gly Phe Leu Glu Leu Ser Asn Val Arg Leu Val Glu Glu Met Thr  
 225 230 235 240  
 Asp Leu Ile Thr Ala Gln Arg Ala Tyr Glu Ala Asn Ser Lys Ser Ile

245	250	255
Gln Thr Ala Asp Ala Met Leu Gln	Thr Val Asn Ser Leu Lys Arg	
260	265	270

(2) INFORMATION FOR SEQ ID NO:672:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 271 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - ii) MOLECULE TYPE: protein
  - iii) HYPOTHETICAL: YES
  - vi) ORIGINAL SOURCE:
    - (A) ORGANISM: Helicobacter pylori
  - ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION 1...271
  - xii) SEQUENCE DESCRIPTION: SEQ ID NO:673

Leu	Leu	Ser	Leu	Val	Lys	Gly	Lys	Thr	Met	Leu	Arg	Ser	Leu	Tyr	Ser
1				5					10					15	
Ala	Thr	Ser	Gly	Met	Leu	Ala	Gln	Gln	Thr	His	Ile	Asp	Thr	Thr	Ser
						20			25					30	
Asn	Asn	Ile	Ala	Asn	Val	Asn	Thr	Thr	Gly	Phe	Lys	Lys	Ser	Arg	Ala
						35		40				45			
Asp	Phe	Asn	Asp	Leu	Phe	Tyr	Gln	Ala	Met	Gln	Tyr	Ala	Gly	Thr	Asn
						50		55			60				
Thr	Ser	Asn	Thr	Thr	Leu	Ser	Pro	Asp	Gly	Met	Glu	Val	Gly	Leu	Gly
						65		70		75				80	
Val	Arg	Pro	Ser	Ala	Ile	Thr	Lys	Met	Phe	Ser	Gln	Gly	Ser	Pro	Lys
						85			90				95		
Glu	Thr	Glu	Asn	Asn	Leu	Asp	Ile	Ala	Ile	Thr	Gly	Lys	Gly	Phe	Phe
						100			105				110		
Gln	Val	Gln	Leu	Pro	Asp	Gly	Thr	Thr	Ala	Tyr	Thr	Arg	Ser	Gly	Asn
						115			120			125			
Phe	Lys	Leu	Asp	Glu	Gln	Gly	Asn	Leu	Val	Thr	Ser	Glu	Gly	Tyr	Leu
						130		135			140				
Leu	Ile	Pro	Gln	Ile	Thr	Leu	Pro	Glu	Asp	Thr	Thr	Gln	Val	Asn	Ile
						145		150		155				160	
Gly	Val	Asp	Gly	Thr	Val	Ser	Val	Thr	Gln	Gly	Leu	Gln	Thr	Thr	Ser
						165			170				175		
Asn	Val	Ile	Gly	Gln	Ile	Thr	Leu	Ala	Asn	Phe	Val	Asn	Pro	Ala	Gly
						180			185			190			
Leu	His	Ser	Met	Gly	Asp	Asn	Leu	Phe	Ser	Ile	Thr	Asn	Ala	Ser	Gly
						195		200			205				
Asp	Ala	Ile	Val	Gly	Asn	Pro	Asp	Ser	Gln	Gly	Leu	Gly	Lys	Leu	Arg
						210		215			220				
Gln	Gly	Phe	Leu	Glu	Leu	Ser	Asn	Val	Arg	Leu	Val	Glu	Glu	Met	Thr
						225		230			235			240	
Asp	Leu	Ile	Thr	Ala	Gln	Arg	Ala	Tyr	Glu	Ala	Asn	Ser	Lys	Ser	Ile
						245			250			255			
Gln	Thr	Ala	Asp	Ala	Met	Leu	Gln	Thr	Val	Asn	Ser	Leu	Lys	Arg	
						260			265			270			

(2) INFORMATION FOR SEQ ID NO:673:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 78 amino acids

562

(B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673

Val	Tyr	Ala	Leu	Met	Val	Ala	Phe	Phe	Ala	Tyr	Met	Ser	Tyr	Cys	Leu
1				5						10				15	
Gly	Tyr	Gln	Phe	Ser	Lys	Phe	Val	Ser	Lys	Asn	Asn	Ile	Ser	Ser	Leu
				20				25				30			
Ser	Ser	Leu	Leu	Ser	Ser	Cys	Val	Arg	Val	Val	Ser	Val	Leu	Ile	Leu
				35				40				45			
Ser	Leu	Ser	Leu	Glu	Leu	Arg	Tyr	Phe	Ser	Pro	Leu	Thr	Ile	Ile	
				50			55			60					
Thr	Met	His	Phe	Ala	Leu	Thr	Leu	Ile	Ile	Leu	Phe	Phe	Phe		
	65				70					75					

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674

Met	Arg	Ser	Trp	Met	Lys	Lys	Tyr	Phe	Thr	Leu	Leu	Gln	Ser			
1				5				10				15				
Ser	Val	Val	Leu	Ala	Val	Phe	Ile	Gly	Cys	Ser	Ser	Thr	Arg	Asn	His	
				20			25					30				
Thr	Phe	Ser	Ala	Leu	Ser	Asn	Gln	Glu	Asn	Thr	Asp	Asp	Lys	Leu	Pro	
				35			40					45				
Val	Val	His	Ser	Ile	Lys	Thr	Ile	Asn	Asp	Val	Ser	Ser	Val	Gly	Phe	
				50			55					60				
Glu	Trp	Ser	Lys	Val	Ala	Asp	Thr	Tyr	Asp	Ile	Asp	Gly	Phe	Val	Leu	
	65				70			75				80				
Tyr	Arg	Leu	Lys	Lys	Asp	Ser	Lys	Leu	Lys	Arg	Ile	Ala	Thr	Ile	Lys	
				85			90					95				
Asn	Pro	Tyr	Ala	Thr	His	Tyr	Tyr	Asp	Glu	Gly	Leu	Glu	Thr	Glu	Ser	
	100				105							110				
Ser	Tyr	Thr	Tyr	Gln	Leu	Ala	Thr	Tyr	Lys	Gly	Asp	Lys	Ile	Ser	Lys	
	115				120							125				
Leu	Ser	Glu	Pro	Ile	Leu	Val	Lys	Thr	Ser	Phe	Ile	Asn	Pro	Val	Glu	

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130	135	140
Ser Val Phe Ala Ser Leu Glu Tyr Pro Lys Ser Val Lys Val Phe Trp		
145	150	155
Ser Pro His Pro Asn Pro Ser Val Ser Lys Tyr Ile Ile Gln Arg Gln		160
165	170	175
Asn Lys Asp Gly Lys Phe Leu Asn Val Gly Ala Val Lys Asn Arg Leu		
180	185	190
Phe Val Glu Phe Phe Asp Lys Asp Leu Glu Asp Gly Gln Lys Tyr Arg		
195	200	205
Tyr Gln Ile Ile Ala Glu Asn Phe Met Gly Asp Lys Ser Arg Pro Ser		
210	215	220
Val Ile Val Glu Gly Lys Thr Lys Asp Leu Pro Lys Glu Ile Ala Asn		
225	230	235
Val Arg Val Ser Gln Asn Leu Thr Arg Gln Ile Glu Leu Ser Trp Asp		240
245	250	255
Lys Ser Pro Glu Glu Asp Val Ile Ala Tyr Arg Ile Tyr Ala Ser Asn		
260	265	270
Asn Arg Asn Asp Lys Tyr Lys Phe Ile Ala Gln Thr Thr Asn Thr Ser		
275	280	285
Tyr Val Asp Lys Ile Glu Lys Asp Asn Leu Thr Arg Tyr Tyr Lys Val		
290	295	300
Val Ala Val Asp Lys Thr His Leu Glu Gly Ala Leu Pro Lys Glu Pro		
305	310	315
Ala Met Gly Glu Thr Ser Asp Arg Pro Glu Ala Pro Ile Ile Thr Lys		320
325	330	335
Gly Thr Ile Gln Asp Ser Ser Ala Leu Ile Gln Trp Glu Asn Asn Pro		
340	345	350
Ser Pro Lys Ile Ala Thr Tyr Ala Val Tyr Arg Phe Glu Ala Asn Ser		
355	360	365
Lys Thr Pro Leu Arg Phe Gly Asn Ile Thr Gln Asn Gln Phe Val Asp		
370	375	380
Lys Asp Met Lys Val Gly Val Ala Tyr Arg Tyr Gln Val Val Ser Val		
385	390	395
		400

## (2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675

Met Gln Asn Gly Tyr Tyr Ala Ala Thr Gly Ala Met Ala Thr Gln Phe		
1	5	10
Asn Arg Leu Asp Leu Thr Ser Asn Asn Leu Ala Asn Leu Asn Thr Asn		15
20	25	30
Gly Phe Lys Arg Asp Asp Ala Ile Thr Gly Asp Phe Leu Arg Leu Tyr		
35	40	45
Gln Glu Tyr Arg Glu Gln Leu Pro Leu Glu Asp Gln Thr Lys Ala Ser		
50	55	60
Ala Lys Tyr Leu Asn Arg Unk Leu Asn Arg Val Pro Ile Leu Ser Unk		
65	70	75
		80

564

Ile Tyr Thr Unk Arg Unk Leu Gly Unk Val  
 85   90

## (2) INFORMATION FOR SEQ ID NO:675:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...90

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:675

Met Gln Asn Gly Tyr Tyr Ala Ala Thr Gly Ala Met Ala Thr Gln Phe  
 1                         5                     10                     15  
 Asn Arg Leu Asp Leu Thr Ser Asn Asn Leu Ala Asn Leu Asn Thr Asn  
 20                         25                     30  
 Gly Phe Lys Arg Asp Asp Ala Ile Thr Gly Asp Phe Leu Arg Leu Tyr  
 35                         40                     45  
 Gln Glu Tyr Arg Glu Glu Gln Leu Pro Leu Glu Asp Gln Thr Lys Ala Ser  
 50                         55                     60  
 Ala Lys Tyr Leu Asn Arg Unk Leu Asn Arg Val Pro Ile Leu Ser Unk  
 65                         70                     75                     80  
 Ile Tyr Thr Unk Arg Unk Leu Gly Unk Val  
 85                         90

## (2) INFORMATION FOR SEQ ID NO:676:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...126

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:676

Met Leu Pro Thr Lys Thr Arg Ile Arg Asp Pro Asn Lys Gln Glu Leu  
 1                         5                     10                     15  
 Thr Gln Pro Lys Ile Lys Gly Leu Ser Met Gly Lys Ile Leu Ala Ser  
 20                         25                     30  
 Leu Leu Gly Gly Gly Thr Asn Leu Phe Thr Gly Leu Ser Ser Asp Leu  
 35                         40                     45  
 Phe Ser Met Ile Leu Asn Phe Leu Phe Phe Leu Met Leu Met Met Gly

565

50	55	60
Leu Asn Glu Ala Leu Gly Lys Lys Phe Asn Leu Pro Met Asp Asn Ile		
65	70	75
Lys Asn Phe Met Ala Glu Val Leu Lys Asn Gly Phe Asp Ser Ile Lys		80
85	90	95
Asn Met Gly Ser Ala Leu Val Gly Asn Gly Phe Gly Ser Ser Lys Ser		
100	105	110
Asp Lys Thr Thr Asn Lys Met Ser Val Pro Gln Val Arg Leu		
115	120	125

## (2) INFORMATION FOR SEQ ID NO:677:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...195

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:677

Val	Gly	Ala	Met	Pro	Thr	Ile	Gln	Ile	Arg	Unk	Phe	Gly	Ala	Gly	Gly
1															15
Ser	Gly	His	Ser	Asp	Ala	Thr	Leu	Met	Leu	Val	Asn	Gly	Ile	Pro	Val
20															30
Tyr	Met	Ala	Pro	Tyr	Ala	His	Ile	Glu	Leu	Asp	Ile	Phe	Pro	Val	Thr
35															45
Phe	Gln	Ala	Ile	Asp	Arg	Ile	Asp	Val	Ile	Lys	Gly	Gly	Ser	Val	
50															60
Gln	Tyr	Gly	Pro	Asn	Thr	Tyr	Gly	Ile	Val	Asn	Ile	Ile	Thr	Lys	
65															80
Pro	Ile	Pro	Asn	Gln	Trp	Glu	Asn	Gln	Ala	Ala	Glu	Arg	Unk	Thr	Tyr
85															95
Trp	Ala	Lys	Ala	Arg	Asn	Ala	Gly	Phe	Ala	Ala	Pro	Unk	Asp	Lys	Thr
100															110
Gly	Asp	Pro	Ser	Phe	Ile	Lys	Ser	Leu	Gly	Asn	Asn	Leu	Leu	Tyr	Asn
115															125
Thr	Tyr	Val	Arg	Ser	Gly	Gly	Met	Ile	Asn	Lys	His	Val	Gly	Ile	Gln
130															140
Arg	Lys	Leu	Thr	Gly	Leu	Glu	Ala	Lys	Ala	Leu	Gly	Thr	Ile	Ala	Pro
145															160
Leu	Val	Phe	Gln	Thr	Ile	Gly	Trp	Met	Gly	Ser	Met	Thr	Ser	Met	Lys
165															175
Ala	Met	Gly	Leu	Lys	Pro	Ile	Thr	Asn	Thr	Thr	Ile	Leu	Ala	Ile	Unk
180															190
Gln	Pro	Gly													
195															

## (2) INFORMATION FOR SEQ ID NO:677:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677

Val	Gly	Ala	Met	Pro	Thr	Ile	Gln	Ile	Arg	Unk	Phe	Gly	Ala	Gly	Gly
1							5			10			15		
Ser	Gly	His	Ser	Asp	Ala	Thr	Leu	Met	Leu	Val	Asn	Gly	Ile	Pro	Val
							20			25			30		
Tyr	Met	Ala	Pro	Tyr	Ala	His	Ile	Glu	Leu	Asp	Ile	Phe	Pro	Val	Thr
							35			40			45		
Phe	Gln	Ala	Ile	Asp	Arg	Ile	Asp	Val	Ile	Lys	Gly	Gly	Gly	Ser	Val
							50			55			60		
Gln	Tyr	Gly	Pro	Asn	Thr	Tyr	Gly	Gly	Ile	Val	Asn	Ile	Ile	Thr	Lys
							65			70			75		80
Pro	Ile	Pro	Asn	Gln	Trp	Glu	Asn	Gln	Ala	Ala	Glu	Arg	Unk	Thr	Tyr
							85			90			95		
Trp	Ala	Lys	Ala	Arg	Asn	Ala	Gly	Phe	Ala	Ala	Pro	Unk	Asp	Lys	Thr
							100			105			110		
Gly	Asp	Pro	Ser	Phe	Ile	Lys	Ser	Leu	Gly	Asn	Asn	Leu	Leu	Tyr	Asn
							115			120			125		
Thr	Tyr	Val	Arg	Ser	Gly	Gly	Met	Ile	Asn	Lys	His	Val	Gly	Ile	Gln
							130			135			140		
Arg	Lys	Leu	Thr	Gly	Leu	Glu	Ala	Lys	Ala	Leu	Gly	Thr	Ile	Ala	Pro
							145			150			155		160
Leu	Val	Phe	Gln	Thr	Ile	Gly	Trp	Met	Gly	Ser	Met	Thr	Ser	Met	Lys
							165			170			175		
Ala	Met	Gly	Leu	Lys	Pro	Ile	Thr	Asn	Thr	Thr	Ile	Leu	Ala	Ile	Unk
							180			185			190		
Gln	Pro	Gly													
		195													

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678

Met	Ala	Asn	Met	Met	Ala	Ala	Ala	Met	Leu	Gly	Ile	Asp	Ser	Cys
1							5			10			15	
Pro	Ile	Glu	Gly	Tyr	Asp	Gln	Glu	Lys	Val	Glu	Ala	Tyr	Leu	Glu

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Lys	Gly	Tyr	Leu	Asn	Thr	Ala	Glu	Phe	Gly	Val	Ser	Val	Met	Ala	Ser
35							40						45		
Phe	Gly	Tyr	Arg	Asn	Gln	Glu	Ile	Thr	Pro	Lys	Thr	Arg	Trp	Lys	Thr
50							55					60			
Glu	Val	Ile	Tyr	Glu	Val	Ile	Glu								
65							70								

## (2) INFORMATION FOR SEQ ID NO:679:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...111

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:679

Met	Ala	Gly	Leu	Val	Leu	Met	Val	Leu	Leu	Ala	Ser	Tyr	Glu	Ser	Phe
1						5			10				15		
Val	Ser	Lys	Leu	Asp	Lys	Val	Asp	Ala	Ser	Glu	Ile	Thr	Trp	Leu	Lys
						20			25				30		
His	Thr	Asp	Phe	Asn	Ala	Leu	Lys	Leu	Lys	Val	Ser	Leu	Ser	Ile	Val
						35			40				45		
Ala	Ile	Ser	Ala	Ile	Phe	Leu	Leu	Lys	Arg	Tyr	Met	Ser	Leu	Glu	Asp
						50			55				60		
Val	Leu	Ser	Ser	Ile	Pro	Lys	Asp	Thr	Pro	Leu	Ser	His	Asn	Pro	Ile
						65			70				75		80
Phe	Trp	Gln	Val	Val	Ile	His	Leu	Val	Phe	Val	Cys	Ser	Ala	Leu	Leu
						85			90				95		
Thr	Ala	Val	Thr	Asn	Asn	Ile	Ala	Phe	Ser	Gln	Lys	Glu	Arg	His	
						100			105				110		

## (2) INFORMATION FOR SEQ ID NO:680:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...142

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:680

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Met Ile Thr Ile Val Ile Ala Lys Ala Gly Asn Ile Val Lys Unk Asp  
 1               5               10               15  
 Ile Phe Thr His Ile Ser Asp Ile Lys Met Gly Leu Ile Lys Gly Gly  
 20              25              30  
 Gln Trp Gly Val Ile Gly Leu Gly Asn Ile Gly Lys Arg Val Ala Lys  
 35              40              45  
 Leu Ala Gln Ala Phe Gly Ala Lys Val Val Tyr Phe Ser Pro Lys Asp  
 50              55              60  
 Lys Lys Glu Glu Tyr Glu Arg Leu Ser Leu Glu Glu Leu Leu Lys Thr  
 65              70              75              80  
 Ser Gly Ile Ile Ser Ile His Ala Pro Leu Asn Glu Ser Thr Arg Asp  
 85              90              95  
 Leu Ile Ala Leu Lys Glu Leu Gln Ser Leu Lys Asp Gly Ala Ile Leu  
 100            105            110  
 Ile Asn Val Gly Arg Gly Gly Ile Val Asn Glu Lys Unk Leu Ala Unk  
 115            120            125  
 Unk Leu Glu Thr Thr Asp Leu Tyr Tyr Ala Ser Asp Val Phe  
 130            135            140

## (2) INFORMATION FOR SEQ ID NO:681:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681

Val Asn Phe Asn Ala Lys Asn Ile Ser Ile Asp Asn Leu Val Glu Ile  
 1               5               10               15  
 Asn Asn Arg Val Gly Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val  
 20              25              30  
 Leu Thr Leu Gln Ala Ser Glu Gly Ile Thr Unk Ser Lys Asn Ala Glu  
 35              40              45  
 Ile Ser Leu Tyr Asp Gly Ala Thr Unk Ile Trp Leu Gln Thr Gly  
 50              55              60

## (2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 310 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...310

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:682

```

Met Arg Thr Leu Ile Leu Ser Leu Leu Lys His Ala Ile Leu Met Gly
1      5          10        15
Met Leu Leu Lys Glu Cys Gln Glu Lys Leu Lys Arg Ser Leu Asn Leu
20     25          30
Ser Ala Asn His Cys Val Leu Ser Ala Gly Tyr Gly Ala Ser Ser Ala
35     40          45
Ile Lys Lys Phe Gln Glu Ile Leu Gly Val Cys Ile Pro Ser Lys Thr
50     55          60
Lys Lys Asn Leu Glu Pro Tyr Leu Lys Asp Met Ala Leu Lys Arg Val
65     70          75        80
Ile Val Gly Pro Tyr Glu His His Ser Asn Glu Val Ser Trp Arg Glu
85     90          95
Gly Leu Cys Glu Val Val Arg Ile Pro Leu Asn Glu His Gly Leu Leu
100    105         110
Asp Leu Glu Ile Leu Glu Gln Thr Leu Lys Lys Thr Pro Asn Ser Leu
115    120         125
Val Ser Val Ser Ala Ala Ser Asn Val Thr Gly Ile Leu Thr Pro Leu
130    135         140
Lys Glu Val Ser Ser Leu Cys Lys Glu Tyr Arg Ala Ile Leu Ala Leu
145    150         155        160
Asp Leu Ala Asn Phe Ser Ala His Ala Asn Pro Lys Asp Cys Glu Tyr
165    170         175
Gln Thr Gly Phe Tyr Ala Pro His Lys Leu Leu Gly Gly Val Gly Gly
180    185         190
Cys Gly Leu Leu Gly Ile Ser Lys Asp Leu Ile Asp Thr Gln Ile Pro
195    200         205
Thr Ser Phe Ser Ala Gly Gly Val Ile Lys Tyr Ala Asn Arg Thr Arg
210    215         220
His Glu Phe Ile Asp Glu Leu Pro Leu Arg Glu Glu Phe Gly Thr Pro
225    230         235        240
Gly Leu Leu Gln Phe Tyr Arg Ser Ala Leu Ala Tyr Gln Leu Arg Asp
245    250         255
Glu Cys Gly Leu Asp Phe Ile His Lys Lys Glu Asn Asn Leu Leu Arg
260    265         270
Val Leu Val Tyr Gly Leu Lys Asp Leu Pro Ala Ile Asn Ile Tyr Gly
275    280         285
Asn Leu Thr Ala Ser Arg Val Gly Val Val Thr Phe Asn Ile Gly Gly
290    295         300
Ile Ser Pro Tyr Asp Leu
305    310

```

## (2) INFORMATION FOR SEQ ID NO:683:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 169 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...169

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683

(2) INFORMATION FOR SEQ ID NO:684:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 84 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684

(2) INFORMATION FOR SEQ ID NO:684:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 84 amino acids  
    (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684

Met	Arg	Unk	Glu	Lys	Ile	Met	Thr	Asn	Phe	Glu	Lys	Unk	Ile	Ala	Gln
1			5						10					15	
Asn	Arg	Leu	Lys	Thr	Asn	Ala	Val	Leu	Thr	Thr	Tyr	Cys	Ala	Ile	Phe
			20					25					30		
Ala	Phe	Ile	Gly	Leu	Leu	Val	Asp	Ala	Ile	Arg	Ile	Asn	Ala	Asn	Asp
			35				40				45				
Leu	Gly	Ile	Ala	Leu	Phe	Lys	Leu	Met	Thr	Phe	Gln	Ile	Phe	Pro	Thr
			50				55			60					
Unk	Thr	Ile	Val	Met	Phe	Val	Val	Ala	Phe	Val	Ile	Unk	Unk	Ser	Leu
			65			70			75				80		
Tyr	Pro	Lys	Phe												

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685

Met	Unk	Met	Ser	His	Ile	Ile	Lys	Ser	Ile	Glu	Ala	Leu	Asp	Asp	Tyr
1					5				10				15		
Thr	Ile	Arg	Phe	Thr	Leu	Asn	Gly	Pro	Glu	Ala	Pro	Phe	Leu	Ala	Asn
					20			25			30				
Leu	Gly	Met	Asp	Phe	Leu	Ser	Ile	Leu	Ser	Lys	Asp	Tyr	Ala	Asp	Tyr
					35			40			45				
Leu	Ala	Gln	Asn	Asn	Lys	Lys	Asp	Glu	Leu	Ala	Lys	Unk	Pro	Val	Gly
					50			55			60				
Thr	Gly	Pro	Phe	Lys	Phe	Phe	Leu	Trp	Asn	Lys	Arg				
					65			70			75				

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685

Met	Unk	Met	Ser	His	Ile	Ile	Lys	Ser	Ile	Glu	Ala	Leu	Asp	Asp	Tyr
														15	
1															
															10
Thr	Ile	Arg	Phe	Thr	Leu	Asn	Gly	Pro	Glu	Ala	Pro	Phe	Leu	Ala	Asn
															30
															20
															25
Leu	Gly	Met	Asp	Phe	Leu	Ser	Ile	Leu	Ser	Lys	Asp	Tyr	Ala	Asp	Tyr
															45
															35
															40
Leu	Ala	Gln	Asn	Asn	Lys	Lys	Asp	Glu	Leu	Ala	Lys	Unk	Pro	Val	Gly
															50
															55
Thr	Gly	Pro	Phe	Lys	Phe	Phe	Leu	Trp	Asn	Lys	Arg				
															60
65															70
															75

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 196 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686

Leu	Met	Arg	Lys	Ile	Phe	Ser	Tyr	Ile	Ser	Lys	Val	Leu	Leu	Phe	Ile
1															15
															10
Gly	Val	Val	Tyr	Ala	Glu	Pro	Asp	Ser	Lys	Val	Glu	Ala	Leu	Glu	Gly
															30
20															25
Arg	Lys	Gln	Glu	Ser	Ser	Leu	Asp	Lys	Lys	Ile	Arg	Gln	Glu	Leu	Lys
															45
															35
35															40
Ser	Lys	Glu	Leu	Lys	Asn	Lys	Glu	Leu	Lys	Asn	Lys	Asp	Leu	Lys	Asn
															50
															55
50															60
Lys	Glu	Glu	Lys	Glu	Thr	Lys	Ala	Lys	Arg	Lys	Pro	Arg	Ala	Glu	
65															80
Val	His	His	Gly	Asp	Ala	Lys	Asn	Pro	Thr	Pro	Lys	Ile	Thr	Pro	Pro
															95
85															90
Lys	Ile	Lys	Gly	Ser	Ser	Lys	Gly	Val	Gln	Asn	Gln	Gly	Val	Gln	Asn
100															110
Asn	Ala	Pro	Lys	Pro	Glu	Glu	Lys	Asp	Thr	Thr	Pro	Gln	Ala	Thr	Glu
115															125
Lys	Asn	Lys	Glu	Thr	Ser	Pro	Ser	Ser	Gln	Phe	Asn	Ser	Ile	Phe	Gly

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130	Asn Pro Asn Asn Ala Thr Asn Asn Thr Leu Glu Asp Lys Val Val Gly
145	150 155 160
Gly Ile Ser Leu Leu Val Asn Gly Ser Pro Ile Thr Leu Tyr Gln Ile	
165	170 175
Gln Glu Gln Glu Lys Ser Lys Val Ser Unk Ala Unk Ala Arg Asp	
180	185 190
Arg Leu Unk Unk	
195	

## (2) INFORMATION FOR SEQ ID NO:686:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686

Leu Met Arg Lys Ile Phe Ser Tyr Ile Ser Lys Val Leu Leu Phe Ile	
1 5 10 15	
Gly Val Val Tyr Ala Glu Pro Asp Ser Lys Val Glu Ala Leu Glu Gly	
20 25 30	
Arg Lys Gln Glu Ser Ser Leu Asp Lys Lys Ile Arg Gln Glu Leu Lys	
35 40 45	
Ser Lys Glu Leu Lys Asn Lys Glu Leu Lys Asn Lys Asp Leu Lys Asn	
50 55 60	
Lys Glu Glu Lys Glu Thr Lys Ala Lys Arg Lys Pro Arg Ala Glu	
65 70 75 80	
Val His His Gly Asp Ala Lys Asn Pro Thr Pro Lys Ile Thr Pro Pro	
85 90 95	
Lys Ile Lys Gly Ser Ser Lys Gly Val Gln Asn Gln Gly Val Gln Asn	
100 105 110	
Asn Ala Pro Lys Pro Glu Glu Lys Asp Thr Thr Pro Gln Ala Thr Glu	
115 120 125	
Lys Asn Lys Glu Thr Ser Pro Ser Ser Gln Phe Asn Ser Ile Phe Gly	
130 135 140	
Asn Pro Asn Asn Ala Thr Asn Asn Thr Leu Glu Asp Lys Val Val Gly	
145 150 155 160	
Gly Ile Ser Leu Leu Val Asn Gly Ser Pro Ile Thr Leu Tyr Gln Ile	
165 170 175	
Gln Glu Gln Glu Lys Ser Lys Val Ser Unk Ala Unk Ala Arg Asp	
180 185 190	
Arg Leu Unk Unk	
195	

## (2) INFORMATION FOR SEQ ID NO:687:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687

Val	Leu	Trp	Val	Leu	Tyr	Phe	Leu	Thr	Ser	Leu	Phe	Ile	Cys	Ser	Leu
1															15
															10
Ile	Val	Leu	Trp	Ser	Lys	Lys	Ser	Met	Leu	Phe	Val	Asp	Asn	Ala	Asn
															30
															20
Lys	Ile	Gln	Gly	Phe	His	His	Ala	Arg	Thr	Pro	Arg	Ala	Gly	Gly	Leu
															45
															35
Gly	Ile	Phe	Leu	Ser	Phe	Ala	Ala	Cys	Tyr	Leu	Glu	Pro	Phe	Glu	
															50
															55
Met	Pro	Phe	Lys	Gly	Pro	Phe	Val	Phe	Leu	Gly	Leu	Ser	Leu	Val	Phe
															80
															65
															70
Leu	Ser	Gly	Phe	Leu	Glu	Asp	Ile	Asn	Leu	Ser	Leu	Ser	Pro	Lys	Ile
															95
															85
Arg	Leu	Ile	Leu	Gln	Ala	Val	Gly	Val	Val	Cys	Ile	Ile	Ser	Ser	Thr
															110
															100
Pro	Leu	Val	Val	Ser	Asp	Phe	Ser	Pro	Leu	Phe	Ser	Leu	Pro	Tyr	Phe
															115
															120
Ile	Ala	Phe	Leu	Phe	Ala	Ile	Phe	Tyr	Ala	Gly	Gly	Tyr	Gln		125
															130
															135
															140

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 86 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688

Met	Ala	Cys	Lys	Phe	Cys	Pro	Lys	Ile	Arg	Lys	Thr	Asp	Trp	Ile	Phe
1															15
															10
Ile	Leu	Ile	Ala	Ala	Leu	Gly	Phe	Tyr	Ser	Val	Asn	Lys	Leu	Gly	Tyr
															30
															20
Ala	Pro	Lys	Phe	Asn	Thr	Pro	Thr	Pro	Lys	Ser	Ser	Arg	Pro	Leu	Ser
															45
															35
Arg	Pro	Ile	Glu	Lys	Pro	Asn	Asn	Met	Thr	Glu	Glu	Glu	Arg	Lys	Lys
															50
															55
Arg	Phe	Ile	Glu	Leu	Gln	Lys	Ala	Cys	Leu	Leu	His	Lys	Asp	Lys	Lys
															60
															65
Ala	Cys	Glu	Glu	Val	Phe										70
															75
															80

## (2) INFORMATION FOR SEQ ID NO:689:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...121

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:689

Val	Asp	Ser	Ile	Leu	Ile	Asp	Glu	Ala	Arg	Thr	Pro	Leu	Ile	Ile	Ser
1						5						10			15
Gly	Pro	Val	Asp	Arg	Arg	Met	Glu	Asn	Tyr	Asn	Lys	Ala	Asp	Glu	Val
						20						25			30
Ala	Lys	Ser	Met	Gln	Val	Glu	Val	Asp	Phe	Thr	Ile	Asp	Glu	Lys	Asn
						35					40			45	
Arg	Ala	Ile	Leu	Ile	Thr	Glu	Glu	Gly	Ile	Lys	Lys	Ala	Glu	Asn	Leu
						50				55		60			
Phe	Gly	Val	Asp	Asn	Leu	Tyr	Lys	Ile	Glu	Asn	Ala	Ala	Leu	Ser	His
						65				70		75			80
His	Leu	Asp	Gln	Ala	Leu	Lys	Ala	Asn	Tyr	Leu	Phe	Phe	Ile	Asp	Lys
						85				90			95		
Asp	Tyr	Ile	Val	Ala	Asn	Asn	Glu	Val	Val	Ile	Val	Asp	Lys	Phe	Thr
						100				105			110		
Asp	Arg	Leu	Asn	Glu	Gly	Glu	Ala	Leu							
						115						120			

## (2) INFORMATION FOR SEQ ID NO:690:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...59

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:690

Met	Thr	Ile	Thr	Thr	Leu	Ser	Phe	Leu	Phe	Thr	Thr	Pro	Glu	Val	Phe
1							5			10			15		
Val	Asn	Gln	Asp	Phe	Pro	Trp	Leu	Ser	Gly	Ala	Gly	Arg	Leu	Val	Val
							20			25			30		

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Lys	Asp	Leu	Ala	Leu	Phe	Ala	Gly	Gly	Leu	Phe	Val	Ala	Gly	Phe	Asp
	35				40						45				
Arg	Asn	Ala	Ile	Trp	Arg	Val	Lys	Gly	Phe	Ala					
	50					55									

## (2) INFORMATION FOR SEQ ID NO:691:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...142

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:691

Val	Phe	Ser	Gly	Asn	Lys	Arg	Ala	Ile	Asn	Tyr	Arg	Thr	Ile	Val	Ser
1				5					10				15		
Ala	Phe	Val	Ile	Gln	Val	Ala	Leu	Gly	Ala	Leu	Ala	Leu	Tyr	Val	Pro
				20				25				30			
Leu	Gly	Arg	Glu	Ile	Leu	Gln	Gly	Leu	Ala	Ser	Gly	Ile	Gln	Ser	Val
				35			40			45					
Ile	Gly	Tyr	Gly	Tyr	Glu	Gly	Val	Arg	Phe	Leu	Phe	Gly	Asn	Leu	Ala
		50			55			60							
Pro	Asn	Ala	Lys	Gly	Asp	Gln	Gly	Ile	Gly	Gly	Phe	Ile	Phe	Ala	Ile
	65				70			75			80				
Asn	Val	Leu	Ala	Ile	Ile	Ile	Phe	Phe	Ala	Ser	Leu	Ile	Ser	Leu	Leu
					85			90			95				
Tyr	Tyr	Leu	Lys	Ile	Met	Pro	Leu	Val	Ile	Asn	Leu	Ile	Gly	Gly	Ala
					100			105			110				
Leu	Gln	Lys	Cys	Leu	Gly	Thr	Ser	Lys	Ala	Glu	Ser	Met	Ser	Ala	Ala
					115			120			125				
Ala	Asn	Unk	Unk	Val	Ala	His	Thr	Glu	Asp	Unk	Leu	Ser	His		
				130			135			140					

## (2) INFORMATION FOR SEQ ID NO:692:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...80

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:692

**SUBSTITUTE SHEET (RULE 26)**

Met Leu Val Gly Ile Ser Asn Ala Ile Asn Ile Ile Asp Gly Phe Asn  
 1 5 10 15  
 Gly Leu Ala Ser Gly Ile Cys Ala Ile Ala Leu Leu Val Ile His Tyr  
 20 25 30  
 Ile Asp Unk Ser Ser Leu Ser Cys Leu Leu Ala Tyr Met Val Leu Gly  
 35 40 45  
 Val Tyr Gly Val Lys Unk Pro Phe Arg Lys Asp Phe Leu Gly Arg Ser  
 50 55 60  
 Gly Gly Arg Ile Phe Trp Val Trp Unk Unk Phe Leu Ser Cys Ile  
 65 70 75 80

## (2) INFORMATION FOR SEQ ID NO:693:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693

Met Lys Arg Ser Ser Val Phe Ser Phe Leu Val Ala Phe Leu Leu Val  
 1 5 10 15  
 Val Gly Cys Ser His Lys Met Asp Asn Lys Thr Val Ala Gly Asp Val  
 20 25 30  
 Ser Thr Lys Ala Val Gln Thr Ala Pro Val Thr Thr Glu Pro Ala Pro  
 35 40 45  
 Glu Lys Glu Glu Pro Lys Gln Glu Pro Ala Pro Val Val Glu Glu Lys  
 50 55 60  
 Pro Ala Ile Glu Ser Gly Thr Ile Ile Ala Ser Ile Tyr Phe Asp Phe  
 65 70 75 80  
 Asp Lys Tyr Glu Ile Lys Glu Ser Asp Gln Glu Thr Leu Asp Glu Ile  
 85 90 95  
 Val Gln Lys Ala Lys Glu Asn His Met Gln Val Leu Leu Glu Gly Asn  
 100 105 110  
 Thr Asp Glu Phe Gly Ser Ser Glu Tyr Asn Gln Ala Leu Gly Val Lys  
 115 120 125  
 Arg Thr Leu Ser Val Lys Asn Ala Leu Val Ile Lys Gly Val Glu Lys  
 130 135 140  
 Asp Met Ile Lys Thr Ile Ser Phe Gly Glu Ser Lys Pro Lys Cys Val  
 145 150 155 160  
 Gln Lys Thr Arg Glu Cys Tyr Arg Glu Asn Arg Arg Val Asp Val Lys  
 165 170 175  
 Leu Val Lys

## (2) INFORMATION FOR SEQ ID NO:693:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693

Met	Lys	Arg	Ser	Ser	Val	Phe	Ser	Phe	Leu	Val	Ala	Phe	Leu	Leu	Val
1					5				10				15		
Val	Gly	Cys	Ser	His	Lys	Met	Asp	Asn	Lys	Thr	Val	Ala	Gly	Asp	Val
					20				25				30		
Ser	Thr	Lys	Ala	Val	Gln	Thr	Ala	Pro	Val	Thr	Thr	Glu	Pro	Ala	Pro
					35				40			45			
Glu	Lys	Glu	Glu	Pro	Lys	Gln	Glu	Pro	Ala	Pro	Val	Val	Glu	Glu	Lys
	50				55				60						
Pro	Ala	Ile	Glu	Ser	Gly	Thr	Ile	Ile	Ala	Ser	Ile	Tyr	Phe	Asp	Phe
	65				70				75			80			
Asp	Lys	Tyr	Glu	Ile	Lys	Glu	Ser	Asp	Gln	Glu	Thr	Leu	Asp	Glu	Ile
	85				90				95						
Val	Gln	Lys	Ala	Lys	Glu	Asn	His	Met	Gln	Val	Leu	Glu	Gly	Asn	
	100				105				110						
Thr	Asp	Glu	Phe	Gly	Ser	Ser	Glu	Tyr	Asn	Gln	Ala	Leu	Gly	Val	Lys
	115				120				125						
Arg	Thr	Leu	Ser	Val	Lys	Asn	Ala	Leu	Val	Ile	Lys	Gly	Val	Glu	Lys
	130				135				140						
Asp	Met	Ile	Lys	Thr	Ile	Ser	Phe	Gly	Glu	Ser	Lys	Pro	Lys	Cys	Val
	145				150				155			160			
Gln	Lys	Thr	Arg	Glu	Cys	Tyr	Arg	Glu	Asn	Arg	Arg	Val	Asp	Val	Lys
	165				170				175						
Leu	Val	Lys													

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694

Met	Leu	His	Lys	Lys	Tyr	Arg	Pro	Asn	Val	Ala	Ala	Ile	Ile	Met	Ser
1					5				10					15	
Pro	Asp	Tyr	Pro	Asn	Thr	Cys	Glu	Val	Phe	Ile	Ala	Glu	Arg	Ile	Asp
					20				25			30			
Ile	Glu	Gly	Ala	Trp	Gln	Phe	Pro	Gln	Gly	Gly	Ile	Asp	Glu	Gly	Glu

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35	40	45
Thr Pro Leu Glu Ala Leu Tyr Arg Glu Leu Leu Glu		Glu Ile Gly Thr
50	55	60
Asn Glu Ile Glu Ile Leu Ala Gln Tyr Pro Arg		
65	70	75

## (2) INFORMATION FOR SEQ ID NO:695:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...99

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:695

Val Met Leu Met Ala Ile Phe Thr Pro Tyr Ile Leu Ile Leu Lys Met			
1	5	10	15
Met Lys Lys Ser Met Ser Leu Phe Ala Asn Met Gly Leu Glu Gln Ile			
20	25	30	
Phe Cys Asn Arg Asp Ile Lys Asp Leu Asn Asp Phe Val Phe Gly Ile			
35	40	45	
Glu Val Gly Leu Asp Ser Asn Ala Arg Lys Asn Arg Ser Arg Lys Ala			
50	55	60	
Met Glu Asn His Leu Ile Gly Leu Phe Val Gln Ala Gln Leu Asn Phe			
65	70	75	80
Lys Glu Gln Val Asp Ile Arg Glu Phe Glu Asp Leu Arg Gln Ala Phe			
85	90	95	
Gly Asn Asp			

## (2) INFORMATION FOR SEQ ID NO:696:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...209

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:696

Met Ile Arg Leu Ala Ala Phe Phe Leu Ala Leu Ala Cys Ala Ile Thr			
1	5	10	15

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Pro Lys Ser Arg Leu Leu Leu Lys Asn Val Leu Leu Asn Pro Thr Arg  
 20 25 30  
 Ile Glu Ala Phe Glu Val Leu Lys Lys Met Gly Ala His Ile Glu Tyr  
 35 40 45  
 Val Ile Gln Ser Lys Asp Leu Glu Val Ile Gly Asp Ile Tyr Ile Glu  
 50 55 60  
 His Ala Pro Leu Lys Ala Ile Ser Ile Asp Gln Asn Ile Ala Ser Leu  
 65 70 75 80  
 Ile Asp Glu Ile Pro Ala Leu Ser Ile Ala Met Leu Phe Ala Lys Gly  
 85 90 95  
 Lys Ser Met Val Arg Asn Ala Lys Asp Leu Arg Ala Lys Glu Ser Asp  
 100 105 110  
 Arg Ile Lys Ala Val Val Ser Asn Phe Lys Ala Leu Gly Ile Glu Cys  
 115 120 125  
 Glu Glu Phe Glu Asp Gly Phe Tyr Ile Glu Gly Leu Gly Asp Ala Ser  
 130 135 140  
 Gln Leu Lys Gln His Phe Ser Lys Ile Lys Pro Pro Ile Ile Lys Ser  
 145 150 155 160  
 Phe Asn Asp His Arg Ile Ala Met Ser Phe Ala Val Leu Thr Leu Ala  
 165 170 175  
 Leu Pro Leu Glu Ile Asp Asn Leu Glu Cys Ala Asn Ile Ser Phe Pro  
 180 185 190  
 Thr Phe Gln Leu Trp Leu Asn Leu Phe Lys Lys Arg Ser Leu Asn Gly  
 195 200 205  
 Asn

## (2) INFORMATION FOR SEQ ID NO:697:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...75

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:697

Val Gly Ser Leu Lys Phe Leu Asn Ala Met Gly Val Asp Leu Lys Val  
 1 5 10 15  
 Lys Glu Ser Ala Asn Ile Met Val Gly Phe Ala Lys Asn Lys Thr Leu  
 20 25 30  
 Cys Ala Leu Phe Ile Leu Glu Glu Arg Leu Lys Ala Asn Ala Lys Glu  
 35 40 45  
 Val Ile Gln Ala Leu Gln Asn Gln Gly Leu Glu Leu Glu Ile Leu Ser  
 50 55 60  
 Gly Asp Asn Glu Ser Ser Val Lys Glu Cys Ala  
 65 70 75

## (2) INFORMATION FOR SEQ ID NO:698:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698

Met	Glu	Ala	Leu	Asn	Ala	Leu	Asn	Ala	Gln	Ser	Asp	Glu	Gln	Ile	Leu
1	5								10					15	
Cys	Glu	Gly	Tyr	Phe	Val	Leu	Leu	Gln	Ile	Leu	Glu	Pro	Met	Ile	Pro
									20					25	30
His	Thr	Ala	Trp	Glu	Leu	Ser	Glu	Arg	Leu	Phe	Lys	Arg	Glu	Asn	Phe
								35			40		45		
Lys	Pro	Ile	Glu	Val	Asp	Glu	Ser	Ala	Leu	Ile	Glu	Asp	Phe	Met	Thr
								50			55		60		
Leu	Gly	Leu	Thr	Ile	Asn	Gly	Lys	Arg	Arg	Ala	Glu	Leu	Lys	Val	Asn
								65			70		75		80
Ile	Asn	Ala	Ser	Lys	Glu	Glu	Ile	Ile	Ile	Leu	Ala	Lys	Lys	Glu	Leu
								85			90		95		
Glu	Lys	Tyr	Leu	Glu	Asn	Ala	Ser	Val	Lys	Lys	Glu	Ile	Tyr	Val	Pro
								100			105		110		
Asn	Lys	Leu	Val	Asn	Phe	Val	Thr	Ala							
								115			120				

(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699

Met	Lys	Glu	Ser	Ile	Lys	Tyr	Leu	Leu	Glu	Ser	Val	Gly	Leu	Val	Leu
1	5								10					15	
Leu	Met	Ser	Val	Asn	Pro	Gly	Phe	Gly	Gly	Gln	Lys	Phe	Leu	Asp	Leu
									20		25		30		
Val	Leu	Glu	Lys	Cys	Leu	Lys	Val	Lys	Glu	Leu	Ile	Lys	Arg	Tyr	Asn
								35		40		45			
Pro	Ser	Cys	Leu	Leu	Glu	Val	Asp	Gly	Gly	Val	Asn	Asp	Lys	Asn	Ile
								50		55		60			
Phe	Glu	Leu	Gln	Gln	Ala	Gly	Val	Asp	Val	Val	Val	Ser	Gly	Ser	Tyr
								65		70		75		80	
Ile	Phe	Glu	Ser	Lys	Asp	Unk	Lys	Leu	Ala	Ile	Glu	Gly	Leu	Gln	Asn
								85		90		95			

**SUBSTITUTE SHEET (RULE 26)**

Val Arg Gln Pro Leu Ala  
100

## (2) INFORMATION FOR SEQ ID NO:700:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...131

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:700

Val	His	Asp	Gly	Val	Leu	Gly	Trp	Val	Gly	Phe	Thr	Leu	Ile	Ala	Ser
1				5					10				15		
Met	Tyr	His	Met	Thr	Pro	Arg	Leu	Phe	Lys	Arg	Glu	Ile	Tyr	Ser	Gly
	20						25					30			
Arg	Leu	Val	Asp	Phe	Gln	Phe	Trp	Ile	Met	Thr	Leu	Gly	Ile	Val	Leu
	35				40				45						
Tyr	Phe	Ser	Ser	Met	Trp	Ile	Ala	Gly	Ile	Thr	Gln	Gly	Met	Met	Trp
	50				55				60						
Arg	Asp	Val	Asp	Gln	Tyr	Gly	Asn	Leu	Thr	Tyr	Gln	Phe	Ile	Asp	Thr
	65				70				75				80		
Val	Lys	Ala	Leu	Ile	Pro	Tyr	Tyr	Asn	Ile	Arg	Gly	Val	Gly	Gly	Leu
	85							90				95			
Met	Tyr	Phe	Ile	Gly	Phe	Ile	Ile	Phe	Ala	Tyr	Asn	Ile	Phe	Met	Thr
	100					105						110			
Ile	Thr	Ala	Gly	Lys	Lys	Leu	Glu	Arg	Glu	Pro	Asn	Tyr	Ala	Thr	Pro
	115					120				125					
Met	Ala	Lys													
	130														

## (2) INFORMATION FOR SEQ ID NO:701:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...441

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:701

Met Ile Thr Leu Phe Ser Phe Gly Ala Phe Ala Tyr Tyr Phe Val Ser

1	5	10	15
Ser Gln Ile Ser His Glu Asn Tyr Gln Asn Glu Met Arg His Tyr Gln			
20	25	30	
Phe Val Thr Thr Ile Asn Glu Ile Leu Asn Asn Tyr Ser Asp Tyr Arg			
35	40	45	
Ala Ile Glu Asp Tyr Leu Tyr Lys Ile Gly Phe Arg Glu Thr Thr Ile			
50	55	60	
Glu Asn Leu Glu Lys Val Leu Ala Lys Arg Arg His Gln Leu His His			
65	70	75	80
Arg Asn Ile Trp Tyr Ala Glu Val Phe Lys Phe Ser Asp Met Val Phe			
85	90	95	
Ile Leu Leu Lys Lys Asp Glu His Phe Val Leu Tyr Lys Asp Leu His			
100	105	110	
Ser Val Ser Tyr Arg Asn Tyr Phe Leu Ala Ile Thr Val Gly Leu Leu			
115	120	125	
Leu Ile Leu Phe Leu Phe Leu Phe Val Leu Gln Ser Leu Leu Pro Leu			
130	135	140	
Arg Glu Leu Arg Ser Gln Val Lys Arg Phe Ala Gln Gly Asp Lys Ser			
145	150	155	160
Val Ser Cys Lys Ser Lys Gln Lys Asp Glu Ile Gly Asp Leu Ala Asn			
165	170	175	
Glu Phe Asp Asn Cys Ile Gln Lys Ile Asn Ala Met Asn Glu Ser Arg			
180	185	190	
Val Leu Phe Leu Arg Ser Ile Met His Glu Leu Arg Thr Pro Ile Thr			
195	200	205	
Lys Gly Lys Ile Leu Ser Ser Met Leu Lys Glu Glu Leu Ser Cys Lys			
210	215	220	
Arg Phe Ser Ser Ile Phe Asp His Leu Asn Met Leu Ile Glu Gln Phe			
225	230	235	240
Ala Arg Ile Glu Gln Leu Ala Ser Lys Asn Tyr Gly Ser Asn Lys Glu			
245	250	255	
Lys Phe Leu Met Ser Asp Leu Ile Asp Lys Ile Glu Lys Met Leu Leu			
260	265	270	
Ile Asp Glu Asp Lys Lys Ser Pro Ile His Val Ser Ser Asn Tyr			
275	280	285	
Ile Ile Glu Ala Asp Phe Glu Leu Phe Ala Ile Ala Leu Lys Asn Met			
290	295	300	
Ile Asp Asn Ala Ile Lys Tyr Ser Asp Asp Lys Gln Val Phe Leu Asp			
305	310	315	320
Phe Ile Gly Asn Asn Leu Val Val Ser Asn Lys Ser Lys Pro Leu Lys			
325	330	335	
Glu Asp Phe Glu Lys Tyr Leu Gln Pro Tyr Phe Lys Ser Ser Asn Pro			
340	345	350	
Ser Gln Ala His Gly Phe Gly Leu Gly Met Tyr Ile Ile Lys Asn Ala			
355	360	365	
Leu Glu Ala Met Gly Leu Asn Leu Ser Tyr His Tyr Ser Asn Gly Arg			
370	375	380	
Ile Cys Phe Thr Ile His Asp Cys Val Phe Asn Ser Phe Tyr Asp Leu			
385	390	395	400
Glu Ala Asp Asn Glu Glu Leu Pro Pro Glu Asn Leu Arg Glu Val			
405	410	415	
Lys Gly Met Lys Gly Thr Glu Lys Ala Asn Cys Gly Val Lys Glu Lys			
420	425	430	
Gln Lys Glu Arg Thr Cys Ser Asn Asp			
435	440		

## (2) INFORMATION FOR SEQ ID NO:702:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 127 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702

Val	Leu	Leu	Leu	Ser	Arg	Met	Gly	Ile	Ala	Phe	Ala	His	Ser	Ile	Phe
1						5				10				15	
Trp	Ser	Ile	Thr	Ala	Ser	Leu	Val	Ile	Arg	Val	Ala	Pro	Arg	Asn	Lys
						20			25				30		
Lys	Gln	Gln	Ala	Leu	Gly	Leu	Leu	Ala	Leu	Gly	Ser	Ser	Leu	Ala	Met
						35			40			45			
Ile	Leu	Gly	Leu	Pro	Leu	Gly	Arg	Ile	Ile	Gly	Gln	Ile	Leu	Asp	Trp
						50			55			60			
Arg	Ser	Thr	Phe	Gly	Val	Ile	Gly	Gly	Val	Ala	Thr	Leu	Ile	Met	Leu
65						70			75			80			
Leu	Met	Trp	Lys	Leu	Leu	Pro	His	Leu	Pro	Ser	Arg	Asn	Ala	Gly	Thr
						85			90			95			
Leu	Ala	Ser	Val	Pro	Ile	Leu	Met	Lys	Arg	Pro	Leu	Leu	Val	Gly	Ile
						100			105			110			
Tyr	Leu	His	Val	Asn	His	Gly	Tyr	Phe	Trp	Ala	Phe	His	His	Leu	
						115			120			125			

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703

Met	Gly	Thr	Leu	Ile	Glu	Lys	Trp	Phe	Gly	Phe	Ser	Gln	Ile	Arg	Glu
1							5		10				15		
Glu	Leu	Glu	Ala	Arg	Ile	Ser	Glu	Leu	Glu	Asp	Glu	Asn	Thr	Glu	Leu
							20		25			30			
Leu	Arg	Glu	Arg	Glu	Tyr	Leu	Ala	Ala	Glu	Thr	Ser	Glu	Leu	Lys	Asp
						35			40			45			
Ala	Asn	Asp	Gln	Leu	Arg	Gln	Asn	Asp	Lys	Leu	Phe	Ile	Thr	Lys	
							50		55			60			
Asp	Lys	Leu	Thr	Lys	Glu	Asn	Thr	Glu	Leu	Phe	Ala	Glu	Asn	Glu	Ser
65							65		70			75		80	
Leu	Ser	Val	Lys	Ile	Ser	Gly	Leu	Glu	His	Ser	Asn	Asp	Gln	Leu	Trp
							85		90			95			
Gln	Asn	Asn	Asn	Lys	Leu	Thr	Lys	Glu	Lys	Ala	Glu	Leu	Lys	Thr	Glu
						100			105			110			
Lys	Asp	Ile	Leu	Ala	Lys	Glu	Asn	Thr	Arg	Leu	Leu	Ala	Ala	Arg	Asp

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115	120	125
Arg Leu Thr Glu Glu Lys Arg Glu Leu Thr Thr Glu	Lys Glu Arg Leu	
130	135	140
Lys Arg Glu Asn Thr Glu Leu Thr His Lys Ile Thr Glu	Leu Thr Lys	
145	150	155
Glu Asn Lys Ala Leu Thr Thr Glu Asn Asp Lys Leu Asn His Gln Val		160
165	170	175
Thr Ala Leu Thr Asn Glu Arg Asp Ser Leu Glu Gln Glu Arg Ala Arg		
180	185	190
Leu Gln Asp Ala His Gly Phe Leu Glu Lys Arg Cys Thr Asn Leu Glu		
195	200	205
Lys Glu Asn Gln Arg Leu Thr Asp Lys Leu Lys Gln Leu Glu Ser Ala		
210	215	220
Gln Lys Ser Leu Glu Asn Thr Asn Asn Gln Leu Arg Gln Ala Leu Glu		
225	230	235
Asn Ser Asn Val Gln Leu Ala Gln Ala Lys Glu Unk Ile Ala Ile Glu		240
245	250	255
Unk Ser Glu Leu Unk Arg Arg Asn Arg Thr Leu Glu Glu Leu Arg Gly		
260	265	270
Tyr Gly Ser Gln Lys Unk Ile Trp Thr Tyr Thr Unk Gly Val		
275	280	285

## (2) INFORMATION FOR SEQ ID NO:703:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...286

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:703

Met Gly Thr Leu Ile Glu Lys Trp Phe Gly Phe Ser Gln Ile Arg Glu			
1	5	10	15
Glu Leu Glu Ala Arg Ile Ser Glu Leu Glu Asp Glu Asn Thr Glu Leu			
20	25	30	
Leu Arg Glu Arg Glu Tyr Leu Ala Ala Glu Thr Ser Glu Leu Lys Asp			
35	40	45	
Ala Asn Asp Gln Leu Arg Gln Lys Asn Asp Lys Leu Phe Ile Thr Lys			
50	55	60	
Asp Lys Leu Thr Lys Glu Asn Thr Glu Leu Phe Ala Glu Asn Glu Ser			
65	70	75	80
Leu Ser Val Lys Ile Ser Gly Leu Glu His Ser Asn Asp Gln Leu Trp			
85	90	95	
Gln Asn Asn Asn Lys Leu Thr Lys Glu Lys Ala Glu Leu Lys Thr Glu			
100	105	110	
Lys Asp Ile Leu Ala Lys Glu Asn Thr Arg Leu Leu Ala Ala Arg Asp			
115	120	125	
Arg Leu Thr Glu Glu Lys Arg Glu Leu Thr Thr Glu Lys Glu Arg Leu			
130	135	140	
Lys Arg Glu Asn Thr Glu Leu Thr His Lys Ile Thr Glu Leu Thr Lys			
145	150	155	160
Glu Asn Lys Ala Leu Thr Thr Glu Asn Asp Lys Leu Asn His Gln Val			
165	170	175	

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Thr Ala Leu Thr Asn Glu Arg Asp Ser Leu Glu Gln Glu Arg Ala Arg  
 180 185 190  
 Leu Gln Asp Ala His Gly Phe Leu Glu Lys Arg Cys Thr Asn Leu Glu  
 195 200 205  
 Lys Glu Asn Gln Arg Leu Thr Asp Lys Leu Lys Gln Leu Glu Ser Ala  
 210 215 220  
 Gln Lys Ser Leu Glu Asn Thr Asn Asn Gln Leu Arg Gln Ala Leu Glu  
 225 230 235 240  
 Asn Ser Asn Val Gln Leu Ala Gln Ala Lys Glu Unk Ile Ala Ile Glu  
 245 250 255  
 Unk Ser Glu Leu Unk Arg Arg Asn Arg Thr Leu Glu Glu Leu Arg Gly  
 260 265 270  
 Tyr Gly Ser Gln Lys Unk Ile Trp Thr Tyr Thr Unk Gly Val  
 275 280 285

## (2) INFORMATION FOR SEQ ID NO:704:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...110

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:704

Val Leu Arg Lys Leu Leu Gly Lys Asn Cys Ile Glu Thr His Lys Gly  
 1 5 10 15  
 Val Gly Tyr Arg Leu Thr His Tyr Glu Lys Lys Ser Leu Lys Leu Phe  
 20 25 30  
 Leu Gly Thr Tyr Leu Gly Ser Ser Phe Val Leu Met Leu Val Ile Ser  
 35 40 45  
 Val Leu Ala Phe Asn Tyr Glu Lys Asn Glu Lys Ile Lys Unk Ile Arg  
 50 55 60  
 Met Asp Met Asp Lys Met Ala Ser Lys Ile Ala Ser Glu Ile Ile Gln  
 65 70 75 80  
 Leu His Met Gln Thr His Ala Asp Tyr His Asn Ala Leu Asn Ala Leu  
 85 90 95  
 Ile Ser Arg Tyr Lys Asp Val Ser Ile Unk Leu Unk Asp Thr  
 100 105 110

## (2) INFORMATION FOR SEQ ID NO:704:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

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## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...110

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:704

Val Leu Arg Lys Leu Leu Gly Lys Asn Cys Ile Glu Thr His Lys Gly  
 1 5 10 15  
 Val Gly Tyr Arg Leu Thr His Tyr Glu Lys Ser Leu Lys Leu Phe  
 20 25 30  
 Leu Gly Thr Tyr Leu Gly Ser Ser Phe Val Leu Met Leu Val Ile Ser  
 35 40 45  
 Val Leu Ala Phe Asn Tyr Glu Lys Asn Glu Lys Ile Lys Unk Ile Arg  
 50 55 60  
 Met Asp Met Asp Lys Met Ala Ser Lys Ile Ala Ser Glu Ile Ile Gln  
 65 70 75 80  
 Leu His Met Gln Thr His Ala Asp Tyr His Asn Ala Leu Asn Ala Leu  
 85 90 95  
 Ile Ser Arg Tyr Lys Asp Val Ser Ile Unk Leu Unk Asp Thr  
 100 105 110

## (2) INFORMATION FOR SEQ ID NO:705:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...115

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:705

Met Arg Ile Ile Ile Arg Leu Leu Ser Phe Lys Met Asn Ala Phe Leu  
 1 5 10 15  
 Lys Leu Ala Leu Ala Ser Leu Met Gly Gly Leu Trp Tyr Ala Phe Asn  
 20 25 30  
 Gly Glu Gly Ser Glu Ile Val Ala Ile Gly Ile Phe Val Leu Ile Leu  
 35 40 45  
 Phe Val Phe Phe Ile Arg Pro Val Ser Phe Gln Asp Pro Glu Lys Arg  
 50 55 60  
 Glu Glu Tyr Ile Glu Arg Leu Lys Lys Asn His Glu Arg Lys Met Ile  
 65 70 75 80  
 Leu Gln Asp Lys Gln Lys Glu Glu Gln Met Arg Leu Tyr Gln Ala Lys  
 85 90 95  
 Lys Glu Arg Glu Ser Arg Gln Lys Gln Asp Leu Lys Glu Gln Met Lys  
 100 105 110  
 Lys Tyr Ser  
 115

## (2) INFORMATION FOR SEQ ID NO:706:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids

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(B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706

Val	Arg	Ser	Cys	Lys	Gln	Ile	Phe	Asp	Lys	Gly	Leu	Lys	Pro	Tyr	Tyr
1						5			10					15	
Lys	His	Ser	Val	Cys	Leu	Lys	Pro	Phe	Arg	Phe	Cys	Phe	Leu	Lys	
						20			25			30			
Ile	His	Ala	Tyr	Gln	Gln	Arg	Tyr	Arg	Ala	Phe	Ala	Leu	Thr	Leu	Phe
						35			40			45			
Ser	Cys	Lys	Phe	Phe	Asn	Ala	Cys	Lys	Ile	Phe	Ile	Pro	Ile	Ile	Asp
						50			55			60			
Phe	Lys	Ile	Val	Phe	Ile	Pro	Ile	Leu	Lys	His	Gln	Ala	Lys	Leu	Lys
						65			70			75			80
Arg	Val	Ser	Asn	Ala	Tyr										
						85									

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707

Met	Cys	Gly	Met	Gly	Phe	Ile	Gly	Phe	Lys	Thr	Lys	Leu	Thr	Gln	Thr
1						5			10				15		
Lys	Ala	Phe	Ile	Ile	Leu	Ile	Pro	Ile	Phe	Gln	Asp	Arg	Ala	Val	Lys
						20			25			30			
Ala	Ala	Thr	Arg	Ser	Ala	Pro	Ile	Gln	Leu	Ile	Cys				
						35			40						

(2) INFORMATION FOR SEQ ID NO:708:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 560 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear**SUBSTITUTE SHEET (RULE 26)**

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708

Met Gly Asn Phe Asn Ser Tyr Gly Asp Leu Val Phe Asn Leu Ser His  
 1 5 10 15  
 Ser Val Ser His Ala Ile Ile Asn Thr Gln Gly Thr Ala Thr Ile Met  
 20 25 30  
 Ala Asn Asn Asn Pro Leu Ile Gln Phe Asn Ala Ser Ser Lys Glu Val  
 35 40 45  
 Gly Thr Tyr Thr Leu Ile Asp Ser Ala Lys Ala Ile Tyr Tyr Gly Tyr  
 50 55 60  
 Asn Asn Gln Ile Thr Gly Gly Ser Ser Leu Asp Asn Tyr Leu Lys Leu  
 65 70 75 80  
 Tyr Ala Leu Ile Asp Ile Asn Gly Lys His Met Val Met Thr Asp Asn  
 85 90 95  
 Gly Leu Thr Tyr Asn Gly Gln Ala Val Ser Val Lys Asp Gly Gly Leu  
 100 105 110  
 Val Val Gly Phe Lys Asp Ser Gln Asn Gln Tyr Ile Tyr Thr Ser Ile  
 115 120 125  
 Leu Tyr Asn Lys Val Lys Ile Ala Val Ser Asn Asp Pro Ile Asn Asn  
 130 135 140  
 Pro Gln Ala Pro Thr Leu Lys Gln Tyr Ile Ala Gln Ile Gln Gly Val  
 145 150 155 160  
 Gln Ser Val Asp Ser Ile Unk Gln Ala Gly Gly Asn Gln Ala Ile Asn  
 165 170 175  
 Trp Leu Asn Lys Ile Phe Glu Thr Lys Gly Ser Pro Leu Phe Ala Pro  
 180 185 190  
 Tyr Tyr Leu Glu Ser His Ser Thr Lys Asp Leu Thr Thr Ile Ala Gly  
 195 200 205  
 Asp Ile Ala Asn Thr Leu Glu Val Ile Ala Asn Pro Asn Phe Lys Asn  
 210 215 220  
 Asp Ala Thr Asn Ile Leu Gln Ile Asn Thr Tyr Thr Gln Gln Met Ser  
 225 230 235 240  
 Arg Leu Ala Lys Leu Ser Asp Thr Ser Thr Phe Ala Arg Ser Asp Phe  
 245 250 255  
 Leu Glu Arg Leu Glu Ala Leu Lys Asn Lys Arg Phe Ala Asp Ala Ile  
 260 265 270  
 Pro Asn Ala Met Asp Val Ile Leu Lys Tyr Ser Gln Arg Asn Arg Val  
 275 280 285  
 Lys Asn Asn Val Trp Ala Thr Gly Val Gly Ala Ser Phe Ile Ser  
 290 295 300  
 Gly Gly Thr Unk Thr Leu Tyr Gly Ile Asn Unk Gly Tyr Asp Arg Phe  
 305 310 315 320  
 Ile Lys Gly Val Ile Val Gly Gly Tyr Ala Ala Tyr Gly Tyr Ser Gly  
 325 330 335  
 Phe His Ala Asn Ile Thr Gln Ser Gly Ser Ser Asn Val Asn Val Gly  
 340 345 350  
 Val Tyr Ser Arg Ala Phe Ile Lys Arg Ser Glu Leu Thr Met Ser Leu  
 355 360 365  
 Asn Glu Thr Trp Gly Tyr Asn Lys Thr Phe Ile Asn Ser Tyr Asp Pro  
 370 375 380  
 Leu Leu Ser Ile Ile Asn Gln Ser Tyr Arg Tyr Asp Thr Trp Thr Thr  
 385 390 395 400  
 Asp Ala Lys Ile Asn Tyr Gly Tyr Asp Phe Met Phe Lys Asp Lys Ser  
 405 410 415

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Val Ile Phe Lys Pro Gln Val Gly Leu Ser Tyr Tyr Tyr Ile Gly Leu  
 420 425 430  
 Ser Gly Leu Arg Gly Ile Met Asp Asp Pro Ile Tyr Asn Gln Phe Arg  
 435 440 445  
 Ala Asn Ala Asp Pro Asn Lys Lys Ser Val Leu Thr Ile Asn Phe Ala  
 450 455 460  
 Leu Glu Ser Arg His Tyr Phe Asn Lys Asn Ser Tyr Tyr Phe Val Ile  
 465 470 475 480  
 Ala Asp Val Gly Arg Asp Leu Phe Ile Asn Ser Met Gly Asp Lys Met  
 485 490 495  
 Val Arg Phe Ile Gly Asn Asn Thr Leu Ser Tyr Arg Asp Gly Gly Arg  
 500 505 510  
 Tyr Asn Thr Phe Ala Ser Ile Ile Thr Gly Gly Glu Ile Arg Leu Phe  
 515 520 525  
 Lys Thr Phe Tyr Val Asn Ala Gly Ile Gly Ala Arg Phe Gly Leu Asp  
 530 535 540  
 Tyr Lys Asp Ile Asn Ile Thr Gly Asn Ile Gly Met Unk Unk Unk Phe  
 545 550 555 560

## (2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 124 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709

Leu Met Thr Lys Ser Leu Lys Leu Ile Gln Lys Gly Val Lys Asn Leu  
 1 5 10 15  
 Tyr Glu Thr Leu Lys Asn Arg Ala Leu Glu His Gln Asp Thr Leu Met  
 20 25 30  
 Val Gly Arg Ser His Gly Val Phe Gly Glu Pro Ile Thr Phe Gly Leu  
 35 40 45  
 Val Leu Ala Leu Phe Ala Asp Glu Ile Lys Arg His Leu Lys Ala Leu  
 50 55 60  
 Asp Leu Thr Met Glu Phe Ile Unk Val Gly Ala Ile Ser Gly Ala Met  
 65 70 75 80  
 Gly Asn Phe Ala His Ala Pro Leu Glu Leu Glu Leu Ala Cys Gly  
 85 90 95  
 Phe Leu Gly Leu Lys Thr Ala Asn Ile Ser Asn Gln Val Ile Gln Arg  
 100 105 110  
 Asp Arg Tyr Ala Gly Leu His Ala Ile Trp Leu Phe  
 115 120

## (2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 124 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709

Leu	Met	Thr	Lys	Ser	Leu	Lys	Leu	Ile	Gln	Lys	Gly	Val	Lys	Asn	Leu
1					5				10					15	
Tyr	Glu	Thr	Leu	Lys	Asn	Arg	Ala	Leu	Glu	His	Gln	Asp	Thr	Leu	Met
						20			25				30		
Val	Gly	Arg	Ser	His	Gly	Val	Phe	Gly	Glu	Pro	Ile	Thr	Phe	Gly	Leu
					35			40			45				
Val	Leu	Ala	Leu	Phe	Ala	Asp	Glu	Ile	Lys	Arg	His	Leu	Lys	Ala	Leu
					50			55		60					
Asp	Leu	Thr	Met	Glu	Phe	Ile	Unk	Val	Gly	Ala	Ile	Ser	Gly	Ala	Met
					65			70		75			80		
Gly	Asn	Phe	Ala	His	Ala	Pro	Leu	Glu	Leu	Glu	Glu	Leu	Ala	Cys	Gly
					85			90			95				
Phe	Leu	Gly	Leu	Lys	Thr	Ala	Asn	Ile	Ser	Asn	Gln	Val	Ile	Gln	Arg
					100			105			110				
Asp	Arg	Tyr	Ala	Gly	Leu	His	Ala	Ile	Trp	Leu	Phe				
					115			120							

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710

Leu	Ser	Asp	Ala	Ser	Lys	Arg	Ser	Leu	Asn	Pro	Thr	Leu	Met	Met	Asn
1					5			10			15				
Asn	Asn	Asn	Thr	Leu	Pro	Lys	Pro	Leu	Glu	Glu	Ser	Leu	Asp	Leu	Lys
					20			25			30				
Glu	Phe	Ile	Ala	Leu	Phe	Lys	Thr	Phe	Phe	Ala	Lys	Glu	Arg	Gly	Ser
					35			40			45				
Ile	Ala	Leu	Glu	Asn	Asp	Leu	Lys	Gln	Ala	Phe	Thr	Tyr	Leu	Asn	Glu
					50			55		60					
Val	Asp	Ala	Ile	Gly	Leu	Pro	Ala	Pro	Unk	Lys	Arg	Glu	Arg	Lys	Arg
					65			70		75		80			
Ser	Tyr	Cys	Cys	Gln	Thr	His	Gln	Ile	Arg	Asp	Ala	Pro	Phe	Arg	
					85			90			95				

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## (2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 95 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710

Leu	Ser	Asp	Ala	Ser	Lys	Arg	Ser	Leu	Asn	Pro	Thr	Leu	Met	Met	Asn
1				5					10				15		
Asn	Asn	Asn	Thr	Leu	Pro	Lys	Pro	Leu	Glu	Glu	Ser	Leu	Asp	Leu	Lys
				20				25				30			
Glu	Phe	Ile	Ala	Leu	Phe	Lys	Thr	Phe	Phe	Ala	Lys	Glu	Arg	Gly	Ser
				35				40			45				
Ile	Ala	Leu	Glu	Asn	Asp	Leu	Lys	Gln	Ala	Phe	Thr	Tyr	Leu	Asn	Glu
				50				55			60				
Val	Asp	Ala	Ile	Gly	Leu	Pro	Ala	Pro	Unk	Lys	Arg	Glu	Arg	Lys	Arg
	65			70				75			80				
Ser	Tyr	Cys	Cys	Gln	Thr	His	Gln	Ile	Arg	Asp	Ala	Pro	Phe	Arg	
				85				90			95				

## (2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 80 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711

Leu	Pro	Ile	Ile	Leu	Unk	Val	Ile	Val	Met	Met	Phe	Phe	Ser	Lys	Ile
1					5				10				15		
Val	Gly	Asp	Phe	Ile	Glu	Lys	His	Tyr	Arg	Val	Lys	Thr	Leu	Ala	Phe
					20			25			30				
Val	Phe	Leu	Leu	Val	Val	Gly	Val	Phe	Leu	Phe	Leu	Glu	Gly	Leu	His
					35			40			45				
Leu	His	Ile	Asn	Lys	Asn	Tyr	Leu	Tyr	Ala	Gly	Ile	Gly	Phe	Ala	Leu
	50			55					60						
Leu	Ile	Glu	Cys	Leu	Unk	Ile	Phe	Ile	Glu	Lys	Lys	Met	Lys	Lys	Ser
	65				70				75			80			

## (2) INFORMATION FOR SEQ ID NO:711:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711

Leu	Pro	Ile	Ile	Leu	Unk	Val	Ile	Val	Met	Met	Phe	Phe	Ser	Lys	Ile
1															15
Val	Gly	Asp	Phe	Ile	Glu	Lys	His	Tyr	Arg	Val	Lys	Thr	Leu	Ala	Phe
															30
Val	Phe	Leu	Leu	Val	Val	Gly	Val	Phe	Leu	Phe	Leu	Glu	Gly	Leu	His
															45
Leu	His	Ile	Asn	Lys	Asn	Tyr	Leu	Tyr	Ala	Gly	Ile	Gly	Phe	Ala	Leu
															60
Leu	Ile	Glu	Cys	Leu	Unk	Ile	Phe	Ile	Glu	Lys	Lys	Met	Lys	Lys	Ser
															80
65															
70															
75															
80															

## (2) INFORMATION FOR SEQ ID NO:712:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712

Met	Glu	Ser	Asn	Gln	Ser	Leu	Pro	Met	Ala	Leu	Ile	Ser	Cys	Ser	Pro
1															15
Asn	Ala	Lys	Gly	Ala	Asp	Ile	Lys	Gly	Tyr	Asn	Gly	Leu	Val	Gly	Glu
															30
Leu	Ile	Glu	Arg	Asn	Phe	Gln	Arg	Tyr	Gly	Val	Pro	Leu	Leu	Ser	
35															
40															
45															
Thr	Leu	Thr	Asn	Gly	Leu	Leu	Ile	Gly	Ile	Thr	Ser	Ala	Leu	Asn	Asn
50															
55															
60															
Arg	Gly	Asn	Lys	Glu	Glu	Val	Thr	Asn	Phe	Phe	Gly	Asp	Tyr	Leu	Leu
65															
70															
75															
80															
Leu	Gln	Leu	Met	Arg	Gln	Ser	Gly	Met	Gly	Ile	Asn	Gln	Val	Val	Asn
85															
90															
95															

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Gln Ile Leu Arg Asp Lys Ser Lys Ile Ala Pro Ile Val Val Ile Arg  
 100 105 110  
 Glu Gly Ser Arg Val Phe Ile Ser Pro Asn Thr Asp Ile Phe Phe Pro  
 115 120 125  
 Ile Pro Arg Glu Asn Glu Val Ile Ala Glu Phe Leu Lys  
 130 135 140

## (2) INFORMATION FOR SEQ ID NO:713:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...51

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713

Val Asn Phe Tyr Leu Ser Pro Lys Asp Tyr His His Tyr His Ala Pro  
 1 5 10 15  
 Cys Asp Leu Glu Ile Leu Glu Ala Arg Tyr Phe Ala Gly Lys Leu Leu  
 20 25 30  
 Pro Val Asn Lys Pro Ser Leu His Lys Lys Gln Asn Leu Phe Val Gly  
 35 40 45  
 Asn Glu Arg  
 50

## (2) INFORMATION FOR SEQ ID NO:714:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714

Met Asp Ile Leu Lys Ala Glu His Leu Asn Lys Gln Ile Lys Lys Thr  
 1 5 10 15  
 Lys Ile Val Ser Asp Val Ser Leu Glu Val Lys Ser Gly Glu Val Val  
 20 25 30  
 Gly Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr Thr Phe Tyr Met  
 35 40 45  
 Ile Cys Gly Leu Leu Glu Pro Ser Gly Ser Val Tyr Leu Asn Asp

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50	55	60
Val Asp Leu Ala Lys Tyr Pro Leu His Lys Arg Ser Asn Leu Gly Ile		
65	70	75
Gly Tyr Leu Pro Gln Glu Ser Ser Ile Phe Lys Glu Leu Ser Val Glu		80
85	90	95
Glu Asn Leu Ala Leu Ala Gly Glu Ser Thr Phe Lys Asn Ser Lys Glu		
100	105	110
Ser Glu Glu Lys Met Glu Ser Leu Leu Asp Ala Phe Asn Ile Gln Ala		
115	120	125
Ile Arg Glu Arg Lys Gly Met Ser Leu Ser Gly Gly Glu Arg Arg Arg		
130	135	140
Val Glu Ile Ala Arg Ala Leu Met Lys Asn Pro Lys Phe Val Leu Leu		
145	150	155
Asp Glu Pro Phe Ala Gly Val Asp Pro Ile Ala Val Ile Asp Ile Gln		160
165	170	175
Arg Ile Ile Glu Ser Leu Ile Gly Leu Asn Ile Gly Val Leu Ile Thr		
180	185	190
Asp His Asn Val Arg Glu Thr Leu Ser Val Cys His Arg Ala Tyr Val		
195	200	205
Ile Lys Ser Gly Thr Leu Leu Ala Ala Gly Thr Leu Met Lys Phe Met		
210	215	220
Lys Thr Leu Trp Cys Val Ser Ile Ile		
225	230	

## (2) INFORMATION FOR SEQ ID NO:715:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...265

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:715

Met Ile Lys Ala Arg Phe Lys Lys Arg Leu Leu Gly Ser Arg Gly Ala		
1	5	10
Phe Asp Leu Asn Ile Asp Leu Glu Ile Lys Glu Ala Glu Val Val Ala		15
20	25	30
Leu Leu Gly Glu Ser Gly Ala Gly Lys Ser Thr Ile Leu Arg Ile Leu		
35	40	45
Ala Gly Leu Glu Ala Val Ser Ser Gly Tyr Ile Glu Ala Asn His Ser		
50	55	60
Val Trp Leu Asp Thr Gln Lys Ile Phe Leu Lys Pro Gln Gln Arg		
65	70	75
Lys Ile Gly Phe Val Phe Gln Asp Tyr Ala Leu Phe Pro His Leu Asn		80
85	90	95
Val Tyr Gln Asn Ile Ala Phe Ala His Pro Lys Asp Lys Asn Lys Ile		
100	105	110
His Glu Val Leu Arg Leu Met Arg Leu Glu Asn Leu Ser Gln Gln Lys		
115	120	125
Ile Pro Lys Leu Ser Gly Gly Gln Ala Gln Arg Val Ala Leu Ala Arg		
130	135	140
Ala Leu Ile Ala Ala Lys Asn Leu Leu Leu Asp Glu Pro Leu Asn		
145	150	155
		160

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Ala Leu Asp Asn Ala Leu Lys Asn Glu Val Gln Gln Gly Leu Leu Asp  
 165 170 175  
 Phe Ile Lys Arg Glu Asn Leu Ser Val Leu Leu Val Ser His Asp Pro  
 180 185 190  
 Asn Glu Ile Thr Lys Leu Ala Arg Thr Phe Leu Phe Leu Asn Asn Gly  
 195 200 205  
 Val Ile Asp Pro Asn Gln Glu Asn Arg Leu Phe Ser Asn Arg Leu Leu  
 210 215 220  
 Val Lys Pro Leu Phe Glu Asp Glu Asn Tyr Cys His Tyr Glu Val Ile  
 225 230 235 240  
 Pro Gln Thr Ile Ser Leu Pro Lys Asp Cys Leu Asn Pro Thr Phe Lys  
 245 250 255  
 Leu Asp Phe Ile Gln Asn Lys Lys Phe  
 260 265

## (2) INFORMATION FOR SEQ ID NO:715:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...265

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:715

Met Ile Lys Ala Arg Phe Lys Arg Leu Leu Gly Ser Arg Gly Ala  
 1 5 10 15  
 Phe Asp Leu Asn Ile Asp Leu Glu Ile Lys Glu Ala Glu Val Val Ala  
 20 25 30  
 Leu Leu Gly Glu Ser Gly Ala Gly Lys Ser Thr Ile Leu Arg Ile Leu  
 35 40 45  
 Ala Gly Leu Glu Ala Val Ser Ser Gly Tyr Ile Glu Ala Asn His Ser  
 50 55 60  
 Val Trp Leu Asp Thr Gln Lys Lys Ile Phe Leu Lys Pro Gln Gln Arg  
 65 70 75 80  
 Lys Ile Gly Phe Val Phe Gln Asp Tyr Ala Leu Phe Pro His Leu Asn  
 85 90 95  
 Val Tyr Gln Asn Ile Ala Phe Ala His Pro Lys Asp Lys Asn Lys Ile  
 100 105 110  
 His Glu Val Leu Arg Leu Met Arg Leu Glu Asn Leu Ser Gln Gln Lys  
 115 120 125  
 Ile Pro Lys Leu Ser Gly Gly Gln Ala Gln Arg Val Ala Leu Ala Arg  
 130 135 140  
 Ala Leu Ile Ala Ala Lys Asn Leu Leu Asp Glu Pro Leu Asn  
 145 150 155 160  
 Ala Leu Asp Asn Ala Leu Lys Asn Glu Val Gln Gln Gly Leu Leu Asp  
 165 170 175  
 Phe Ile Lys Arg Glu Asn Leu Ser Val Leu Leu Val Ser His Asp Pro  
 180 185 190  
 Asn Glu Ile Thr Lys Leu Ala Arg Thr Phe Leu Phe Leu Asn Asn Gly  
 195 200 205  
 Val Ile Asp Pro Asn Gln Glu Asn Arg Leu Phe Ser Asn Arg Leu Leu  
 210 215 220  
 Val Lys Pro Leu Phe Glu Asp Glu Asn Tyr Cys His Tyr Glu Val Ile

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225	230	235	240
Pro Gln Thr Ile Ser Leu Pro Lys Asp Cys		Leu Asn Pro Thr Phe Lys	
245	250	255	
Leu Asp Phe Ile Gln Asn Lys Lys Phe			
260	265		

## (2) INFORMATION FOR SEQ ID NO:716:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716

Met Lys Glu Ile Val Thr Ile Glu Asn Val Ser Phe Asn Tyr His Asn  
 1               5                   10                   15  
 Arg Ala Ile Phe Lys Asp Phe Asn Leu Ser Ile Gln Glu Gly Asp Phe  
 20              25                   30  
 Leu Cys Val Leu Gly Glu Ser Gly Ser Gly Lys Ser Thr Leu Leu Gly  
 35              40                   45  
 Leu Ile Leu Gly Leu Leu Lys Pro Ser Leu Gly Ser Val Lys Ile Phe  
 50              55                   60  
 Asn Glu Thr Leu Ser Asn Asn Ala Phe Leu Arg Gln Lys Ile Gly Tyr  
 65              70                   75                   80  
 Ile Ala Gln Gly Asn Ser Leu Phe Pro His Leu Asn Ala Leu Gln Asn  
 85              90                   95  
 Met Thr Phe Cys Leu Asn Leu Gln Gly Ile Asn Lys Gln Ala Ala Gln  
 100            105                   110  
 Lys Glu Ala Lys Ala Leu Ala Leu Lys Met Gly Leu Asp Glu Ser Leu  
 115            120                   125  
 Met Asp Lys Phe Pro Asn Glu Leu Ser Gly Gly Gln Ala Lys Glu Trp  
 130            135                   140  
 Ala Leu Leu Gly Gly Leu Ser Thr Gly Gln Asn Ser Phe Tyr  
 145            150                   155

## (2) INFORMATION FOR SEQ ID NO:717:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature

## (B) LOCATION 1...191

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:717

Met Ile Phe Pro Glu Arg Phe Gln Asn Ala Phe Leu Gly Leu Ser Glu  
 1 5 10 15  
 Leu Phe Tyr Tyr Ala Ser Ser Leu Ser Phe Tyr Thr Ile Leu Ser Leu  
 20 25 30  
 Ser Pro Ile Leu Leu Phe Val Phe Ser Leu Phe Val Ser His Tyr Leu  
 35 40 45  
 Gln Ala His Ser Gly Glu Met Glu Ala Leu Ile Phe Pro Asn Ala Pro  
 50 55 60  
 Lys Leu Ile Gly Ala Ile Lys Asp Phe Leu Glu Asn Phe Lys Lys Thr  
 65 70 75 80  
 Asp Met Thr Leu Gly Thr Leu Glu Glu Val Ser Ile Val Val Ala Leu  
 85 90 95  
 Val Leu Phe Cys Glu Asn Tyr Arg Ser Ile Ala Ser Lys Ile Phe Asp  
 100 105 110  
 Ala Lys Pro Arg Asp Tyr Ala His Phe Lys Gly Lys Glu Ile Phe Leu  
 115 120 125  
 Phe Trp Gly Phe Gly Thr Thr Leu Val Phe Leu Phe Ala Leu Pro Leu  
 130 135 140  
 Val Val Phe Phe Asp Ile Lys Ile Gln Val Phe Phe Glu Asp Lys Asp  
 145 150 155 160  
 Ser Ser Leu Leu His Val Leu Arg Trp Ile Gly Thr Tyr Ala Phe Phe  
 165 170 175  
 Leu Ile Leu Phe Thr Ile Pro Thr Asn Lys Val Phe Lys Leu Lys  
 180 185 190

## (2) INFORMATION FOR SEQ ID NO:718:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...243

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:718

Met Val Leu Met Ile Phe Thr Ser Ile Leu Lys Ile Ala Leu Lys Val  
 1 5 10 15  
 Leu Ser Glu Arg Lys Lys Asn Arg Tyr Gly Phe Pro Arg Ile Phe Asp  
 20 25 30  
 Val Ala Asp Ile Glu Gln Glu Glu Arg Glu Val Ile Glu Trp Arg Glu  
 35 40 45  
 Lys Lys Lys Ala Ser Lys Gln Ser Tyr Lys Gln Asn Leu Gln Ile Asn  
 50 55 60  
 Lys Ile Ala Asn Asp Leu Lys Arg Asp Lys Ile Val Asp Lys Arg Thr  
 65 70 75 80  
 Ile Leu Ser Val Ile Asp Ala Asp Ile Glu Arg Gly Phe Ile Pro Pro  
 85 90 95  
 Lys Asp Leu Leu Lys Gln Leu Glu Lys Ile Ser Ala Ser Leu Ser Lys  
 100 105 110  
 Asp Ile Val Ile Thr Ile Lys Gln Val Glu Lys Leu Glu Leu Asn Tyr

115	120	125
Ala Leu Ile Asp Asn Ile Gln His Asn Thr Leu Asp Asp Thr Leu Asp		
130	135	140
Phe Thr Phe Ile Val Gly Asp Ser Leu Ser Val Gln Ser Leu Tyr Val		
145	150	155
Thr Phe Asn Leu Val Ile Asp Ile Asp Arg Pro Met Ser Glu Gln Phe		160
165	170	175
Leu Asn Unk Ile Gly Lys Leu Gly Ser Phe Glu Ser Arg Glu Gln Ala		
180	185	190
Leu Glu Trp Val Arg Leu Ser Gln Thr Lys Leu Ile Ile Glu Thr Pro		
195	200	205
Lys Glu Ala Leu Lys Asn Ala Glu Leu Ser Gln Ile Glu Glu Ile Leu		
210	215	220
Thr Gly Cys Ile Phe Asn Gly Ala Tyr Arg Leu Gln Asn Asp Leu Lys		
225	230	235
Lys Gly Arg		240

## (2) INFORMATION FOR SEQ ID NO:719:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...236

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:719

Val Ser Glu Val Ala Ser Val Gly Gly Phe Val Lys Asp Tyr Glu Val		
1	5	10
Thr Leu Gln Asn Asp Ser Leu Ile Arg Tyr Asn Leu Ser Leu Glu Gln		15
20	25	30
Val Ala Asn Ala Ile Lys Asn Ser Asn Asn Asp Thr Gly Gly Gly Val		
35	40	45
Ile Leu Glu Asn Gly Phe Glu Lys Ile Ile Arg Ser His Gly Tyr Ile		
50	55	60
Gln Ser Leu Asn Asp Leu Glu Glu Ile Val Val Lys Lys Glu Gly Ala		
65	70	75
Ile Pro Leu Lys Ile Lys Asp Ile Ala Ser Val Val Arg Leu Ala Pro Lys		80
85	90	95
Pro Arg Arg Gly Ala Ala Asn Leu Asn Gly Asp Lys Glu Val Val Gly		
100	105	110
Gly Ile Val Met Val Arg Tyr His Ala Asp Thr Tyr Lys Val Leu Lys		
115	120	125
Ala Ile Lys Glu Lys Ile Ala Thr Leu Gln Ala Ser Asn Pro Asp Val		
130	135	140
Lys Ile Thr Ser Val Tyr Asp Arg Ser Glu Leu Ile Glu Lys Gly Ile		
145	150	155
Asp Asn Leu Ile His Thr Leu Ile Glu Glu Ser Val Ile Val Leu Val		160
165	170	175
Ile Ile Ala Ile Phe Leu Leu His Phe Arg Ser Ala Leu Val Val Ile		
180	185	190
Ile Thr Leu Pro Leu Arg Val Cys Ile Ser Phe Leu Leu Met Ser Tyr		
195	200	205

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Phe Asn Ile Glu Ala Ser Ile Met Ser Leu Gly Gly Ile Ala Ile Ala  
 210                215                220  
 Ile Gly Ala Met Val Asn Ala Ala Ile Val Met Val  
 225                230                235

## (2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 175 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720

Val Glu Thr Phe Leu Arg Ile Phe Glu Lys Asp Ile Phe Asn Thr Pro  
 1                5                10                15  
 Tyr Lys Leu Glu Val Ile Asn Ala Thr Glu Gly Gly Ala Arg Ile Lys  
 20                25                30  
 Gly Thr Lys Glu Met Pro Phe Lys Glu Val Cys Glu Lys Ile Asp Lys  
 35                40                45  
 Ser Lys Pro Lys Pro Pro Ile Asn Leu Ile Tyr Pro Thr Gln Ser Glu  
 50                55                60  
 Gln Ala Lys Asn Leu Lys Ile Ala Lys Lys Cys Glu Glu Ile Ile  
 65                70                75                80  
 Lys Tyr Ala Asn Glu Lys Lys Thr Gln Val Glu Glu Ala Phe Leu Lys  
 85                90                95  
 Val Ala Glu Phe Leu Glu Lys Val Glu Lys Leu His Glu Lys Asn Lys  
 100                105                110  
 Leu Glu Glu Leu Asp Phe Glu Glu Leu Glu Asn Leu Ser Ala Glu Ile  
 115                120                125  
 Asp Asn Val Lys Glu Leu Phe Asp Asp Lys Arg Phe Asn Ser Tyr Phe  
 130                135                140  
 Met Asp Ala Ile Gln Ser Tyr Ile Phe His Gln Glu Leu His Ile Ala  
 145                150                155                160  
 Glu Ile Val Cys Lys Lys Thr Ser Asn Glu Asp Gly Ile Lys Gly  
 165                170                175

## (2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 226 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

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- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...226

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:721

```

Met Lys Thr Pro Cys Asn Ala Tyr Phe Leu Lys Thr Pro Pro Lys Asn
1      5          10          15
Lys Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Phe Leu Leu
20     25          30
Leu Ala Ser Ala Leu Trp Leu Ile Pro Arg Ser Ala Ile Glu Unk Lys
35     40          45
Pro Leu Val Val Ala Thr Lys Pro Ser Ser Glu Gln Tyr Ile Leu Gly
50      55          60
Glu Ile Leu Ser Leu Leu Glu Lys His His Ile Pro Ile Lys Arg
65      70          75          80
Ala Phe Gly Ile Gly Gly Thr Met Asn Ile His Pro Ala Leu Ile
85     90          95
Arg Gly Asp Phe Asp Leu Tyr Val Glu Tyr Thr Gly Thr Ala Trp Val
100    105         110
Asn Thr Leu Lys Asn Pro Leu Thr Gln Lys Val Asp Phe Glu Thr Ile
115    120         125
Lys Lys Arg Tyr Glu Lys Glu Phe Asn Leu Leu Trp Val Gly Leu Leu
130    135         140
Gly Phe Asn Asn Thr Tyr Ser Leu Ala Ile Ser Lys Glu Asp Ala Gln
145    150         155         160
Lys Tyr Ala Ile Glu Thr Phe Ser Asp Leu Ala Phe His Ser Pro Asn
165    170         175
Phe Asp Phe Gly Ala Glu Unk Asp Phe Phe Glu Arg Glu Asp Ala Phe
180    185         190
Lys Gly Leu Ile Lys Ala Tyr Arg Phe His Phe Arg Ser Leu His Glu
195    200         205
Met Unk Ile Asn Leu Arg Tyr Lys Ser Phe Glu Ser Leu Ile Arg Unk
210    215         220
Thr Leu
225

```

## (2) INFORMATION FOR SEQ ID NO:722:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 79 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...79

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:722

```

Val Met Val Tyr Lys Leu Pro Lys His Gln Gln Asn Lys Val Met Ile
1      5          10          15
Leu Gly Leu Gly Leu Ala Met Ile Thr Arg Ile Gly Leu Leu Gly Ser
20     25          30
Leu Phe Phe Ile Ser His Leu Gln Lys Pro Leu Phe Ala Ile Ala Gly
35     40          45
Met Ser Phe Ser Trp Arg Asp Val Val Leu Leu Gly Gly Ala Phe
50      55          60

```

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Leu Ala Phe Lys Ala Leu Val Glu Leu Lys Arg Ala Asp Leu Ser  
 65                   70                   75

## (2) INFORMATION FOR SEQ ID NO:723:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...64

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:723

Val Lys Phe Ser Val Leu Thr Leu Phe Pro Gln Leu Ile Leu Pro Tyr  
 1               5                   10                   15  
 Phe Glu Asp Ser Ile Leu Lys Arg Ala Leu Glu Lys Asn Leu Phe Glu  
 20              25                   30  
 Leu Glu Val Leu Asn Leu Arg Asp Phe Ser Ala Asn Lys Tyr Gln Lys  
 35              40                   45  
 Ala Unk Ser His Ala His Trp Trp Gly Cys Gly Ala Asn Phe Arg Pro  
 50              55                   60

## (2) INFORMATION FOR SEQ ID NO:723:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...64

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:723

Val Lys Phe Ser Val Leu Thr Leu Phe Pro Gln Leu Ile Leu Pro Tyr  
 1               5                   10                   15  
 Phe Glu Asp Ser Ile Leu Lys Arg Ala Leu Glu Lys Asn Leu Phe Glu  
 20              25                   30  
 Leu Glu Val Leu Asn Leu Arg Asp Phe Ser Ala Asn Lys Tyr Gln Lys  
 35              40                   45  
 Ala Unk Ser His Ala His Trp Trp Gly Cys Gly Ala Asn Phe Arg Pro  
 50              55                   60

## (2) INFORMATION FOR SEQ ID NO:724:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 138 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...138
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:724

Leu Trp Arg Thr Pro Lys Thr Pro Leu Val Ile Lys Pro Tyr Leu Lys  
 1               5               10               15  
 Ser Met Ser Asp Ser Glu Ile Phe Ala Unk Unk Cys Val Gly Met Ala  
 20              25              30  
 Ser Val Unk Gly Pro Val Leu Ala Gly Tyr Ala Ser Met Gly Ile Pro  
 35              40              45  
 Leu Pro Tyr Leu Ile Ala Ala Ser Phe Met Ser Ala Pro Gly Gly Leu  
 50              55              60  
 Leu Phe Ala Lys Thr Ile Tyr Pro Gln Asn Glu Thr Ile Ser Ser His  
 65              70              75              80  
 Ala Asp Val Ser Ala Glu Glu His Val Asn Ile Ile Glu Ala Unk Ala  
 85              90              95  
 Unk Gly Ala Ser Thr Gly Unk His Leu Ala Leu His Val Gly Ala Met  
 100            105            110  
 Leu Leu Ala Phe Val Gly Met Val Ala Leu Val Asn Gly Leu Leu Gly  
 115            120            125  
 Val Val Gly Gly Phe Leu Gly Met Glu His  
 130            135

## (2) INFORMATION FOR SEQ ID NO:724:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 138 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...138
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:724

Leu Trp Arg Thr Pro Lys Thr Pro Leu Val Ile Lys Pro Tyr Leu Lys  
 1               5               10               15  
 Ser Met Ser Asp Ser Glu Ile Phe Ala Unk Unk Cys Val Gly Met Ala  
 20              25              30  
 Ser Val Unk Gly Pro Val Leu Ala Gly Tyr Ala Ser Met Gly Ile Pro  
 35              40              45

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Leu Pro Tyr Leu Ile Ala Ala Ser Phe Met Ser Ala Pro Gly Gly Leu  
 50 55 60  
 Leu Phe Ala Lys Thr Ile Tyr Pro Gln Asn Glu Thr Ile Ser Ser His  
 65 70 75 80  
 Ala Asp Val Ser Ala Glu Glu His Val Asn Ile Ile Glu Ala Unk Ala  
 85 90 95  
 Unk Gly Ala Ser Thr Gly Unk His Leu Ala Leu His Val Gly Ala Met  
 100 105 110  
 Leu Leu Ala Phe Val Gly Met Val Ala Leu Val Asn Gly Leu Leu Gly  
 115 120 125  
 Val Val Gly Gly Phe Leu Gly Met Glu His  
 130 135

## (2) INFORMATION FOR SEQ ID NO:725:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 210 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...210

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:725

Met Phe Val Val Phe Ile Glu Gly Phe Gly Leu Ala Ile Ser Leu Cys  
 1 5 10 15  
 Ala Ala Val Gly Ala Gln Ser Leu Phe Ile Val Glu Arg Gly Met Ala  
 20 25 30  
 Arg Asn Tyr Val Phe Leu Ile Cys Ala Leu Cys Phe Met Cys Asp Ile  
 35 40 45  
 Val Leu Met Ser Met Gly Val Phe Gly Val Gly Ala Tyr Phe Ala Lys  
 50 55 60  
 Asn Leu Tyr Leu Ser Leu Phe Leu Asn Leu Phe Gly Ala Val Phe Thr  
 65 70 75 80  
 Gly Phe Tyr Ala Phe Leu Ala Leu Lys Thr Leu Phe Gln Thr Phe Lys  
 85 90 95  
 Lys Lys Gln Val Gln Thr Pro Lys Lys Leu Ser Leu Lys Lys Thr Leu  
 100 105 110  
 Leu Phe Thr Leu Gly Val Thr Leu Leu Asn Pro Gln Val Tyr Leu Glu  
 115 120 125  
 Met Val Phe Leu Ile Gly Ala Ser Ala Met Ser Phe Asn Leu Val Gln  
 130 135 140  
 Lys Phe Val Phe Leu Ala Gly Thr Leu Ser Ala Ala Phe Ser Trp Leu  
 145 150 155 160  
 Leu Leu Leu Cys Thr Met Ser Leu Arg Tyr Gly Ser Lys Leu Leu Asn  
 165 170 175  
 Asn Gln Lys Ile Phe Met Gly Val Asn Leu Phe Val Thr Ala Ile Met  
 180 185 190  
 Gly Thr Leu Ser Val Thr Leu Phe Arg Asp Phe Leu Ala Leu Leu Ser  
 195 200 205  
 Lys Thr  
 210

## (2) INFORMATION FOR SEQ ID NO:726:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 296 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...296
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:726

Val	Lys	Pro	Lys	Ser	Met	Lys	Glu	Lys	Leu	Arg	Gly	Ala	Met	Val	Asn
1					5				10					15	
Ile	Leu	Arg	Ile	Lys	Met	Ile	Glu	Ile	Ser	Glu	Trp	Leu	Gln	Lys	Leu
					20				25					30	
Asp	Asp	Ala	Leu	Asp	Lys	Val	Val	Ala	Lys	Lys	Glu	Pro	Glu	Ser	Phe
					35				40					45	
Leu	Lys	Pro	Ile	Ile	Ser	Pro	Ile	Glu	Asp	Tyr	Gln	Lys	Ser	Val	Arg
					50				55					60	
Gln	Ile	Gln	Ala	Gln	Phe	Thr	Asp	Ala	Pro	Lys	Phe	Asn	Glu	Glu	Gly
					65				70					80	
Ala	Tyr	Pro	Gln	Phe	Leu	Ser	Cys	Gly	Leu	Leu	Gln	Val	Arg	Gly	Lys
					85				90					95	
Asn	Gly	Ala	Asn	Met	Glu	Phe	Leu	Leu	Pro	Lys	Val	Tyr	Pro	Phe	Pro
					100				105					110	
Pro	Lys	Ser	Leu	Tyr	Ile	Glu	His	Glu	Lys	Asp	Gly	Gln	Phe	Leu	Arg
					115				120					125	
Glu	Met	Leu	Met	Arg	Leu	Leu	Ser	Ser	Ala	Pro	Leu	Val	Gln	Leu	Glu
					130				135					140	
Val	Ile	Leu	Ile	Asp	Ala	Leu	Ser	Leu	Gly	Gly	Ile	Phe	Asn	Leu	Ala
					145				150					160	
Arg	Arg	Leu	Leu	Asp	Lys	Asn	Asn	Asp	Phe	Ile	Tyr	Gln	Gln	Arg	Ile
					165				170					175	
Leu	Thr	Glu	Ser	Lys	Glu	Ile	Glu	Glu	Ala	Leu	Lys	His	Leu	His	Glu
					180				185					190	
Tyr	Leu	Lys	Val	Asn	Leu	Gln	Glu	Lys	Leu	Ala	Gly	Phe	Arg	Asp	Phe
					195				200					205	
Val	His	Tyr	Asn	Glu	Asn	Ala	Lys	Asp	Ser	Leu	Pro	Leu	Lys	Ala	Leu
					210				215					220	
Phe	Leu	Ser	Gly	Val	Asp	Ala	Leu	Ser	Lys	Asp	Ala	Leu	Tyr	Tyr	Leu
					225				230					240	
Glu	Lys	Ile	Met	Arg	Phe	Gly	Ser	Lys	Asn	Gly	Val	Leu	Ser	Phe	Val
					245				250					255	
Asn	Leu	Glu	Ser	Glu	Lys	Asn	Asn	Gln	Ser	Ala	Glu	Asp	Leu	Lys	Arg
					260				265					270	
Tyr	Ala	Glu	Phe	Phe	Lys	Asp	Arg	Thr	Ser	Phe	Glu	Unk	Leu	Lys	Tyr
					275				280					285	
Leu	Asn	Val	Glu	Ile	Ile	Ser	Asp								
					290				295						

## (2) INFORMATION FOR SEQ ID NO:727:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 94 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

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- (iii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...94
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:727

Val Leu Ile Ser Val Met Ile Gly Gln Asn Gln Val Leu Gly Phe Ile  
1 5 10 15  
Gly Thr Asn Phe Lys Gln Glu Leu Val Val Asp Phe Ile Val Pro Ser  
20 25 30  
Ala Glu Ile Asn Ile Gly Asn Gln Val Ile Thr Ser Gly Leu Asp Gly  
35 40 45  
Ile Phe Gly Ala Gly Val Phe Val Gly Glu Val Ser Ser Val Glu Asp  
50 55 60  
His Tyr Thr Tyr Lys Ser Ala Val Leu Lys Asn Ala Phe Leu Ser Glu  
65 70 75 80  
Ala Lys Leu Leu Arg His Val Phe Leu Ser Gly Val Lys Asn  
85 90

## (2) INFORMATION FOR SEQ ID NO:728:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 83 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...83
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:728

Met Glu Ala Gln Leu Arg Phe Thr Gly Val Gly Gly Gln Gly Val Leu  
1 5 10 15  
Leu Ala Gly Glu Ile Leu Ala Glu Ala Lys Ile Val Ser Gly Gly Tyr  
20 25 30  
Gly Thr Lys Thr Ser Thr Tyr Thr Ser Gln Val Arg Gly Gly Pro Thr  
35 40 45  
Lys Val Asp Ile Leu Leu Asp Lys Asp Glu Ile Ile Phe Pro Tyr Ala  
50 55 60  
Lys Glu Gly Glu Ile Asp Phe Met Leu Ser Val Ala Gln Ile Ser Tyr  
65 70 75 80  
Asn Gln Phe

## (2) INFORMATION FOR SEQ ID NO:729:

- (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 203 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729

Met	Gln	Ala	Trp	Val	Asp	Lys	Pro	Val	Leu	Leu	Glu	Pro	Asp	Ser	Asn
1				5					10				15		
Ala	Gln	Tyr	Ala	Ala	Val	Ile	Glu	Ile	Asp	Val	Ala	Glu	Ile	Thr	Glu
					20			25				30			
Pro	Ile	Leu	Ala	Cys	Pro	Asn	Asp	Pro	Asp	Asp	Val	Ala	Thr	Leu	Ser
					35		40				45				
Glu	Val	Leu	Ala	Asp	Thr	Thr	Gly	Lys	Arg	Pro	His	Ala	Ile	Asp	Glu
					50		55		60						
Val	Phe	Ile	Gly	Ser	Cys	Met	Thr	Asn	Ile	Gly	His	Phe	Arg	Ala	Phe
					65		70		75		80				
Gly	Glu	Ile	Val	Lys	Asn	Ala	Pro	Pro	Ser	Gln	Ala	Arg	Leu	Trp	Val
					85		90			95					
Val	Pro	Pro	Ser	Lys	Met	Asp	Glu	Gln	Glu	Leu	Ile	Asn	Glu	Gly	Tyr
					100		105			110					
Tyr	Ala	Ile	Phe	Gly	Ala	Ala	Gly	Ala	Arg	Thr	Glu	Val	Pro	Gly	Cys
					115		120			125					
Ser	Leu	Cys	Met	Gly	Asn	Gln	Ala	Arg	Val	Arg	Asp	Asn	Ala	Val	Val
					130		135			140					
Phe	Ser	Thr	Ser	Thr	Arg	Asn	Phe	Asp	Asn	Arg	Met	Gly	Arg	Gly	Ala
					145		150		155		160				
Lys	Val	Tyr	Leu	Gly	Ser	Ala	Glu	Leu	Gly	Ala	Ala	Cys	Ala	Leu	Leu
					165		170			175					
Gly	Arg	Ile	Pro	Thr	Lys	Glu	Glu	Tyr	Met	Asn	Leu	Val	Ser	Glu	Lys
					180		185			190					
Leu	Glu	Ser	Gln	Lys	Asp	Lys	Ile	Tyr	Arg	Ser					
					195		200								

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 220 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730

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Val Gly Asn Ala Gly Val Ala Leu Ala Gly Leu Met Ser Asp Glu Ile  
 1 5 10 15  
 Tyr Leu Cys Ala Leu Asp Cys Ala Tyr Ile Lys Gly Phe Lys Lys His  
 20 25 30  
 Ala Gln Asn Ser Tyr Tyr Gly Asp Glu Lys Glu Ile Asp Thr Ser Ser  
 35 40 45  
 Leu Ile Ser Val Glu Gly Asn Val Glu Gly Tyr Glu Thr Phe Ser Asp  
 50 55 60  
 Ser Leu Phe Leu Leu Ser Lys Glu Arg Ile Glu Glu Ala Leu His Tyr  
 65 70 75 80  
 Tyr Gln Pro Lys Lys Val Tyr Asn Leu Ser Tyr Gly Ala Lys Ile Lys  
 85 90 95  
 His Ala Val Ser Leu Asn His Ser Gln Val Lys Leu Lys Gln Ile Asn  
 100 105 110  
 Lys Gln Asp Ala Ile Val Arg Ile Lys Ser Met Phe Ser Pro Arg Ser  
 115 120 125  
 Asn His Ala Lys Asp Leu Lys Asn Leu Gln Lys Asn Leu Ile Arg Phe  
 130 135 140  
 Lys Glu Asp Phe Phe Thr His Leu Asn Thr Pro Cys Lys Thr Lys Gln  
 145 150 155 160  
 Glu Ala Phe Glu Trp Val Asp Ser Leu Ser Gly Phe Cys Gln Thr Ala  
 165 170 175  
 Ser Ala Lys Thr Pro Thr Ile Gly Ile Leu Phe Glu Gly Ser Val Ala  
 180 185 190  
 His Ile Leu Gln Ser Val Leu Ile Val Ser Leu His Leu Lys Glu Asn  
 195 200 205  
 Glu Leu Thr Leu Leu Ser Asn Ser Leu Lys Thr Pro  
 210 215 220

## (2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 116 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731

Val Met Asn Phe Phe Val Gly Gly Leu Ser Ile Val Cys Asn Val Val  
 1 5 10 15  
 Val Ile Thr Tyr Ser Ala Leu His Pro Thr Ala Pro Val Glu Gly Ala  
 20 25 30  
 Glu Asp Ile Val Gln Val Ser His His Leu Thr Ser Phe Tyr Gly Pro  
 35 40 45  
 Ala Thr Gly Leu Leu Phe Gly Phe Thr Tyr Leu Tyr Ala Ala Ile Asn  
 50 55 60  
 His Thr Phe Gly Leu Asp Trp Arg Pro Tyr Ser Trp Tyr Ser Leu Phe  
 65 70 75 80  
 Val Ala Ile Asn Thr Val Pro Ala Ala Ile Leu Ser His Tyr Ser Asp  
 85 90 95  
 Met Leu Asp Asp His Lys Val Leu Gly Ile Thr Glu Gly Asp Trp Trp  
 100 105 110  
 Ala Ile Ile Unk

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## (2) INFORMATION FOR SEQ ID NO:731:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...116

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:731

Val	Met	Asn	Phe	Phe	Val	Gly	Gly	Leu	Ser	Ile	Val	Cys	Asn	Val	Val
1					5					10				15	
Val	Ile	Thr	Tyr	Ser	Ala	Leu	His	Pro	Thr	Ala	Pro	Val	Glu	Gly	Ala
			20					25					30		
Glu	Asp	Ile	Val	Gln	Val	Ser	His	His	Leu	Thr	Ser	Phe	Tyr	Gly	Pro
			35				40				45				
Ala	Thr	Gly	Leu	Leu	Phe	Gly	Phe	Thr	Tyr	Leu	Tyr	Ala	Ala	Ile	Asn
			50				55			60					
His	Thr	Phe	Gly	Leu	Asp	Trp	Arg	Pro	Tyr	Ser	Trp	Tyr	Ser	Leu	Phe
			65			70			75				80		
Val	Ala	Ile	Asn	Thr	Val	Pro	Ala	Ala	Ile	Leu	Ser	His	Tyr	Ser	Asp
			85				90				95				
Met	Leu	Asp	Asp	His	Lys	Val	Leu	Gly	Ile	Thr	Glu	Gly	Asp	Trp	Trp
			100				105				110				
Ala	Ile	Ile	Unk												
			115												

## (2) INFORMATION FOR SEQ ID NO:732:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...248

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:732

Met	Gln	Lys	Ser	Ile	Phe	Lys	Ile	Thr	Leu	Leu	Leu	Val	Phe	Leu	Phe
1					5				10				15		
Leu	Arg	Asn	Ala	Val	Gly	Leu	Asp	Asp	Lys	Lys	Ala	Ala	Pro	Lys	Ser
				20					25				30		

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Val Gln Asn Thr Pro Lys Asn Leu Pro Pro Ile Gln Leu Arg Leu Asp  
 35 40 45  
 Gln Ala Tyr Glu Asp Leu Ile Lys Met Leu Asp Asn Met Gly Lys Ser  
 50 55 60  
 Thr Gln Tyr Glu Phe Pro Lys Ile Lys Glu Ile Leu Glu Gln Ser Glu  
 65 70 75 80  
 Glu Glu Trp Leu Gly Val Ala His Glu Glu Cys Val Ala Leu Val Met  
 85 90 95  
 Leu Ile Ser Pro Lys Ala Ser Ile Glu Asn Ser Pro Ile Tyr Lys Asn  
 100 105 110  
 Cys Tyr Glu Ala Tyr Val Lys Gln Arg Ile His Asp Leu Tyr Asp Phe  
 115 120 125  
 Tyr Ile Glu Gly Lys Lys Val Lys Arg Lys Ile Lys Lys Ala His Glu  
 130 135 140  
 His Glu Met Ala Leu Asn Lys Ser Gln Pro Leu Lys Lys Glu Pro Pro  
 145 150 155 160  
 Lys Ser Glu Asn Lys Lys Gly Leu Thr Lys Pro Ser Leu Lys Asp Ala  
 165 170 175  
 Lys Ile Pro Lys Gly Tyr Tyr Leu Gln Ile Gly Ala Phe Leu Asn Ser  
 180 185 190  
 Pro Ser Lys Asp Phe Leu Gln Thr Leu Lys Thr Phe Pro His Gln Met  
 195 200 205  
 Glu Glu Lys Asp Ser Leu Thr His Tyr Leu Ile Gly Pro Tyr Lys Thr  
 210 215 220  
 Lys Glu Glu Ala Leu Lys Gln Leu Glu Asn Ala Ala Lys Ser Phe Lys  
 225 230 235 240  
 Asn Lys Pro Ala Leu Val Glu Lys  
 245

## (2) INFORMATION FOR SEQ ID NO:733:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...150

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:733

Met Gln Glu Ile Leu Ile Pro Leu Lys Glu Lys Ser Tyr Lys Val Phe  
 1 5 10 15  
 Leu Gly Glu Leu Pro Glu Ile Lys Leu Lys Gln Lys Ala Leu Ile Ile  
 20 25 30  
 Ser Asp Ser Ile Val Ala Gly Leu His Leu Pro Tyr Leu Leu Glu Arg  
 35 40 45  
 Leu Asn Ala Leu Glu Val Arg Val Cys Val Ile Glu Ser Gly Glu Lys  
 50 55 60  
 Tyr Lys Asn Phe His Ser Leu Glu Arg Ile Leu Asn Asn Ala Phe Glu  
 65 70 75 80  
 Met Gln Leu Asn Arg His Ser Leu Met Ile Ala Leu Gly Gly Val  
 85 90 95  
 Ile Ser Asp Met Val Gly Phe Ala Ser Ser Ile Tyr Phe Arg Gly Ile  
 100 105 110  
 Asp Phe Ile Asn Ile Pro Tyr Asp Phe Thr Arg Ser Ser Gly Cys Glu

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115	120	125
Arg Gly Gly Glu Asn Arg Asp Gln His Ala Leu Trp Gln Glu Pro Asn		
130	135	140
Arg Ile Val Pro Pro Ala		
145	150	

## (2) INFORMATION FOR SEQ ID NO:734:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734

Val	Leu	Leu	Gly	Lys	His	Ser	Gly	Ala	Gly	Leu	Leu	Ser	Ala	Leu	Unk
1								5		10					15
Ala	Leu	Ser	Phe	Gly	Ser	Gly	Val	Val	Ser	Ile	Gln	Ala	Leu	Glu	Cys
								20		25					30
Glu	Ile	Thr	Ser	Asn	Asn	Lys	Pro	Leu	Glu	Leu	Val	Phe	Cys	Glu	Asn
								35		40					45
Phe	Pro	Lys	Lys	Leu	Ser	Ala	Phe	Ala	Leu	Gly	Met	Gly	Leu	Glu	Asn
								50		55					60
Ile	Pro	Lys	Asp	Phe	Lys	Tys	Trp	Leu	Glu	Leu	Ala	Pro	Cys	Val	Leu
								65		70					80
Asp	Ala	Gly	Val	Phe	Tyr	His	Lys	Glu	Val	Leu	Gln	Ala	Leu	Glu	Lys
								85		90					95
Glu	Val	Ile	Leu	Thr	Pro	His	Pro	Lys	Glu	Phe	Leu	Ser	Leu	Leu	Lys
								100		105					110
Ser	Val	Gly	Ile	Asn	Ile	Ser	Met	Leu	Glu	Leu	Leu	Asp	Asn	Lys	Leu
								115		120					125
Glu	Ile	Ala	Arg	Asp	Phe	Ser	Gln	Lys	Tyr	Pro	Lys	Val	Val	Leu	Leu
								130		135					140
Leu	Lys	Gly	Ala	Asn	Thr	Leu	Ile	Ala	His	Gln	Gly	Arg	Val	Phe	Ile
								145		150					160
Asn	Asn	Leu	Gly	Ser	Val	Ala	Leu	Ala	Lys	Ala	Gly	Ser	Gly	Asp	Val
								165		170					175
Leu	Ala	Gly	Leu	Ile	Val	Ser	Leu	Leu	Ser	Gln	Asn	Tyr	Thr	Pro	Leu
								180		185					190
Unk	Ala	Ala	Ile	Asn	Ala	Ser	Leu	Ala	His	Ala	Leu	Ala	Gly	Leu	Unk
								195		200					205
Phe	Lys	Asn	Unk	Unk	Ala	Leu	Thr	Pro	Unk	Asp	Leu	Ile	Glu	Lys	Unk
								210		215					220
Lys	Arg	Leu													
								225							

## (2) INFORMATION FOR SEQ ID NO:734:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734

Val	Leu	Leu	Gly	Lys	His	Ser	Gly	Ala	Gly	Leu	Leu	Ser	Ala	Leu	Unk
1					5				10				15		
Ala	Leu	Ser	Phe	Gly	Ser	Gly	Val	Val	Ser	Ile	Gln	Ala	Leu	Glu	Cys
			20				25						30		
Glu	Ile	Thr	Ser	Asn	Asn	Lys	Pro	Leu	Glu	Leu	Val	Phe	Cys	Glu	Asn
			35				40					45			
Phe	Pro	Lys	Lys	Leu	Ser	Ala	Phe	Ala	Leu	Gly	Met	Gly	Leu	Glu	Asn
	50				55				60						
Ile	Pro	Lys	Asp	Phe	Lys	Trp	Leu	Glu	Leu	Ala	Pro	Cys	Val	Leu	
	65				70			75				80			
Asp	Ala	Gly	Val	Phe	Tyr	His	Lys	Glu	Val	Leu	Gln	Ala	Leu	Glu	Lys
			85				90					95			
Glu	Val	Ile	Leu	Thr	Pro	His	Pro	Lys	Glu	Phe	Leu	Ser	Leu	Leu	Lys
			100				105					110			
Ser	Val	Gly	Ile	Asn	Ile	Ser	Met	Leu	Glu	Leu	Leu	Asp	Asn	Lys	Leu
	115						120					125			
Glu	Ile	Ala	Arg	Asp	Phe	Ser	Gln	Lys	Tyr	Pro	Lys	Val	Val	Leu	Leu
	130				135				140						
Leu	Lys	Gly	Ala	Asn	Thr	Leu	Ile	Ala	His	Gln	Gly	Arg	Val	Phe	Ile
	145					150			155				160		
Asn	Asn	Leu	Gly	Ser	Val	Ala	Leu	Ala	Lys	Ala	Gly	Ser	Gly	Asp	Val
						165			170			175			
Leu	Ala	Gly	Leu	Ile	Val	Ser	Leu	Leu	Ser	Gln	Asn	Tyr	Thr	Pro	Leu
			180				185					190			
Unk	Ala	Ala	Ile	Asn	Ala	Ser	Leu	Ala	His	Ala	Leu	Ala	Gly	Leu	Unk
			195				200					205			
Phe	Lys	Asn	Unk	Unk	Ala	Leu	Thr	Pro	Unk	Asp	Leu	Ile	Glu	Lys	Unk
	210					215					220				
Lys	Arg	Leu													
	225														

(2) INFORMATION FOR SEQ ID NO:735:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735

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Met Arg Ile Leu His Tyr Gly Gly Glu Leu Pro Cys Asp Cys Pro Lys  
 1 5 10 15  
 Arg Ile Ala Gly Leu Asp Phe Ala Leu Lys Ile Leu Thr Asn Ile Thr  
 20 25 30  
 Ser Asp His Leu Asp Phe His Gln Asn Ile Glu Asn Tyr Arg Asp Ala  
 35 40 45  
 Lys Asn Ser Phe Phe Lys Asp Glu Gly Leu Lys Val Ile Asn Arg Asp  
 50 55 60  
 Glu Thr Asn Ala Leu Phe Asn Pro Ile Asn Ala Arg Thr Tyr Ala Leu  
 65 70 75 80  
 Asp Lys Lys Ala His Leu Asn Val Gln Ala Phe Ser Leu Asn Pro Ser  
 85 90 95  
 Ile Ser Ala Ser Leu Cys Tyr Gln His Asp Leu Arg Asp Pro Asn Leu  
 100 105 110  
 Lys Glu Thr Ala Leu Ile His Ser Pro Leu Leu Gly Arg Tyr Asn Leu  
 115 120 125  
 Tyr Asn Ile Leu Ala Gly Val Leu Gly Val Lys Leu Leu Thr Gln Leu  
 130 135 140  
 Pro Leu Glu Thr Ile Ala Pro Leu Leu Glu Asn Phe Tyr Gly Val Lys  
 145 150 155 160  
 Gly Arg Leu Glu Ile Val His Ser Lys Pro Leu Val Val Val Asp Phe  
 165 170 175  
 Ala His Thr Thr Asp Gly Met Gln Gln Val Phe  
 180 185

## (2) INFORMATION FOR SEQ ID NO:736:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...198

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:736

Val Ser Ile Lys Glu Glu Ser Gln Thr Leu Ala Asp Ile Thr Phe Gln  
 1 5 10 15  
 Asn Tyr Phe Arg Met Phe Ser Lys Leu Ser Gly Met Thr Gly Thr Ala  
 20 25 30  
 Gln Thr Glu Ala Thr Glu Phe Leu Glu Ile Tyr Asn Leu Glu Val Val  
 35 40 45  
 Ser Ile Pro Thr Asn Leu Ala Ile Lys Arg Lys Asp Leu Asn Asp Leu  
 50 55 60  
 Ile Tyr Lys Ser Glu Lys Glu Lys Phe Asp Ala Val Ile Leu Lys Ile  
 65 70 75 80  
 Lys Glu Leu His Asp Lys Gly Gln Pro Val Leu Val Gly Thr Ala Ser  
 85 90 95  
 Ile Glu Lys Ser Glu Thr Leu His Ala Leu Leu Lys Lys Glu Arg Ile  
 100 105 110  
 Pro His Thr Val Leu Asn Ala Lys Gln His Thr Lys Glu Ala Glu Ile  
 115 120 125  
 Ile Lys Asp Ala Gly Leu Lys Gly Ala Val Thr Ile Ala Thr Asn Met  
 130 135 140

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Ala Gly Arg Gly Val Asp Ile Lys Leu Thr Asp Glu Val Lys Glu Leu  
 145           150           155           160  
 Gly Gly Leu Tyr Ile Ile Gly Thr Glu Arg His Glu Ser Arg Arg Ile  
 165           170           175  
 Asp Asn Gln Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp Pro Gly Val  
 180           185           190  
 Ser Gln Phe Tyr Leu Ser  
 195

## (2) INFORMATION FOR SEQ ID NO:737:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...208

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:737

Val Val Ala Asp Glu Val Arg Lys Leu Ala Glu Lys Thr Gln Lys Ala  
 1           5           10           15  
 Thr Lys Glu Ile Ala Val Val Lys Ser Met Gln Gln Glu Ala Asn  
 20           25           30  
 Asp Ile Gln Thr Asn Thr His Asp Ile Asn Ser Ile Val Gly Ser Ile  
 35           40           45  
 Lys Gly Asp Val Glu Glu Leu Lys Ser Thr Val Lys Asn Asn Met Ile  
 50           55           60  
 Val Ala Gln Ala Ala Lys Tyr Thr Ile Tyr Asn Ile Asn Asn Arg Val  
 65           70           75           80  
 Phe Cys Gly Unk Ala Lys Leu Asp His Val Val Phe Lys Asn Asn Leu  
 85           90           95  
 Tyr Gly Met Val Unk Leu Val Ser Ile Pro Leu Thr Leu Pro Ala His  
 100          105          110  
 Lys Ser Unk Arg Leu Gly Lys Trp Tyr Tyr Glu Gly Ala Gly Lys Glu  
 115          120          125  
 Asn Phe Ala Asn Thr Ser Gly Tyr Arg Ala Leu Glu Ser His His Ala  
 130          135          140  
 Ser Val His Ala Glu Ala Asn Asp Leu Val Lys Ala Val Gln Glu Asp  
 145          150          155          160  
 His Val Thr Asp Ser Lys Tyr Leu Glu His Lys Val His Leu Met Glu  
 165          170          175  
 Asp Ser Ala Lys His Val Lys Glu Asn Ile Asp Lys Met Phe Tyr Glu  
 180          185          190  
 Lys Gln Asp Glu Leu Asn Lys Ile Ile Glu Lys Ile Gln Lys Gly Glu  
 195          200          205

## (2) INFORMATION FOR SEQ ID NO:738:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738

Met	Asn	Thr	Ser	Lys	Lys	Leu	Gly	Asn	Pro	Leu	Leu	Phe	Leu	His	Asp	
1								5						10		15
Asn	Lys	Ile	Leu	Leu	Phe	Val	Val	Gly	Val	Ser	Met	Gly	Gly	Trp	Ala	
								20			25			30		
Thr	Ser	Lys	Ile	Tyr	Gln	Phe	Glu	Ser	Ala	Leu	Glu	Pro	Ile	His	Phe	
								35			40			45		
Lys	Phe	Ala	Arg	Lys	Leu	Ser	Leu	Ser	Pro	Phe	Leu	Asn	Leu	Ser	His	
								50			55			60		
Leu	Val	Arg	Asn	Lys	Pro	Leu	Asn	Thr	Thr	Asp	Gly	Gly	Phe	Met	Leu	
								65			70			75	80	
Pro	Leu	Tyr	His	Glu	Leu	Ala	Thr	Gln	Tyr	Pro	Leu	Leu	Leu	Lys	Phe	
								85			90			95		
Asp	Gln	Gln	Asn	Asn	Pro	Arg	Glu	Leu	Leu	Arg	Pro	Asn	Thr	Leu	Asn	
								100			105			110		
His	Gln	Leu	Gln	Pro	Ser	Leu	Thr	Pro	Phe	Lys	Asp	Cys	Ala	Val	Met	
								115			120			125		
Ala	Phe	Arg	Asn	His	Ser	Phe	Lys	Asp	Ser	Leu	Met	Leu	Glu	Thr	Cys	
								130			135			140		
Lys	Thr	Pro	Thr	Asp	Trp	Gln	Lys	Pro	Ile	Ser	Thr	Asn	Leu	Lys	Asn	
								145			150			155	160	
Leu	Asp	Asp	Ser	Leu	Asn	Leu	Leu	Asn	Leu	Asn	Gly	Ile	Leu	Tyr	Leu	
								165			170			175		
Ile	His	Asn	Pro	Ser	Asp	Leu	Ser	Leu	Arg	Arg	Lys	Glu	Leu	Trp	Leu	
								180			185			190		
Ser	Lys	Leu	Glu	Asn	Gln	Gln	Leu	Ile								
								195			200					

(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739

Met	Ser	Ile	Gln	His	Phe	Arg	Val	Ala	Leu	Ile	Pro	Phe	Phe	Ala	Ala
1								5			10			15	
Phe	Cys	Leu	Pro	Val	Phe	Ala	His	Pro	Glu	Thr	Leu	Val	Lys	Val	Lys
								20			25			30	

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Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	Asp
35												45			
Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	Phe	Arg	Pro	Glu	Glu	Arg	Phe
50					55							60			
Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	Leu	Cys	Gly	Ala	Val	Leu	Ser
65					70					75					80
Arg	Ile	Asp	Ala	Gly	Gln	Glu	Gln	Leu	Gly	Arg	Arg	Ile	Tyr	Ser	
												85	90	95	
Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	Val	Thr	Glu	Lys	His	Leu	Thr
									100	105			110		
Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Ser	Arg	Trp	Cys	His	Asn	His	
												115	120	125	

## (2) INFORMATION FOR SEQ ID NO:740:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 79 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740

Val	Asn	Val	Gly	Val	Pro	Phe	Ser	Tyr	Gln	Val	Ser	Ala	Thr	Phe	Gln
1									5					10	15
Asn	Ser	Arg	Leu	Ser	Ser	Leu	Leu	Glu	Thr	Leu	Lys	Lys	Ser	Phe	Leu
									20					25	30
Glu	Lys	Pro	Leu	Ile	Glu	Ser	Ser	Ala	Asn	Lys	Ile	Ala	Asp	Ile	Phe
									35					40	45
Ser	Lys	Ala	Val	Leu	Phe	Leu	Ala	Phe	Val	Ser	Phe	Leu	Leu	Trp	Gln
									50					55	60
Phe	Gly	Leu	Gly	Asn	Phe	Glu	Lys	Ser	Phe	Asn	Gly	Val	Tyr		
									65					70	75

## (2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 49 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...49

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741

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Met Leu Met Val Asn Gly Tyr Gln Ile Thr Met His Lys Gly Tyr Lys  
 1 5 10 15  
 Val Gly Phe Phe Thr Ser Gly Tyr Asn Pro Asp Phe Ala Gln Thr Ile  
 20 25 30  
 Gln Asn Arg Ser Tyr Leu Met Ser Ser Tyr Glu Leu Ser Phe Leu Arg  
 35 40 45  
 Asn

## (2) INFORMATION FOR SEQ ID NO:742:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...412

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:742

Met Val Gln Phe Gln Asn Thr Leu Ile Lys Phe His Ala Leu Ser Phe  
 1 5 10 15  
 Lys Asn Ala Asn Leu Ile Tyr Asn Ala Lys Leu Asn Lys Thr Cys Tyr  
 20 25 30  
 Lys Glu Asn Ser Asn Thr Ile Ile Leu Arg Ile Lys Met Leu Thr Gln  
 35 40 45  
 Glu Asp Val Leu Asn Ala Leu Lys Thr Ile Ile Tyr Pro Asn Phe Glu  
 50 55 60  
 Lys Asp Ile Val Ser Phe Gly Phe Val Lys Asn Ile Thr Leu His Asp  
 65 70 75 80  
 Asn Gln Leu Gly Leu Leu Ile Glu Ile Pro Ser Ser Ser Glu Glu Thr  
 85 90 95  
 Ser Ala Ile Leu Arg Glu Asn Ile Ser Lys Ala Met Gln Glu Lys Gly  
 100 105 110  
 Val Lys Ala Leu Asn Leu Asp Ile Lys Thr Pro Pro Lys Pro Gln Ala  
 115 120 125  
 Pro Lys Pro Thr Thr Lys Asn Leu Ala Lys Asn Ile Lys His Val Val  
 130 135 140  
 Met Ile Ser Ser Gly Lys Gly Val Gly Lys Ser Thr Thr Ser Val  
 145 150 155 160  
 Asn Leu Ser Ile Ala Leu Ala Asn Leu Asn Gln Lys Val Gly Leu Leu  
 165 170 175  
 Asp Ala Asp Val Tyr Gly Pro Asn Ile Pro Arg Met Met Gly Leu Gln  
 180 185 190  
 Asn Ala Asp Val Ile Met Asp Pro Ser Gly Lys Lys Leu Ile Pro Leu  
 195 200 205  
 Lys Ala Phe Gly Val Ser Val Met Ser Met Gly Leu Leu Tyr Asp Glu  
 210 215 220  
 Gly Gln Ser Leu Ile Trp Arg Gly Pro Met Leu Met Arg Ala Ile Glu  
 225 230 235 240  
 Gln Met Leu Ser Asp Ile Ile Trp Gly Asp Leu Asp Val Leu Val Val  
 245 250 255  
 Asp Met Pro Pro Arg Asn Arg Arg Cys Ala Ala His Ala Ala Gln Ala  
 260 265 270

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Val Pro Leu Ser Ala Gly Ile Thr Val Thr Pro Gln Ile Val Ser  
 275 280 285  
 Leu Asp Asp Ala Lys Arg Ser Leu Asp Met Phe Lys Lys Leu His Ile  
 290 295 300  
 Pro Ile Ala Gly Ile Val Glu Asn Met Gly Ser Phe Val Cys Glu His  
 305 310 315 320  
 Cys Lys Lys Glu Ser Glu Ile Phe Gly Ser Asn Ser Met Ser Gly Leu  
 325 330 335  
 Leu Glu Ala Tyr Asn Thr Gln Ile Leu Ala Lys Leu Pro Leu Glu Pro  
 340 345 350  
 Lys Val Arg Leu Gly Gly Asp Lys Gly Glu Pro Ile Val Ile Ser His  
 355 360 365  
 Pro Thr Ser Val Ser Ala Lys Ile Phe Glu Lys Met Ala Lys Asp Leu  
 370 375 380  
 Ser Ala Phe Leu Asp Lys Val Glu Arg Glu Lys Leu Ala Asp Asn Lys  
 385 390 395 400  
 Asp Ile Gln Pro Thr Gln Thr His Ala Tyr Ser His  
 405 410

## (2) INFORMATION FOR SEQ ID NO:743:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...89

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:743

Met Gly Val Val Ile Gly Glu Thr Thr Glu Ile Gly Asp Asp Val Thr  
 1 5 10 15  
 Ile Tyr His Gly Val Thr Leu Gly Gly Thr Gly Lys Phe Lys Gly Lys  
 20 25 30  
 Arg His Pro Thr Leu Gly Asn Arg Val Val Val Gly Ala Gly Ala Lys  
 35 40 45  
 Val Leu Gly Ala Ile Cys Val Gly Asp Asp Val Arg Ile Gly Ala Asn  
 50 55 60  
 Ala Val Val Leu Ser Asp Leu Pro Thr Gly Ser Thr Ala Val Gly Ala  
 65 70 75 80  
 Lys Ala Lys Thr Ile Thr Lys Asp Arg  
 85

## (2) INFORMATION FOR SEQ ID NO:744:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744

```

Met Leu Ser Phe Ile Ser Ala Phe Asp Lys Arg Gly Val Ser Ile Arg
1      5          10          15
Leu Leu Thr Ala Leu Leu Leu Phe Ser Leu Gly Leu Ala Lys Asp
20     25          30
Leu Glu Ile Gln Thr Phe Val Ala Lys Tyr Leu Ser Lys Asn Gln Lys
35     40          45
Ile Gln Ala Leu Gln Glu Gln Ile Asp Ala Leu Asp Ser Gln Glu Lys
50     55          60
Val Val Ser Lys Trp Asp Asn Pro Ile Leu Tyr Leu Gly Tyr Asn Asn
65     70          75          80
Ala Asn Val Ser Asp Phe Phe Arg Leu Asp Ser Thr Leu Met Gln Asn
85     90          95
Met Ser Leu Gly Leu Ser Gln Lys Val Asp Leu Asn Gly Lys Lys Leu
100    105         110
Thr Gln Ser Lys Met Ile Asn Leu Glu Lys Gln Lys Lys Ile Leu Glu
115    120         125
Leu Lys Lys Thr Lys Gln Gln Leu Val Ile Asn Leu Met Ile Asn Gly
130    135         140
Ile Glu Asn Tyr Lys Asn Gln Gln Glu Ile Glu Leu Leu Asn Thr Ala
145    150         155         160
Ile Lys Asn Leu Glu Asn Thr Leu Tyr Gln Ala Asn His Ser Ser Ser
165    170         175
Pro Asp Leu Ile Glu Ile Asp Lys Leu Glu Asn Leu Lys Ile Ala Asn
180    185         190

```

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745

```

Val Unk Leu Tyr Leu Ala Leu Thr Leu Ser Leu Gly Ile Ala Met Leu
1      5          10          15
Leu Val Glu Met Leu Ile Gly Asn Leu Gly Lys Lys Asp Val Val Ser
20     25          30
Asn Tyr Gln Ile Leu Asp Pro Lys Arg Lys Lys Tyr Tyr Pro Phe Thr
35     40          45
Ser Phe Phe Ile Leu Gly Gly Pro Leu Ile Leu Ser Phe Tyr Ala Val
50     55          60
Val Leu Gly Trp Val Leu Tyr Tyr Leu Phe Val Val Thr Phe Asp Leu
65     70          75          80

```

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Pro	Lys	Asp	Leu	Unk	Gln	Ala	Lys	Met	Gln	Phe	Unk	Met	Leu	Gln	Asn
				85					90				95		
Gly	Ser	Leu	Ile	Trp	Pro	Val	Ile	Asp	Phe	Ser	Ala	Cys			
				100					105						

## (2) INFORMATION FOR SEQ ID NO:745:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 109 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...109

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:745

Val	Unk	Leu	Tyr	Leu	Ala	Leu	Thr	Leu	Ser	Leu	Gly	Ile	Ala	Met	Leu
1				5					10				15		
Leu	Val	Glu	Met	Leu	Ile	Gly	Asn	Leu	Gly	Lys	Lys	Asp	Val	Val	Ser
					20				25				30		
Asn	Tyr	Gln	Ile	Leu	Asp	Pro	Lys	Arg	Lys	Lys	Tyr	Tyr	Pro	Phe	Thr
					35			40			45				
Ser	Phe	Phe	Ile	Leu	Gly	Gly	Pro	Leu	Ile	Leu	Ser	Phe	Tyr	Ala	Val
					50			55			60				
Val	Leu	Gly	Trp	Val	Leu	Tyr	Tyr	Leu	Phe	Val	Val	Thr	Phe	Asp	Leu
					65			70			75			80	
Pro	Lys	Asp	Leu	Unk	Gln	Ala	Lys	Met	Gln	Phe	Unk	Met	Leu	Gln	Asn
					85				90				95		
Gly	Ser	Leu	Ile	Trp	Pro	Val	Ile	Asp	Phe	Ser	Ala	Cys			
					100				105						

## (2) INFORMATION FOR SEQ ID NO:746:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 116 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...116

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:746

Val	Pro	Ala	Val	Gly	Gly	Ala	Leu	Ile	Trp	Unk	Unk	Ile	Unk	Ile	Tyr
1					5				10			15			
Glu	Leu	Tyr	His	Gly	Unk	Val	Asn	Glu	Unk	Ile	Phe	Unk	Val	Leu	Tyr

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Ser Ile Leu Leu Ile Gly Val	20	Ile Asp Ser Val	25	Ile Lys Pro	30
Leu	35	Asp	40	Lys	45
Ile Val Phe Ile Lys Lys Arg	50	Ile Phe Lys Thr	55	Thr Leu Lys	60
Gly Ile Leu Ile Phe Phe Ser Met Ile Ala Gly	65	Ile Ser Gln Phe	70	Ile	75
Gly Phe Trp Gly Ile Ile Val Gly Pro Thr Ile	85	Thr Ala Phe Phe Ile	90	95	
Ala Leu Leu Arg Leu Tyr Glu Asn Tyr Phe Ile Gln	100	Gln Lys Glu Gln Lys	105		110
Thr Cys Glu Cys	115				

## (2) INFORMATION FOR SEQ ID NO:747:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747

Val Val Val Ile Ile Leu Val Val Val	1	Ile Ile Gln Asn Ser Ser Ser	5	10	15
Leu Lys Glu Glu Arg Glu Gln Glu Arg Ala Ile Lys Pro Asp Thr Lys	20	25	30		
Asn Asn Ser Phe Asn Glu Thr Asn Pro Thr Glu Glu Lys Lys Leu Glu	35	40	45		
Pro Thr Pro Lys Leu Glu Glu Lys His Lys Glu Gln Asp Lys Gln Gly	50	55	60		
Lys Glu Ala Ile Lys Glu Asn Pro Asn Thr Ile Tyr Ile Ile Pro Lys	65	70	75	80	
Arg Asp Ile Trp Val Glu Val Ile Asp Leu Asp Glu Lys Lys Asn Ser	85	90	95		
Phe Gln Lys Val Phe Lys Lys Ser Tyr Pro Leu Glu Ala Lys Asn His	100	105	110		
Arg Leu Leu Leu Arg Phe Gly His Gly His Leu Ile Leu Lys Asn Asn	115	120	125		
His Gln Glu Gln Asp Tyr Asn Asp Ser Lys Thr Arg Arg Phe Leu Tyr	130	135	140		
Glu Pro Asn Lys Gly Leu Thr Leu Ile Asn Glu Ala Gln Tyr Lys Ala	145	150	155	160	
Leu Gln Gln					

## (2) INFORMATION FOR SEQ ID NO:748:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748

```

Met Asp Glu Ile Tyr Gln Ile Ala Lys Asn Lys Thr Leu Ile Val Ile
      5          10          15
1
Ala His Arg Leu Ser Thr Ile Glu Arg Cys Glu Val Ile Ile Asp Met
      20          25          30
Ser Gln His Lys Asp Asn Leu Gly
      35          40

```

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749

```

Val Ala Gly Ser Phe Ile Ile Ala Leu Phe Ser Val Leu Ala Asp Gln
1 5 10 15
Phe Val Ser Val Phe Gln His Glu Asn Ala Leu Gln Arg Leu Phe Ser
20 25 30
Gln Asn Ala Thr Gln Lys Gln Lys Lys Lys Ser Leu Cys
35 40 45

```

(2) INFORMATION FOR SEQ ID NO:750:

#### (ii) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...118

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:750

Met Val Ala Leu Ser Asn Ala Leu Ser Arg Val Phe Gly Ser Val Ala  
 1 5 10 15  
 Gly Tyr Lys Phe Pro Ser Phe Ile Gln Lys Ser Ile Asn Ala Leu Tyr  
 20 25 30  
 Val Lys Ile Phe Lys Ile Asp Leu Ser Glu Phe Glu Pro Leu Glu Asn  
 35 40 45  
 Tyr Lys Ser Leu Asn Ala Leu Phe Met Arg Ser Leu Lys Lys Glu Arg  
 50 55 60  
 Pro Phe Asp Lys Ala Pro Ile Phe Ala Leu Arg Leu Ala Met Ala Leu  
 65 70 75 80  
 Ile Thr Glu Cys Ala Phe Leu Asp Asn Asp Ser Ala Leu Gln Ile Lys  
 85 90 95  
 Gly Met Pro Tyr Lys Ala His Glu Leu Val Gly Glu Ile Asn Pro Leu  
 100 105 110  
 Ser Pro Leu Phe Ser Met  
 115

## (2) INFORMATION FOR SEQ ID NO:751:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...200

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:751

Met Ala Val Leu Lys Lys Met Ile Gly Leu Val Ala Val Leu Ser Val  
 1 5 10 15  
 Leu Leu Ala Arg Asp Asn Pro Phe Glu Pro Glu Ile Asn Ser Lys Asn  
 20 25 30  
 Leu Gln Gly Gly Phe Ser Gly Ile Tyr Asp Asp Tyr Leu Lys Glu Ile  
 35 40 45  
 His Val Asp Leu Pro Thr Ser Ala Arg Ile Leu Lys Lys Ile Thr Leu  
 50 55 60  
 Thr Tyr Gln Asp Ile Asp Gly Ser Ile His Ser Lys Val Val Gly Ile  
 65 70 75 80  
 Asp Lys Ser Ile Asp Trp His Tyr Pro Leu Lys Leu Ser Gln His Thr  
 85 90 95  
 Leu Asn Gln Asp Ala Phe Glu Lys Arg Tyr Gln Ile Gln Asp Phe Asp  
 100 105 110  
 Phe Leu Met Ala Asn Asn Thr Met Ile Leu Arg Ser Pro Tyr Lys Ile  
 115 120 125  
 Leu Arg Ser Phe Val Leu Val Asn Pro Tyr Arg Ile Val Leu Asp Thr  
 130 135 140  
 Gln Lys Gly Pro Leu Asp Ile Tyr Gln Asn Met Asp Leu Asn Gln Lys  
 145 150 155 160  
 Phe Phe Ser His Ile Lys Val Gly Thr His Lys Asp Tyr Tyr Arg Ile  
 165 170 175

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Thr Leu Ile Leu Asp Gly Lys Tyr Arg Tyr Leu Leu Glu Glu Lys Asn  
 180 185 190  
 Gly Ala Tyr Glu Leu Lys Leu Lys  
 195 200

## (2) INFORMATION FOR SEQ ID NO:752:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 79 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...79
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:752

Met Gly Gly Phe Thr Ser Ile Trp His Trp Val Ile Val Leu Leu Val  
 1 5 10 15  
 Ile Val Leu Leu Phe Gly Ala Lys Lys Ile Pro Glu Leu Ala Lys Gly  
 20 25 30  
 Leu Gly Ser Gly Ile Lys Asn Phe Lys Lys Ala Val Lys Asp Asp Glu  
 35 40 45  
 Glu Glu Ala Lys Asn Glu Leu Lys Thr Leu Asp Ala Gln Ala Thr Gln  
 50 55 60  
 Thr Lys Val His Glu Thr Ser Glu Ile Lys Ser Lys Gln Glu Ser  
 65 70 75

## (2) INFORMATION FOR SEQ ID NO:753:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...97
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:753

Leu Thr Thr Lys Ala Cys Trp Leu Leu Arg Val Cys Cys Tyr Arg Ser  
 1 5 10 15  
 Leu Asn Ile Thr Ile Lys Asp Arg Thr Met Lys Thr Asn Gly His Phe  
 20 25 30  
 Lys Asp Phe Ala Trp Lys Lys Cys Phe Leu Gly Ala Ser Val Val Ala  
 35 40 45  
 Leu Leu Val Gly Cys Ser Pro His Ile Ile Glu Thr Asn Glu Val Ala

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50	55	60
Leu Lys Leu Asn Tyr His Pro Ala Ser Glu Lys Val Gln Ala Leu Asp		
65	70	75
Glu Lys Ile Leu Leu Leu Arg Pro Ala Phe Gln Tyr Ser Unk Asn Ile		
85	90	95
Cys		

## (2) INFORMATION FOR SEQ ID NO:753:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753

Leu Thr Thr Lys Ala Cys Trp Leu Leu Arg Val Cys Cys Tyr Arg Ser		
1	5	10
		15
Leu Asn Ile Thr Ile Lys Asp Arg Thr Met Lys Thr Asn Gly His Phe		
20	25	30
Lys Asp Phe Ala Trp Lys Lys Cys Phe Leu Gly Ala Ser Val Val Ala		
35	40	45
Leu Leu Val Gly Cys Ser Pro His Ile Ile Glu Thr Asn Glu Val Ala		
50	55	60
Leu Lys Leu Asn Tyr His Pro Ala Ser Glu Lys Val Gln Ala Leu Asp		
65	70	75
Glu Lys Ile Leu Leu Leu Arg Pro Ala Phe Gln Tyr Ser Unk Asn Ile		
85	90	95
Cys		

## (2) INFORMATION FOR SEQ ID NO:754:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754

626

Leu Ser Glu Trp Gln Thr Phe Cys Leu Lys Asp Leu Gly Lys Ile Val  
 1               5               10               15  
 Gly Gly Ala Thr Pro Pro Thr Asn Asn Pro Lys Asn Tyr Gly Asn Lys  
 20              25              30  
 Ile Ala Trp Ile Thr Pro Lys Asp Leu Ser Thr Leu Gln Gly Arg Tyr  
 35              40              45  
 Ile Lys Lys Gly Ser Arg Ser Ile Ser Arg Leu Gly Phe Lys Ser Cys  
 50              55              60  
 Ser Cys Val Leu Leu Pro Lys His Ala Ile Leu Phe Ser Ser Arg Ala  
 65              70              75              80  
 Pro Ile Gly Tyr Val Ala Ile Ala Glu Lys Arg Leu Cys Thr Asn Gln  
 85              90              95  
 Gly Phe Lys Ser Ile Ile Pro Asn Lys Ile Tyr Phe Glu Phe Leu  
 100             105             110  
 Tyr Tyr Leu Leu Lys Tyr Tyr Lys Asp Asn Ile Ser Asn Ile Gly Gly  
 115             120             125  
 Gly Thr Thr Phe Lys Glu Val Ser Gly Ala Thr Leu Gly Ser Ile Pro  
 130             135             140  
 Ser  
 145

## (2) INFORMATION FOR SEQ ID NO:754:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...145

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:754

Leu Ser Glu Trp Gln Thr Phe Cys Leu Lys Asp Leu Gly Lys Ile Val  
 1               5               10               15  
 Gly Gly Ala Thr Pro Pro Thr Asn Asn Pro Lys Asn Tyr Gly Asn Lys  
 20              25              30  
 Ile Ala Trp Ile Thr Pro Lys Asp Leu Ser Thr Leu Gln Gly Arg Tyr  
 35              40              45  
 Ile Lys Lys Gly Ser Arg Ser Ile Ser Arg Leu Gly Phe Lys Ser Cys  
 50              55              60  
 Ser Cys Val Leu Leu Pro Lys His Ala Ile Leu Phe Ser Ser Arg Ala  
 65              70              75              80  
 Pro Ile Gly Tyr Val Ala Ile Ala Glu Lys Arg Leu Cys Thr Asn Gln  
 85              90              95  
 Gly Phe Lys Ser Ile Ile Pro Asn Lys Ile Tyr Phe Glu Phe Leu  
 100             105             110  
 Tyr Tyr Leu Leu Lys Tyr Tyr Lys Asp Asn Ile Ser Asn Ile Gly Gly  
 115             120             125  
 Gly Thr Thr Phe Lys Glu Val Ser Gly Ala Thr Leu Gly Ser Ile Pro  
 130             135             140  
 Ser  
 145

## (2) INFORMATION FOR SEQ ID NO:755:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 206 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755

Val	Arg	Leu	Asn	Ala	Ala	Val	Val	Asp	Gly	Lys	Tyr	Lys	Ile	Ala	
1						5			10			15			
Leu	Glu	Asp	Gly	Ala	Asn	Ala	Leu	Glu	Tyr	Glu	Pro	Leu	Ser	Asp	Glu
						20			25			30			
Unk	Unk	Lys	Lys	Ile	Asn	Unk	Leu	Val	Lys	Gln	Ala	Ile	Gly	Asp	Asn
						35			40			45			
Gln	Asn	Arg	Gly	Asp	Asp	Val	Ala	Val	Ser	Asn	Phe	Glu	Phe	Asn	Pro
						50			55			60			
Met	Val	Pro	Met	Ile	Asp	Asn	Ala	Thr	Leu	Ser	Glu	Lys	Ile	Tyr	
						65			70			75			80
Lys	Thr	Gln	Lys	Ile	Leu	Gly	Leu	Phe	Met	Phe	Leu	Ile	Lys	Val	Tyr
						85			90			95			
Leu	Val	Phe	Ile	Val	Leu	Phe	Ile	Phe	Tyr	Lys	Val	Ile	Val	Pro	
						100			105			110			
Phe	Ser	Glu	Arg	Met	Leu	Glu	Val	Val	Pro	Asp	Glu	Asp	Lys	Glu	Val
						115			120			125			
Lys	Ser	Met	Phe	Glu	Glu	Met	Asn	Glu	Glu	Glu	Asp	Glu	Leu	Asn	Lys
						130			135			140			
Leu	Gly	Asp	Leu	Arg	Lys	Lys	Val	Glu	Asp	Gln	Leu	Gly	Leu	Asn	Ala
						145			150			155			160
Ser	Phe	Ser	Glu	Glu	Val	Arg	Tyr	Glu	Ile	Ile	Leu	Glu	Lys	Ile	
						165			170			175			
Arg	Gly	Thr	Leu	Lys	Glu	Arg	Pro	Asp	Glu	Ile	Ala	Thr	Leu	Phe	Lys
						180			185			190			
Leu	Leu	Ile	Lys	Asp	Glu	Ile	Ser	Ser	Asp	Ser	Ala	Lys	Gly		
						195			200			205			

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 98 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...98

628

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:756

Val Cys Phe Ile Leu Pro Phe Cys Leu Gly Val Leu Gly Thr Gln Ile  
 1                   5                   10                   15  
 Phe Lys Gln Glu Thr Pro Arg Gln Leu Pro Ile Val Val Val Asp Leu  
 20                 25                 30  
 Asp Lys Thr Thr Ser His Gln Val Ala Phe Glu Leu Gly Ala Thr  
 35                 40                 45  
 Ser Ala Val Glu Ile Lys Tyr Gln Val Thr Ser Leu Ser Glu Ala Lys  
 50                 55                 60  
 Arg Phe Leu Asn Ser Ala Glu Val Tyr Gly Ala Leu Ile Leu Pro Lys  
 65                 70                 75                 80  
 Asp Leu Glu Arg Lys Ile Lys Met Gly Arg Lys Val Unk Phe Ala Leu  
 85                 90                 95  
 Leu Leu

## (2) INFORMATION FOR SEQ ID NO:757:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...197

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:757

Met Lys Gly Leu Trp Leu Val Ile Ser Leu Val Phe Val Gly Phe Leu  
 1                 5                 10                 15  
 Trp Ala Asn Glu Ser Tyr Val Phe Asn Asn Ser Lys Gly Arg Leu Thr  
 20                 25                 30  
 Glu Lys Ser Val Ala Phe Ile Glu Gly Val Ser Lys Glu Leu Tyr Leu  
 35                 40                 45  
 Lys Thr Gly Val Arg Phe Ala Ile Asp Met Thr Asp Phe Glu Lys Asn  
 50                 55                 60  
 Pro Ile Ala Leu Ala Asn Lys Lys Glu Arg Gln Ser Tyr Gln Glu Gly  
 65                 70                 75                 80  
 Phe Leu Lys Gln Leu Lys Pro Pro Phe Val Val Phe Phe Phe Tyr His  
 85                 90                 95  
 Asp Ala Gln Lys Ile Glu Leu Val Ala Asn Pro Lys Asp Leu Leu Asp  
 100                 105                 110  
 Thr Asp Lys Ile Phe Phe Glu Lys Ile Ala Pro Leu Leu Pro Thr Asn  
 115                 120                 125  
 Ala Lys Glu Tyr Thr Pro Gln Arg Ile Ser Ala Met Leu Ile Asn Gly  
 130                 135                 140  
 Tyr Ser Val Ala Val Asp Ala Leu Ala Glu Lys Tyr His Val Asn Ile  
 145                 150                 155                 160  
 Thr Gln Asn Phe Ser Ala Pro Lys Gly Val Thr Phe Val Lys Val Val  
 165                 170                 175  
 Ile Tyr Ile Leu Leu Leu Thr Leu Leu Gly Ala Phe Leu Gly Leu Tyr  
 180                 185                 190  
 Phe Phe Lys Lys Ser  
 195

## (2) INFORMATION FOR SEQ ID NO:758:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...148

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:758

Leu	Val	Gln	Ile	Val	Val	Val	Phe	Tyr	Gly	Leu	Pro	Ala	Leu	Gly	Val
1				5					10						15
Tyr	Met	Asp	Pro	Ile	Pro	Ala	Gly	Ile	Ile	Ala	Phe	Ser	Phe	Asn	Val
				20				25							30
Gly	Ala	Tyr	Ala	Ser	Glu	Thr	Leu	Arg	Ala	Ser	Phe	Leu	Ser	Val	Pro
				35			40								45
Lys	Asp	Gln	Trp	Asp	Ser	Ser	Leu	Ser	Leu	Gly	Leu	Asn	Tyr	Leu	Gln
				50			55								60
Thr	Phe	Trp	His	Val	Ile	Phe	Phe	Gln	Ala	Leu	Lys	Val	Ala	Thr	Pro
				65			70			75					80
Ser	Leu	Ser	Asn	Thr	Phe	Ile	Ser	Leu	Phe	Lys	Glu	Thr	Ser	Leu	Ala
				85			90								95
Ser	Val	Val	Thr	Ile	Ala	Glu	Unk	Phe	Arg	Ile	Ala	Gln	Gln	Lys	Unk
				100			105								110
Asn	Val	Ser	Tyr	Asp	Phe	Unk	Pro	Ile	Tyr	Leu	Glu	Unk	Ala	Leu	Ile
				115			120								125
Tyr	Trp	Leu	Phe	Cys	Leu	Val	Leu	Glu	Val	Ile	Gln	Lys	Arg	Val	Glu
				130			135								140
Lys	Ile	Leu	Asn												
				145											

## (2) INFORMATION FOR SEQ ID NO:758:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...148

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:758

Leu	Val	Gln	Ile	Val	Val	Val	Phe	Tyr	Gly	Leu	Pro	Ala	Leu	Gly	Val
1				5					10						15

630

Tyr Met Asp Pro Ile Pro Ala Gly Ile Ile Ala Phe Ser Phe Asn Val  
 20 25 30  
 Gly Ala Tyr Ala Ser Glu Thr Leu Arg Ala Ser Phe Leu Ser Val Pro  
 35 40 45  
 Lys Asp Gln Trp Asp Ser Ser Leu Ser Leu Gly Leu Asn Tyr Leu Gln  
 50 55 60  
 Thr Phe Trp His Val Ile Phe Phe Gln Ala Leu Lys Val Ala Thr Pro  
 65 70 75 80  
 Ser Leu Ser Asn Thr Phe Ile Ser Leu Phe Lys Glu Thr Ser Leu Ala  
 85 90 95  
 Ser Val Val Thr Ile Ala Glu Unk Phe Arg Ile Ala Gln Gln Lys Unk  
 100 105 110  
 Asn Val Ser Tyr Asp Phe Unk Pro Ile Tyr Leu Glu Unk Ala Leu Ile  
 115 120 125  
 Tyr Trp Leu Phe Cys Leu Val Leu Glu Val Ile Gln Lys Arg Val Glu  
 130 135 140  
 Lys Ile Leu Asn  
 145

## (2) INFORMATION FOR SEQ ID NO:759:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 68 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...68
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:759

Met Cys Ser Lys Lys Ile Arg Asn Leu Ile Leu Cys Phe Gly Phe Ile  
 1 5 10 15  
 Leu Ser Leu Cys Ala Glu Glu Asn Ile Thr Lys Glu Asn Met Thr Glu  
 20 25 30  
 Thr Asn Thr Thr Glu Glu Asn Thr Pro Lys Asp Ala Pro Ile Leu Leu  
 35 40 45  
 Glu Glu Lys Arg Ala Gln Thr Leu Glu Leu Lys Glu Glu Asn Glu Val  
 50 55 60  
 Ala Lys Lys Ile  
 65

## (2) INFORMATION FOR SEQ ID NO:760:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 134 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori

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## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...134

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:760

Val Val Ala Asp Glu Val Arg Asn Leu Ala Gly Arg Thr Gln Lys Ser  
 1 5 10 15  
 Leu Ala Glu Ile Asn Ser Thr Ile Met Val Ile Val Gln Glu Ile Asn  
 20 25 30  
 Asp Val Ser Ser Gln Met Asn Leu Asn Ser Gln Lys Met Glu Arg Leu  
 35 40 45  
 Ser Asp Met Ser Lys Ser Val Gln Glu Thr Tyr Glu Lys Met Ser Ser  
 50 55 60  
 Asn Leu Ser Ser Val Val Leu Asp Ser Asn Gln Ser Met Asp Asp Tyr  
 65 70 75 80  
 Ala Lys Ser Gly His Gln Ile Glu Ala Met Val Ser Asp Phe Ala Glu  
 85 90 95  
 Val Glu Lys Val Ala Ser Lys Thr Leu Ala Asp Ser Ser Asp Ile Leu  
 100 105 110  
 Asn Ile Ala Thr His Val Ser Gly Thr Thr Met Asn Leu Unk Lys Gln  
 115 120 125  
 Val Asn Leu Phe Lys Thr  
 130

## (2) INFORMATION FOR SEQ ID NO:760:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...134

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:760

Val Val Ala Asp Glu Val Arg Asn Leu Ala Gly Arg Thr Gln Lys Ser  
 1 5 10 15  
 Leu Ala Glu Ile Asn Ser Thr Ile Met Val Ile Val Gln Glu Ile Asn  
 20 25 30  
 Asp Val Ser Ser Gln Met Asn Leu Asn Ser Gln Lys Met Glu Arg Leu  
 35 40 45  
 Ser Asp Met Ser Lys Ser Val Gln Glu Thr Tyr Glu Lys Met Ser Ser  
 50 55 60  
 Asn Leu Ser Ser Val Val Leu Asp Ser Asn Gln Ser Met Asp Asp Tyr  
 65 70 75 80  
 Ala Lys Ser Gly His Gln Ile Glu Ala Met Val Ser Asp Phe Ala Glu  
 85 90 95  
 Val Glu Lys Val Ala Ser Lys Thr Leu Ala Asp Ser Ser Asp Ile Leu  
 100 105 110  
 Asn Ile Ala Thr His Val Ser Gly Thr Thr Met Asn Leu Unk Lys Gln  
 115 120 125  
 Val Asn Leu Phe Lys Thr  
 130

## (2) INFORMATION FOR SEQ ID NO:761:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 93 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...93
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:761

Val Leu Lys Thr Leu Ser Ile Arg Leu Val Ile Leu Leu Asn Cys Ser  
 1               5                   10                   15  
 Leu Ala Thr Asn Ala Cys Ser Gly Val Gln Lys Leu Arg Asp Glu Ser  
              20                   25                   30  
 His Arg Tyr Ala Ile Asn Phe His Arg Ser Thr Lys Leu Lys Asn Met  
              35                   40                   45  
 Lys Gln Ile Ala Leu Leu Lys Glu Lys Gly Ile Gly Glu Ala Ser Val  
              50                   55                   60  
 Lys Lys Leu Leu Asp Tyr Phe Gly Ser Phe Glu Ala Ile Glu Lys Ala  
              65                   70                   75                   80  
 Ser Asp Gln Glu Lys Asn Ala Val Leu Lys Lys Arg Lys  
              85                                   90

## (2) INFORMATION FOR SEQ ID NO:762:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 73 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...73
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:762

Val Gly Ile Ile Arg Gly Ile Ile His Arg Pro Glu Leu Ile Leu Leu  
 1               5                   10                   15  
 Asp Glu Pro Phe Ser Ala Leu Asp Ser Leu Asn Arg Lys Asn Leu Gln  
              20                   25                   30  
 Asp Leu Ile Lys Glu Ile His Gln Asn Ser Cys Ala Thr Phe Ile Met  
              35                   40                   45  
 Val Thr His Asp Glu Asn Glu Ala Gln Lys Leu Ala Thr Lys Thr Leu  
              50                   55                   60  
 Glu Ile Lys Ala Leu Lys Gln Glu Gln

## (2) INFORMATION FOR SEQ ID NO:763:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763

Val	Ile	Phe	Ile	Ala	Thr	Ala	Asn	Asn	Ile	Asp	Arg	Ile	Pro	Ala	Pro
1									5			10			15
Leu	Arg	Asp	Arg	Met	Glu	Phe	Ile	Ser	Val	Ser	Ser	Tyr	Thr	Pro	Ser
									20			25			30
Glu	Lys	Glu	Glu	Ile	Ala	Lys	Asn	Tyr	Leu	Ile	Pro	Gln	Glu	Leu	Glu
									35			40			45
Lys	His	Ala	Leu	Lys	Pro	Ser	Glu	Val	Asp	Ile	Ser	His	Glu	Cys	Leu
									50			55			60
Lys	Leu	Ile	Ile	Glu	Lys	Tyr	Thr	Arg	Glu	Ala	Gly	Val	Arg	Asp	Leu
									65			70			75
Arg	Arg	Gln	Ile	Ala	Thr	Ile	Met	Arg	Lys	Ala	Ala	Leu	Lys	Tyr	Leu
									85			90			95
Glu	Asp	Asn	Pro	His	Lys	Lys	Gly	Arg	Thr	Lys	Ser	Glu	Asp	Lys	
									100			105			110
Asp	Lys	Lys	Gly	Gly	Asn	Glu	Glu	Asn	Glu	Lys	Arg	Gly	Glu	Ser	Lys
									115			120			125
Asp	Phe	Cys	Val	Ser	Ile	Thr	Pro	Asp	Asn	Leu	Lys	Glu	Tyr	Leu	Glu
									130			135			140
Arg	Met	Val	Phe	Glu	Ile	Unk	Pro	Ile	Asp	Glu	Glu	Asn	Lys	Ile	Gly
									145			150			155
Ile	Val	Asn	Gly	Leu	Ala	Trp	Thr	Pro	Val	Gly	Gly	Asp	Val	Leu	Lys
									165			170			175
Ile	Glu	Ala	Val	Lys	Ile	Arg	Gly	Lys	Gly	Glu	Leu	Lys	Leu	Thr	Gly
									180			185			190
Ser	Leu	Gly	Asp	Val	Met	Lys	Glu	Ser	Ala	Ile	Ile	Ala	Phe	Ser	Val
									195			200			205
Val	Lys	Val	Leu	Leu	Asp	Asn	Glu	Thr	Leu	Lys	Val	Pro	Lys	Ile	Pro
									210			215			220
Ser	Glu	Thr	Asp	Ala	Glu	Asn	Unk	Lys	Lys	Lys	Val	Leu	Lys	Val	
									225			230			235
Unk	Asn	Ala	Tyr	Asp	Leu	His	Leu	His	Val	Pro	Lys	Gly	Leu	Arg	Leu
									245			250			255
Lys	Thr	Ala	Arg	Ala	Leu	Gly	Ser	Leu	Trp	Arg	Ala				
									260			265			

## (2) INFORMATION FOR SEQ ID NO:764:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764

Met	Glu	Phe	Met	Lys	Phe	Val	Ala	Leu	Gly	Leu	Leu	Ser	Ala	Val	
1				5								15			
Leu	Ser	Ser	Ser	Leu	Leu	Ala	Glu	Gly	Asp	Gly	Val	Tyr	Ile	Gly	Thr
				20			25					30			
Asn	Tyr	Gln	Leu	Gly	Gln	Ala	Arg	Leu	Asn	Ser	Asn	Ile	Tyr	Asn	Thr
				35			40				45				
Gly	Asp	Cys	Thr	Gly	Ser	Val	Val	Gly	Cys	Pro	Pro	Gly	Leu	Thr	Ala
	50				55					60					
Asn	Lys	His	Asn	Pro	Gly	Gly	Thr	Asn	Ile	Asn	Trp	His	Ser	Lys	Tyr
65					70			75				80			
Ala	Asn	Gly	Ala	Leu	Asn	Gly	Phe	Gly	Leu	Asn	Val	Gly	Tyr	Lys	Lys
				85				90				95			
Phe	Phe	Gln	Phe	Lys	Ser	Leu	Asp	Met	Thr	Ser	Lys	Trp	Phe	Gly	Phe
	100				105				110						
Arg	Val	Tyr	Gly	Leu	Phe	Asp	Tyr	Gly	His	Ala	Asp	Leu	Gly	Lys	Gln
	115				120			125							
Val	Tyr	Ala	Pro	Asn	Lys	Ile	Gln	Leu	Asp	Met	Val	Ser	Trp	Gly	Val
	130				135			140							
Gly	Ser	Asp	Leu	Leu	Ala	Asp	Ile	Ile	Asp	Lys	Asp	Asn	Ala	Ser	Phe
145					150			155				160			
Gly	Ile	Phe	Gly	Gly	Val	Ala	Ile	Gly	Gly	Asn	Thr	Trp	Lys	Ser	Ser
	165				170			175							
Ala	Ala	Asn	Tyr	Trp	Lys	Glu	Gln	Ile	Ile	Glu	Ala	Lys	Gly	Pro	Asp
	180				185			190				190			
Val	Cys	Thr	Pro	Thr	Tyr	Cys	Asn	Pro	Asn	Ala	Pro	Tyr	Ser	Thr	Asn
	195				200			205							
Thr	Ser	Thr	Val	Ala	Phe	Gln	Val	Trp	Leu	Asn	Phe	Gly	Val	Arg	Ala
	210				215			220							
Asn	Ile	Tyr	Lys	His	Asn	Gly	Val	Glu	Phe	Gly	Val	Arg	Val	Pro	Leu
225					230			235				240			
Leu	Ile	Asn	Lys	Phe	Leu	Ser	Ala	Gly	Pro	Asn	Ala	Thr	Asn	Leu	Tyr
	245				250			255				255			
Tyr	His	Leu	Lys	Arg	Asp	Tyr	Ser	Leu	Tyr	Leu	Gly	Tyr	Asn	Tyr	Thr
	260				265			270							
Phe															

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

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## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...273

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:764

Met Glu Phe Met Lys Lys Phe Val Ala Leu Gly Leu Leu Ser Ala Val  
 1 5 10 15  
 Leu Ser Ser Ser Leu Leu Ala Glu Gly Asp Gly Val Tyr Ile Gly Thr  
 20 25 30  
 Asn Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser Asn Ile Tyr Asn Thr  
 35 40 45  
 Gly Asp Cys Thr Gly Ser Val Val Gly Cys Pro Pro Gly Leu Thr Ala  
 50 55 60  
 Asn Lys His Asn Pro Gly Gly Thr Asn Ile Asn Trp His Ser Lys Tyr  
 65 70 75 80  
 Ala Asn Gly Ala Leu Asn Gly Phe Gly Leu Asn Val Gly Tyr Lys Lys  
 85 90 95  
 Phe Phe Gln Phe Lys Ser Leu Asp Met Thr Ser Lys Trp Phe Gly Phe  
 100 105 110  
 Arg Val Tyr Gly Leu Phe Asp Tyr Gly His Ala Asp Leu Gly Lys Gln  
 115 120 125  
 Val Tyr Ala Pro Asn Lys Ile Gln Leu Asp Met Val Ser Trp Gly Val  
 130 135 140  
 Gly Ser Asp Leu Leu Ala Asp Ile Ile Asp Lys Asp Asn Ala Ser Phe  
 145 150 155 160  
 Gly Ile Phe Gly Gly Val Ala Ile Gly Gly Asn Thr Trp Lys Ser Ser  
 165 170 175  
 Ala Ala Asn Tyr Trp Lys Glu Gln Ile Ile Glu Ala Lys Gly Pro Asp  
 180 185 190  
 Val Cys Thr Pro Thr Tyr Cys Asn Pro Asn Ala Pro Tyr Ser Thr Asn  
 195 200 205  
 Thr Ser Thr Val Ala Phe Gln Val Trp Leu Asn Phe Gly Val Arg Ala  
 210 215 220  
 Asn Ile Tyr Lys His Asn Gly Val Glu Phe Gly Val Arg Val Pro Leu  
 225 230 235 240  
 Leu Ile Asn Lys Phe Leu Ser Ala Gly Pro Asn Ala Thr Asn Leu Tyr  
 245 250 255  
 Tyr His Leu Lys Arg Asp Tyr Ser Leu Tyr Leu Gly Tyr Asn Tyr Thr  
 260 265 270  
 Phe

## (2) INFORMATION FOR SEQ ID NO:765:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...133

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:765

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Met Asn Tyr Asp Asn Tyr Trp Asp Glu Asp Lys Pro Glu Leu Asn Ile  
 1 5 10 15  
 Thr Pro Leu Val Asp Val Met Leu Val Leu Leu Ala Ile Leu Met Val  
 20 25 30  
 Thr Thr Pro Thr Leu Thr Tyr Lys Glu Glu Ile Ala Leu Pro Ser Gly  
 35 40 45  
 Ser Lys Thr Ala Arg Ala Thr Gln Asp Lys Val Ile Glu Ile Arg Met  
 50 55 60  
 Asp Lys Asp Ala Lys Ile Tyr Ile Asp Ser Gln Thr Tyr Glu Tyr Unk  
 65 70 75 80  
 Ser Phe Pro Asp Thr Phe Asn Leu Leu Ser Lys Lys Tyr Asp Lys Asp  
 85 90 95  
 Thr Arg Val Ser Ile Arg Ala Asp Lys Arg Leu Thr Tyr Asp Lys Val  
 100 105 110  
 Ile Tyr Leu Leu Lys Thr Ile Lys Glu Ala Gly Phe Leu Lys Val Ser  
 115 120 125  
 Leu Ile Thr Ser Pro  
 130

## (2) INFORMATION FOR SEQ ID NO:765:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...133

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:765

Met Asn Tyr Asp Asn Tyr Trp Asp Glu Asp Lys Pro Glu Leu Asn Ile  
 1 5 10 15  
 Thr Pro Leu Val Asp Val Met Leu Val Leu Leu Ala Ile Leu Met Val  
 20 25 30  
 Thr Thr Pro Thr Leu Thr Tyr Lys Glu Glu Ile Ala Leu Pro Ser Gly  
 35 40 45  
 Ser Lys Thr Ala Arg Ala Thr Gln Asp Lys Val Ile Glu Ile Arg Met  
 50 55 60  
 Asp Lys Asp Ala Lys Ile Tyr Ile Asp Ser Gln Thr Tyr Glu Tyr Unk  
 65 70 75 80  
 Ser Phe Pro Asp Thr Phe Asn Leu Leu Ser Lys Lys Tyr Asp Lys Asp  
 85 90 95  
 Thr Arg Val Ser Ile Arg Ala Asp Lys Arg Leu Thr Tyr Asp Lys Val  
 100 105 110  
 Ile Tyr Leu Leu Lys Thr Ile Lys Glu Ala Gly Phe Leu Lys Val Ser  
 115 120 125  
 Leu Ile Thr Ser Pro  
 130

## (2) INFORMATION FOR SEQ ID NO:766:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766

Met	Pro	Pro	Thr	Unk	Pro	Gln	Ala	Ser	Ile	Leu	Arg	Leu	Thr	Leu	Lys
1							5			10			15		
Asn	Pro	Leu	Unk	Unk	Leu	Ser	Arg	Tyr	Ser	Leu	Cys	Leu	Leu	Lys	Lys
							20			25			30		
Thr	Arg	Leu	Gln	Thr	Thr	Ser	Asn	Ser	Ala	Pro	Lys	Ala	Cys	Leu	Ile
	35						40				45				
Ala	Gly	Leu	Leu	Lys	Lys	Ser	Lys	Pro	Phe	Ile	Leu	Asn	Thr	Leu	Lys
	50						55			60					
Ile	Arg	Ser	Leu	Leu	Lys	Pro									
65						70									

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766

Met	Pro	Pro	Thr	Unk	Pro	Gln	Ala	Ser	Ile	Leu	Arg	Leu	Thr	Leu	Lys
1							5			10			15		
Asn	Pro	Leu	Unk	Unk	Leu	Ser	Arg	Tyr	Ser	Leu	Cys	Leu	Leu	Lys	Lys
							20			25			30		
Thr	Arg	Leu	Gln	Thr	Thr	Ser	Asn	Ser	Ala	Pro	Lys	Ala	Cys	Leu	Ile
	35						40				45				
Ala	Gly	Leu	Leu	Lys	Lys	Ser	Lys	Pro	Phe	Ile	Leu	Asn	Thr	Leu	Lys
	50						55			60					
Ile	Arg	Ser	Leu	Leu	Lys	Pro									
65						70									

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767

Met	Gly	Cys	Ser	Phe	Ile	Phe	Lys	Lys	Val	Arg	Val	Tyr	Ser	Lys	Met
1															
															15
Leu	Val	Ala	Leu	Gly	Leu	Ser	Ser	Val	Ile	Gly	Cys	Ala	Met	Asn	
															30
Pro	Ser	Ala	Glu	Thr	Lys	Lys	Pro	Asn	Asp	Ala	Lys	Asn	Gln	Pro	
															45
Val	Gln	Thr	His	Glu	Aрг	Met	Thr	Thr	Ser	Ser	Glu	His	Val	Thr	Pro
															50
															60
Leu	Asp	Phe	Asn	Tyr	Pro	Val	His	Ile	Val	Gln	Ala	Pro	Gln	Asn	His
															65
															80
His	Val	Val	Gly	Ile	Leu	Met	Pro	Arg	Ile	Gln	Val	Ser	Asp	Asn	Leu
															85
															95
Lys	Pro	Tyr	Ile	Asp	Lys	Phe	Gln	Asp	Ala	Leu	Ile	Asn	Gln	Ile	Gln
															100
															110
Thr	Ile	Phe	Glu	Lys	Arg	Gly	Tyr	Gln	Val	Leu	Arg	Phe	Gln	Asp	Glu
															115
															125
Lys	Ala	Leu	Asn	Val	Gln	Asp	Lys	Lys	Ile	Phe	Ser	Val	Leu	Asp	
															130
															135
Leu	Lys	Gly													
															145

(2) INFORMATION FOR SEQ ID NO:768:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768

Met	Asp	Arg	Lys	Leu	Leu	Arg	Leu	Tyr	Gln	Pro	Leu	Asn	Ala	Tyr	Ser
1															
															15
Tyr	Asn	Ser	Asp	Ser	Leu	Phe	Leu	Tyr	Asp	Phe	Ser	Arg	Pro	Phe	Ile
															30
Lys	Asn	Ser	Gly	Ala	Ile	Leu	Asp	Ile	Gly	Ser	Gly	Cys	Gly	Val	Leu
															45
Gly	Leu	Leu	Cys	Ala	Arg	Asp	Asn	Pro	Leu	Ala	Ser	Val	His	Leu	Val
															50
															60
Glu	Lys	Asp	Ser	Lys	Met	Ala	Phe	Cys	Ser	Gln	Lys	Asn	Ala	Leu	Lys

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65	70	75	80												
Phe	Pro	Asn	Ala	Gln	Val	Phe	Glu	Ser	Asp	Phe	Leu	Asp	Phe	Asn	Pro
85							90								95
Pro	Ile	Leu	Tyr	Asp	Ala	Ile	Val	Cys	Asn	Pro	Pro	Phe	Tyr	Ala	Leu
100							105								110
Gly	Ser	Ile	Lys	Ser	Gln	Ile	Lys	Gly	His	Ala	Arg	His	Gln	Ser	Glu
115							120								125
Leu	Asp	Phe	Ala	Ser	Leu	Val	Ala	Lys	Val	Lys	Lys	Cys	Leu	Lys	Pro
130							135								140

## (2) INFORMATION FOR SEQ ID NO:769:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...47

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769

Met	Leu	Ser	Ala	Leu	Val	Met	Leu	Pro	Phe	Met	Glu	Val	Phe	Tyr	Tyr
1						5			10					15	
Phe	Asn	Phe	Pro	Leu	Trp	Leu	Asn	Leu	Phe	Leu	Gly	Gln	Thr	Ile	Gly
20							25							30	
Ala	Val	Ile	Phe	Phe	Lys	Leu	Asp	Lys	Leu	Ile	Phe	Ser	Lys	Lys	
35							40							45	

## (2) INFORMATION FOR SEQ ID NO:770:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770

Met	Asn	Thr	Ile	Ile	Arg	Tyr	Ala	Ser	Leu	Trp	Gly	Leu	Cys	Ile	Thr
1							5			10				15	
Leu	Thr	Leu	Ala	Gln	Thr	Pro	Ser	Lys	Thr	Pro	Asp	Glu	Ile	Lys	Gln
20							25							30	
Ile	Leu	Asn	Asn	Tyr	Ser	His	Lys	Asn	Leu	Lys	Leu	Ile	Asp	Unk	Pro
35							40							45	

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Thr Ser Ser Leu Unk Ala Thr Pro Gly Phe Unk Pro Ser Pro Lys Glu  
 50 55 60  
 Thr Ala Thr Thr Ile Asn Gln Glu Ile Ala Lys Tyr His Glu Lys Ser  
 65 70 75 80  
 Asp Lys Ala Ala Leu Gly Leu Tyr Glu Leu Leu Lys Gly Ala Thr Thr  
 85 90 95  
 Asn Leu Ser Leu Gln Ala Gln Glu Leu Ser Val Lys Gln Ala Met Glu  
 100 105 110  
 Glu Pro His His Arg Gln Ser Asp Val Phe Ala Tyr Phe Glu Arg Glu  
 115 120 125  
 Leu

## (2) INFORMATION FOR SEQ ID NO:771:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...242

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:771

Met Val Leu Phe Leu Ser Ile Phe Lys Lys Ser Phe Asn Asp Phe Leu  
 1 5 10 15  
 Ser Ala Arg Met Leu Leu Ile Asn Leu Gly Pro Ile Leu Leu Ser Leu  
 20 25 30  
 Ala Phe Phe Gly Ala Ile Phe Tyr Tyr Asn Gly Gly Ser Ile Val Asn  
 35 40 45  
 Tyr Cys Gln Thr Leu Leu Pro Gln Ser Leu Asn Asp Tyr Ala His Ser  
 50 55 60  
 Gln Gly Phe Phe Ala Gly Val Phe Ala Trp Val Phe Lys Ala Leu Val  
 65 70 75 80  
 Tyr Phe Leu Ile Phe Trp Ile Val Ile Leu Leu Ser Leu Val Ile Asn  
 85 90 95  
 Ile Phe Ala Ser Ile Phe Tyr Thr Pro Leu Val Val Ser Tyr Leu His  
 100 105 110  
 Gln Lys Tyr Tyr Pro His Val Val Leu Glu Glu Phe Gly Ser Ile Leu  
 115 120 125  
 Phe Ser Ile Lys Tyr Phe Leu Lys Ser Leu Thr Phe Met Leu Leu Phe  
 130 135 140  
 Leu Ala Val Leu Thr Pro Leu Tyr Phe Ile Pro Phe Ile Gly Val Phe  
 145 150 155 160  
 Gly Val Phe Phe Ser Ile Val Pro His Phe His Phe Phe Lys Asn Thr  
 165 170 175  
 Met Ser Leu Asp Ile Ala Ser Met Ile Phe Asn His Gln Ser Tyr Gln  
 180 185 190  
 Asn Leu Leu Lys Gln His Arg Leu Lys His Tyr Arg Phe Ser Phe Phe  
 195 200 205  
 Cys Tyr Leu Phe Ser Leu Ile Pro Phe Phe Asn Phe Phe Ala Thr Leu  
 210 215 220  
 Leu Gln Thr Leu Lys Leu Thr His Tyr Ile Phe Ile Phe Lys Glu Lys  
 225 230 235 240  
 Glu Cys

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## (2) INFORMATION FOR SEQ ID NO:772:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...97

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:772

Met	Gln	Tyr	Ala	Asn	Ala	Tyr	Gln	Ala	Tyr	Gln	His	Asn	Arg	Val	Ser
1															
															15
Val	Glu	Ser	Pro	Ala	Lys	Leu	Ile	Glu	Met	Leu	Tyr	Glu	Gly	Ile	Leu
															20
															25
															30
Arg	Phe	Ser	Ser	Gln	Ala	Lys	Arg	Cys	Ile	Glu	Asn	Glu	Asp	Ile	Glu
															35
															40
															45
Lys	Lys	Ile	Tyr	Tyr	Ile	Asn	Arg	Val	Thr	Asp	Ile	Phe	Thr	Glu	Leu
															50
															55
															60
Leu	Asn	Ile	Leu	Asp	Tyr	Glu	Lys	Gly	Gly	Unk	Val	Ala	Val	Tyr	Leu
															65
															70
															75
Thr	Gly	Leu	Tyr	Thr	His	Gln	Ile	Lys	Val	Leu	Thr	Gln	Ala	Asn	Val
															85
															90
															95
Glu															

## (2) INFORMATION FOR SEQ ID NO:773:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...143

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:773

Met	Met	Phe	Asp	Asn	Thr	Leu	Ile	Asn	Leu	Phe	Glu	Thr	Ala	Pro	Leu
1															
															15
Leu	Thr	Ser	Leu	Leu	Ala	Gly	Ile	Leu	Thr	Phe	Leu	Ser	Pro	Cys	Val
															20
															25
Leu	Pro	Leu	Ile	Pro	Ala	Tyr	Met	Ser	Tyr	Ile	Ser	Gln	Ile	Ser	Leu
															35
															40
															45

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Glu	Asp	Ile	Lys	Asp	Gly	Lys	Ala	Lys	Arg	Val	Ser	Val	Phe	Leu	Lys
50					55				60						
Ser	Leu	Met	Phe	Val	Val	Gly	Phe	Ser	Leu	Val	Phe	Leu	Gly	Val	Gly
65					70				75				80		
Met	Ser	Met	Ala	Lys	Leu	Ile	His	Ser	Phe	Ser	Phe	Ser	Trp	Val	Asn
						85			90				95		
Tyr	Ile	Ala	Gly	Gly	Ile	Val	Ile	Leu	Phe	Gly	Leu	His	Phe	Leu	Gly
						100			105			110			
Val	Phe	Arg	Phe	Ala	Phe	Leu	Tyr	Lys	Thr	Gln	Ser	Val	Gly	Leu	Ala
						115			120			125			
Ser	Lys	Ser	Asn	Ser	Met	Gln	Arg	Phe	Thr	Pro	Phe	Phe	Leu	Ala	
					130			135			140				

## (2) INFORMATION FOR SEQ ID NO:774:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...217

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:774

Met	Pro	Val	Ile	Arg	Val	Leu	Val	Met	Leu	Ala	Thr	Met	Met	Lys
1						5			10			15		
Leu	Val	Lys	Thr	Ala	Lys	Glu	Lys	Lys	Val	Phe	Lys	Asn	Val	Gly
						20			25			30		
Ser	Ile	Met	Gly	Ile	Ala	Phe	Trp	Glu	Ala	Ile	Lys	Asp	Ser	Ile
						35			40			45		
Lys	Gln	Ile	Lys	Ser	Asp	Trp	Ile	Cys	Gly	Asn	Val	Lys	Thr	Ala
						50			55			60		
Asp	Asp	Tyr	Leu	Lys	Thr	His	Pro	Asn	Ser	Trp	Phe	Asn	Ser	Ala
						65			70			75		80
Gly	Val	Thr	Ala	Ile	Thr	Ala	Met	Leu	Met	Asn	Val	Cys	Phe	Ala
						85			90			95		
Asp	Gln	Ser	Lys	Glu	Val	Ala	Gln	Ala	Gln	Lys	Glu	Ala	Glu	Asn
						100			105			110		
Ala	Arg	Asp	Arg	Ala	Asn	Lys	Ser	Gly	Ile	Glu	Leu	Glu	Gln	Glu
						115			120			125		
Gln	Lys	Thr	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Glu	Gln	Glu	Lys	Gln
						130			135			140		
Thr	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Glu	Gln	Glu	Lys	Gln	Lys	Glu
						145			150			155		160
Gln	Glu	Lys	Gln	Lys	Thr	Ser	Asn	Ile	Glu	Thr	Asn	Asn	Gln	Ile
						165			170			175		
Val	Glu	Gln	Glu	Gln	Lys	Thr	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Asn
						180			185			190		
Asn	Thr	Gln	Lys	Asp	Leu	Val	Asn	Lys	Ala	Glu	Gln	Asn	Cys	Gln
						195			200			205		
Asn	His	Asn	Gln	Phe	Phe	Ile	Lys	Asn						
						210			215					

## (2) INFORMATION FOR SEQ ID NO:774:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 217 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774

Met	Pro	Val	Ile	Arg	Val	Leu	Val	Met	Leu	Ala	Thr	Met	Met	Met	Lys
1					5				10						15
Leu	Val	Lys	Thr	Ala	Lys	Glu	Lys	Lys	Val	Phe	Lys	Asn	Val	Gly	Ile
					20				25						30
Ser	Ile	Met	Gly	Ile	Ala	Phe	Trp	Glu	Ala	Ile	Lys	Asp	Ser	Ile	Lys
					35			40							45
Lys	Gln	Ile	Lys	Lys	Ser	Asp	Trp	Ile	Cys	Gly	Asn	Val	Lys	Thr	Ala
					50			55							60
Asp	Asp	Tyr	Leu	Lys	Thr	His	Pro	Asn	Ser	Trp	Phe	Asn	Ser	Ala	Ile
					65			70			75				80
Gly	Val	Thr	Ala	Ile	Thr	Ala	Met	Leu	Met	Asn	Val	Cys	Phe	Ala	Asp
					85			90							95
Asp	Gln	Ser	Lys	Lys	Glu	Val	Ala	Gln	Ala	Gln	Lys	Glu	Ala	Glu	Asn
					100			105							110
Ala	Arg	Asp	Arg	Ala	Asn	Lys	Ser	Gly	Ile	Glu	Leu	Glu	Gln	Glu	Glu
					115			120							125
Gln	Lys	Thr	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Glu	Gln	Glu	Lys	Gln	Lys
					130			135							140
Thr	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Glu
					145			150			155				160
Gln	Glu	Lys	Gln	Lys	Thr	Ser	Asn	Ile	Glu	Thr	Asn	Asn	Gln	Ile	Lys
					165			170							175
Val	Glu	Gln	Glu	Gln	Lys	Thr	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Asn	
					180			185							190
Asn	Thr	Gln	Lys	Asp	Leu	Val	Asn	Lys	Ala	Glu	Gln	Asn	Cys	Gln	Glu
					195			200							205
Asn	His	Asn	Gln	Phe	Phe	Ile	Lys	Asn							
					210			215							

(2) INFORMATION FOR SEQ ID NO:775:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 84 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature

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## (B) LOCATION 1...84

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:775

Val Leu Val Val Gly Lys Pro Asn Glu Ser Tyr Ala Asp Thr His Ala  
 1 5 10 15  
 Arg Ile Glu His Phe Ile Lys Leu Val Asp Phe Lys Gly Glu Ile Val  
 20 25 30  
 Phe Ile Asn Glu Asp Asn Ser Ser Val Glu Ala Tyr Glu Asn Leu Glu  
 35 40 45  
 His Leu Gly Lys Lys Asn Lys Arg Ile Ala Thr Lys Asp Gly Arg Leu  
 50 55 60  
 Asp Ser Leu Ser Ala Cys Arg Ile Leu Glu Arg Tyr Cys Gln Gln Val  
 65 70 75 80  
 Leu Lys Lys Gly

## (2) INFORMATION FOR SEQ ID NO:776:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...75

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:776

Met Val Ile Ser Gly His Phe Thr Thr Tyr Ser Tyr Ile Glu Pro Phe  
 1 5 10 15  
 Ile Ile Gln Ile Ser Gln Phe Ser Pro Asp Ile Thr Thr Leu Met Leu  
 20 25 30  
 Phe Val Phe Gly Leu Ala Gly Val Val Gly Ser Phe Leu Phe Gly Arg  
 35 40 45  
 Leu Tyr Ala Lys Asn Ser Arg Lys Phe Ile Ala Phe Ala Met Val Leu  
 50 55 60  
 Val Ile Cys Pro Gln Pro Leu Ala Phe Cys Val  
 65 70 75

## (2) INFORMATION FOR SEQ ID NO:776:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...75

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:776

Met	Val	Ile	Ser	Gly	His	Phe	Thr	Thr	Tyr	Ser	Tyr	Ile	Glu	Pro	Phe
1					5			10				15			
Ile	Ile	Gln	Ile	Ser	Gln	Phe	Ser	Pro	Asp	Ile	Thr	Thr	Leu	Met	Leu
						20		25				30			
Phe	Val	Phe	Gly	Leu	Ala	Gly	Val	Val	Gly	Ser	Phe	Leu	Phe	Gly	Arg
						35		40			45				
Leu	Tyr	Ala	Lys	Asn	Ser	Arg	Lys	Phe	Ile	Ala	Phe	Ala	Met	Val	Leu
						50		55			60				
Val	Ile	Cys	Pro	Gln	Pro	Leu	Ala	Phe	Cys	Val					
						65		70			75				

## (2) INFORMATION FOR SEQ ID NO:777:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 155 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...155

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:777

Met	Arg	Ile	Leu	Ile	Leu	Lys	Asn	Lys	Pro	Pro	Thr	Leu	Arg	Ser	Lys
1						5			10		15				
Ala	Leu	Thr	Arg	Ser	Trp	Gly	Ile	Asn	Phe	Ser	Leu	Lys	Asn	Thr	Leu
							20		25		30				
Ala	Tyr	Ala	Phe	Met	Gly	Phe	Phe	Asp	Tyr	Ala	His	Ala	Asn	Ser	Ile
						35		40		45					
Lys	Leu	Lys	Asn	Pro	Asn	Tyr	Asn	Ser	Glu	Ala	Ala	Gln	Val	Ala	Ser
						50		55		60					
Gln	Ile	Leu	Gly	Lys	Gln	Glu	Ile	Asn	Arg	Leu	Thr	Asn	Ile	Ala	Asp
						65		70		75		80			
Pro	Arg	Thr	Phe	Glu	Pro	Asn	Met	Leu	Thr	Tyr	Gly	Gly	Ala	Met	Asp
						85		90		95					
Val	Met	Val	Asn	Val	Ile	Asn	Asn	Gly	Ile	Met	Ser	Leu	Gly	Ala	Phe
						100		105		110					
Gly	Gly	Ile	Gln	Leu	Ala	Gly	Asn	Ser	Trp	Leu	Met	Ala	Unk	Pro	Ser
						115		120		125					
Phe	Glu	Gly	Ile	Leu	Gly	Glu	Gln	Ala	Leu	Val	Ser	Arg	Lys	Pro	Leu
						130		135		140					
Leu	Ser	Asn	Phe	Tyr	Ser	Met	Trp	Gly	Leu	Ala					
						145		150		155					

## (2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778

Met	Lys	Ser	Thr	Arg	Ile	Gly	Ser	Lys	Ile	Val	Met	Met	Val	Cys	Ala
1					5					10				15	
Val	Val	Ile	Val	Ile	Ser	Ala	Val	Met	Gly	Val	Ile	Ile	Ser	Tyr	Lys
								20		25			30		
Val	Glu	Ser	Val	Leu	Gln	Ser	Gln	Ala	Thr	Glu	Leu	Leu	Gln	Lys	Lys
					35				40			45			
Ala	Gln	Leu	Val	Ser	Phe	Lys	Ile	Gln	Gly	Ile	Met	Lys	Arg	Ile	Phe
					50			55			60				
Met	Gly	Ala	Asn	Thr	Leu	Glu	Arg	Phe	Leu	Ser	Asp	Glu	Asn	Gly	Ala
					65		70			75			80		
Ile	Asn	Asp	Thr	Leu	Lys	Arg	Arg	Met	Leu	Ser	Glu	Phe	Leu	Leu	Ala
					85			90			95				
Asn	Pro	His	Val	Leu	Leu	Val	Ser	Ala	Ile	Tyr	Thr	Asn	Asn	Glu	
					100			105			110				
Arg	Met	Ile	Thr	Ala	Met	Asn	Met	Asp	Ser	Lys	Ile	Ala	Tyr	Pro	Asn
					115			120			125				
Thr	Ala	Leu	Asn	Glu	Asn	Met	Thr	Unk	Pro	Ile	His	Ser	Leu	Lys	Ser
					130			135			140				
Ile	Thr	Arg	Ser	Unk	Pro	Tyr	Tyr	Lys	Glu	Val	Asn	Unk	Unk	Lys	Ile
					145		150			155			160		
Tyr	Unk	Unk	Unk	Ile	Thr	Leu	Pro	Leu	Unk	Unk	Lys	Asn	Unk	Asn	Unk
					165			170			175				
Ile	Unk	Unk	Leu	Asn	Phe	Unk	Leu	Asn	Ile	Asp	Unk	Phe	Leu	Tyr	Unk
					180			185			190				

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778

Met	Lys	Ser	Thr	Arg	Ile	Gly	Ser	Lys	Ile	Val	Met	Met	Val	Cys	Ala
1					5					10			15		
Val	Val	Ile	Val	Ile	Ser	Ala	Val	Met	Gly	Val	Ile	Ile	Ser	Tyr	Lys
					20			25			30				
Val	Glu	Ser	Val	Leu	Gln	Ser	Gln	Ala	Thr	Glu	Leu	Leu	Gln	Lys	Lys

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35	40	45
Ala Gln Leu Val Ser Phe Lys Ile Gln Gly Ile Met Lys Arg Ile Phe		
50	55	60
Met Gly Ala Asn Thr Leu Glu Arg Phe Leu Ser Asp Glu Asn Gly Ala		
65	70	75
Ile Asn Asp Thr Leu Lys Arg Arg Met Leu Ser Glu Phe Leu Leu Ala		80
85	90	95
Asn Pro His Val Leu Val Ser Ala Ile Tyr Thr Asn Asn Asn Glu		
100	105	110
Arg Met Ile Thr Ala Met Asn Met Asp Ser Lys Ile Ala Tyr Pro Asn		
115	120	125
Thr Ala Leu Asn Glu Asn Met Thr Unk Pro Ile His Ser Leu Lys Ser		
130	135	140
Ile Thr Arg Ser Unk Pro Tyr Tyr Lys Glu Val Asn Unk Unk Lys Ile		
145	150	155
Tyr Unk Unk Unk Ile Thr Leu Pro Leu Unk Unk Lys Asn Unk Asn Unk		160
165	170	175
Ile Unk Unk Leu Asn Phe Unk Leu Asn Ile Asp Unk Phe Leu Tyr Unk		
180	185	190

## (2) INFORMATION FOR SEQ ID NO:779:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...171

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:779

Met Asn Val Lys Lys Glu Lys Pro Gln Ser Gly Lys Ile Asp Arg		
1	5	10
Val Asp Cys Leu Glu Lys Leu Gly Lys Glu Asn Thr Thr Phe Leu Ser		15
20	25	30
Ser Ile Ala Met Gly Ser Ile Gly Gln Leu Ala Ile Pro Ile Pro Gly		
35	40	45
Val Gly Val Leu Ile Gly Gly Phe Val Gly Gly Val Met Ser Lys Thr		
50	55	60
Phe Tyr Asp Val Ser Leu Thr Ile Phe Lys Glu Ala Lys Leu Ala Arg		
65	70	75
Gln Arg Arg Ile Glu Ile Glu Lys Glu Cys Arg Glu Ser Ile Arg Gln		80
85	90	95
Leu Glu Met Tyr Gln Asn Gln Phe Asn Glu Val Phe Glu Arg Tyr Phe		
100	105	110
His Gly Thr Ile Lys Phe Phe Asn Glu Ser Phe Asp Glu Leu Glu Arg		
115	120	125
Ala Leu Cys Ala Gly Asp Ala Asp Leu Ala Ile Ala Val Asn Asn Lys		
130	135	140
Ile Gln Glu Gly Met Gly Gln Glu Leu Leu Phe Asp Asn Lys Gln Glu		
145	150	155
Cys Trp Glu Phe Ile Thr Ser Arg Lys Glu Gly		160
165	170	

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## (2) INFORMATION FOR SEQ ID NO:780:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 141 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...141

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:780

Met	Trp	Pro	Unk	Lys	Leu	Phe	Leu	Lys	Pro	Leu	Lys	Glu	Thr	Ser	Leu
1				5					10			15			
Ala	Leu	Val	Gly	Val	Ala	Lys	Asn	Ile	Lys	Ile	Val	Ala	Leu	Lys	Ala
			20					25				30			
Gly	Leu	Lys	Arg	Ala	Tyr	Leu	Pro	Asn	Arg	Ser	Leu	Ile	Phe	Phe	Leu
	35					40			45						
Ile	Lys	Arg	Tyr	Leu	Arg	Phe	Asp	Lys	Ser	Gln	Pro	Phe	Ile	Ser	Ile
	50				55			60							
Thr	Ala	Leu	Leu	Ala	Phe	Phe	Gly	Val	Ala	Val	Gly	Val	Met	Val	Leu
65					70			75			80				
Ile	Val	Ala	Met	Ala	Ile	Met	Asn	Gly	Met	Ser	Lys	Glu	Phe	Glu	Lys
	85					90			95						
Lys	Leu	Phe	Val	Met	Asn	Tyr	Pro	Leu	Thr	Leu	Tyr	Thr	Ser	Pro	
	100				105			110							
Tyr	Gly	Ile	Ser	Glu	Glu	Val	Val	Gln	Ala	Leu	Glu	Lys	Lys	Phe	Pro
	115					120			125						
Asn	Leu	Pro	Phe	Ser	Unk	Pro	Ile	Cys	Lys	Pro	Lys	Ala			
	130					135			140						

## (2) INFORMATION FOR SEQ ID NO:781:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...70

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:781

Met	Val	Ser	Leu	Leu	Gly	Ala	Leu	Lys	Arg	Thr	Pro	Cys	Thr	Asn	Arg
1				5				10	15						
Phe	Tyr	Leu	Lys	Ala	Leu	Leu	Phe	Ala	Ile	Phe	Tyr	His	Ala	Val	Asn
	20					25			30						
Asn	Phe	Leu	Thr	Gln	Cys	Pro	Pro	His	Gln	Val	Arg	Glu	Phe	Phe	Ser

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35	40	45
Ser Arg His Ala Gln Gly Trp Lys Arg Glu Thr Leu Pro Cys Ala Leu		
50	55	60
Ser Phe Gln Asn Ala Leu		
65	70	

## (2) INFORMATION FOR SEQ ID NO:782:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782

Val His His Leu Unk Arg Leu Leu Asp Ser Gly Ser Glu Arg Cys Ile			
1	5	10	15
Gly Cys Gly Leu Cys Glu Lys Ile Cys Thr Ser Asn Cys Ile Arg Ile			
20	25	30	
Ile Thr His Lys Gly Glu Asp Asn Arg Lys Lys Ile Asp Ser Tyr Thr			
35	40	45	
Ile Asn Leu Gly Arg Cys Ile Tyr Cys Gly Leu Cys Ala Glu Val Cys			
50	55	60	
Pro Glu Leu Ala Ile Val Met Gly Asn Arg Phe Glu Asn Ala Ser Thr			
65	70	75	80
Gln Arg Ser Gln Tyr Gly Ser Lys Ser Glu Phe Leu Thr Ser Glu Gln			
85	90	95	
Asp Ala Lys Asn Cys Ser His Ala Glu Phe Leu Gly Phe Gly Ala Val			
100	105	110	
Ser Pro Asn Tyr Asn Glu Arg Met Gln Ala Thr Pro Leu Asp Tyr Val			
115	120	125	
Gln Glu Pro Ser Lys Glu Glu Ser Lys Glu Glu Phe Unk Thr Ser Pro			
130	135	140	
Glu Ser His Lys Gly Asp Glu Asn Val			
145	150		

## (2) INFORMATION FOR SEQ ID NO:783:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature

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## (B) LOCATION 1...183

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:783

Met Ala Ile Trp Gly Trp Cys Phe Leu Phe Ser Ser Leu Met Trp  
 1               5                                   10                   15  
 Gly Ser Ser Met His Glu Leu Val Leu Arg Ser Gln Ala Leu Gly Phe  
                  20                                   25                   30  
 Glu Thr Arg Leu Val Gln Cys Asp Leu Ser Phe Ser Tyr Glu Arg Phe  
                  35                                   40                   45  
 Ile Ser Lys Thr Lys Arg Ser Leu Ala Val Leu Glu Glu Phe Asp Trp  
                  50                                   55                   60  
 Leu Asn Ser Gly Phe Asp Phe Ser Arg Leu Asn Val Glu Asn Asp Thr  
                  65                                   70                   75                   80  
 Leu Glu Leu Leu Lys Ala Leu Tyr Phe Lys Leu Glu Lys Leu Glu Ser  
                  85                                   90                   95  
 Leu Leu Leu Lys Glu Asn Leu Leu Glu Leu Glu Gln Lys Asp Arg Ile  
                  100                                  105                   110  
 Ile Ala Leu Gly His Gly Leu Val Cys Leu Lys Lys Gln Ser Leu Ile  
                  115                                  120                   125  
 Ala Pro Gln Thr Tyr Tyr Gly Arg Cys Val Leu Glu Gly Lys Ile Leu  
                  130                                  135                   140  
 Ala Phe Phe Gly Val Ala Arg Asp Lys Asp Phe Leu Glu Ile Thr Arg  
                  145                                  150                   155                   160  
 Met His Ala Leu Asp Ile Lys Arg Tyr Asp Ser Phe Ile Val Asp Ser  
                  165                                  170                   175  
 Glu Arg Lys Gly Leu Lys Leu  
                  180

## (2) INFORMATION FOR SEQ ID NO:784:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...67

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:784

Met Pro Glu Asn Ser Lys Leu Gln Pro Ala Lys Leu Gly Lys Asn Phe  
 1               5                                   10                   15  
 Asp Pro Val Asp His Ser Asn Arg Asn Phe Phe Phe Ser Leu Ile Leu  
                  20                                   25                   30  
 Ser Val Leu Leu His Trp Leu Ile Tyr Phe Leu Phe Glu His Arg Glu  
                  35                                   40                   45  
 Asp Phe Phe Pro Ser Lys Pro Lys Leu Val Lys Leu Asn Pro Glu Asn  
                  50                                   55                   60  
 Leu Leu Val  
                  65

## (2) INFORMATION FOR SEQ ID NO:785:

## (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 253 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785

Met	Ala	Tyr	Lys	Tyr	Asp	Arg	Asp	Leu	Glu	Phe	Leu	Lys	Gln	Leu	Glu
1								5	10				15		
Ser	Ser	Asp	Leu	Leu	Asp	Leu	Phe	Glu	Val	Leu	Val	Phe	Gly	Lys	Asp
								20	25				30		
Gly	Glu	Lys	Arg	His	Asn	Glu	Lys	Leu	Thr	Ser	Ser	Ile	Glu	Tyr	Lys
								35	40				45		
Arg	His	Gly	Asp	Asp	Tyr	Ala	Lys	Tyr	Ala	Glu	Arg	Ile	Ala	Glu	Glu
								50	55				60		
Leu	Gln	Tyr	Tyr	Gly	Ser	Asn	Ser	Phe	Ala	Ser	Phe	Ile	Lys	Gly	Glu
								65	70				80		
Gly	Val	Leu	Tyr	Lys	Glu	Ile	Leu	Cys	Asp	Val	Cys	Asp	Lys	Leu	Lys
								85	90				95		
Val	Asn	Tyr	Asn	Lys	Lys	Thr	Glu	Thr	Thr	Leu	Ile	Glu	Gln	Asn	Met
								100	105				110		
Leu	Ser	Lys	Ile	Leu	Glu	Arg	Ser	Leu	Glu	Glu	Met	Asp	Asp	Glu	Glu
								115	120				125		
Val	Lys	Glu	Met	Cys	Asp	Glu	Leu	Ser	Ile	Lys	Asn	Thr	Asp	Asn	Leu
								130	135				140		
Asn	Arg	Gln	Ala	Leu	Ser	Ala	Ala	Thr	Leu	Thr	Leu	Phe	Lys	Met	Gly
								145	150				155		160
Gly	Phe	Lys	Ser	Tyr	Gln	Leu	Ala	Val	Ile	Val	Ala	Asn	Ala	Val	Ala
								165	170				175		
Lys	Thr	Ile	Leu	Gly	Arg	Gly	Leu	Ser	Leu	Ala	Gly	Asn	Gln	Val	Leu
								180	185				190		
Thr	Arg	Thr	Leu	Ser	Phe	Leu	Thr	Gly	Pro	Val	Gly	Trp	Ile	Ile	Thr
								195	200				205		
Gly	Val	Trp	Thr	Ala	Ile	Asp	Ile	Ala	Gly	Pro	Ala	Tyr	Arg	Val	Thr
								210	215				220		
Ile	Pro	Ala	Cys	Ile	Val	Val	Ala	Thr	Leu	Arg	Leu	Lys	Thr	Gln	Gln
								225	230				235		240
Ala	Asn	Glu	Asp	Lys	Lys	Ser	Leu	Gln	Ile	Glu	Ser	Val			
								245	250						

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 253 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

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## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...253

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:785

Met Ala Tyr Lys Tyr Asp Arg Asp Leu Glu Phe Leu Lys Gln Leu Glu  
 1 5 10 15  
 Ser Ser Asp Leu Leu Asp Leu Phe Glu Val Leu Val Phe Gly Lys Asp  
 20 25 30  
 Gly Glu Lys Arg His Asn Glu Lys Leu Thr Ser Ser Ile Glu Tyr Lys  
 35 40 45  
 Arg His Gly Asp Asp Tyr Ala Lys Tyr Ala Glu Arg Ile Ala Glu Glu  
 50 55 60  
 Leu Gln Tyr Tyr Gly Ser Asn Ser Phe Ala Ser Phe Ile Lys Gly Glu  
 65 70 75 80  
 Gly Val Leu Tyr Lys Glu Ile Leu Cys Asp Val Cys Asp Lys Leu Lys  
 85 90 95  
 Val Asn Tyr Asn Lys Lys Thr Glu Thr Leu Ile Glu Gln Asn Met  
 100 105 110  
 Leu Ser Lys Ile Leu Glu Arg Ser Leu Glu Glu Met Asp Asp Glu Glu  
 115 120 125  
 Val Lys Glu Met Cys Asp Glu Leu Ser Ile Lys Asn Thr Asp Asn Leu  
 130 135 140  
 Asn Arg Gln Ala Leu Ser Ala Ala Thr Leu Thr Leu Phe Lys Met Gly  
 145 150 155 160  
 Gly Phe Lys Ser Tyr Gln Leu Ala Val Ile Val Ala Asn Ala Val Ala  
 165 170 175  
 Lys Thr Ile Leu Gly Arg Gly Leu Ser Leu Ala Gly Asn Gln Val Leu  
 180 185 190  
 Thr Arg Thr Leu Ser Phe Leu Thr Gly Pro Val Gly Trp Ile Ile Thr  
 195 200 205  
 Gly Val Trp Thr Ala Ile Asp Ile Ala Gly Pro Ala Tyr Arg Val Thr  
 210 215 220  
 Ile Pro Ala Cys Ile Val Val Ala Thr Leu Arg Leu Lys Thr Gln Gln  
 225 230 235 240  
 Ala Asn Glu Asp Lys Lys Ser Leu Gln Ile Glu Ser Val  
 245 250

## (2) INFORMATION FOR SEQ ID NO:786:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...173

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:786

Val Phe Leu Val Gln Ser Trp Ala Leu Ser Leu Lys Ile Asp Ser Leu  
 1 5 10 15  
 Phe Ser Leu Phe Ser Val Gly Lys Ile Pro Ser Gly Ser Lys Asp Pro  
 20 25 30  
 Phe Ala Leu Arg Arg Leu Ser Phe Gly Leu Leu Lys Ile Ile Ala His

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35	40	45													
Tyr	Gly	Leu	Glu	Phe	Asp	Leu	Lys	Ala	Asp	Leu	Lys	Asn	Leu	Phe	Glu
50						55					60				
Lys	Val	Gly	Val	Tyr	Gln	Ser	Phe	Asp	Leu	Glu	Val	Leu	Glu	Lys	Phe
65						70				75				80	
Leu	Leu	Glu	Arg	Phe	His	Asn	Leu	Ile	Asp	Cys	Asn	Leu	Ser	Ile	Ile
						85			90				95		
Arg	Ser	Val	Leu	Asn	Thr	Asn	Glu	Arg	Asp	Ile	Val	Lys	Ile	Ile	Gln
						100			105			110			
Lys	Val	Lys	Ala	Leu	Lys	Arg	Phe	Leu	Asp	Asn	Pro	Lys	Asn	Ala	Gln
						115			120			125			
Lys	Lys	Glu	Leu	Leu	Phe	Ser	Ala	Phe	Lys	Arg	Leu	Ala	Asn	Ile	Asn
130						135			140						
Lys	Asp	Arg	Asn	Pro	Asn	Glu	Ser	Ser	Gly	Phe	Ser	Thr	Ser	Leu	Phe
145						150			155			160			
Lys	Glu	Leu	Gln	Glu	His	Ala	Leu	Phe	Glu	Ala	Phe	Asn			
						165			170						

## (2) INFORMATION FOR SEQ ID NO:787:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...259

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:787

Met	Ser	Leu	Ala	Pro	Ser	Val	Met	Ala	Gly	Phe	Leu	Phe	Cys	Ala	Gly
1							5		10					15	
Ser	Cys	Ser	Leu	Arg	Phe	Pro	Asn	Tyr	Ser	Lys	Ile	Ile	Ser	Ile	Asp
							20		25					30	
Val	Asp	Thr	Val	Phe	Leu	Gly	Asp	Val	Ala	Ser	Ala	Tyr	Phe	Ala	Leu
							35		40			45			
Asp	Asn	Glu	Pro	Thr	Lys	Leu	Leu	Gly	Met	Val	Arg	Asp	Thr	Phe	Ser
							50		55			60			
His	Leu	Pro	Phe	Glu	Ala	Phe	Cys	Asp	Phe	Cys	Glu	Arg	Thr	Cys	Lys
							65		70		75		80		
Asn	Phe	Lys	Ile	Asp	Leu	Leu	Arg	Phe	Ser	Gln	Asn	Glu	Leu	Lys	Arg
							85		90			95			
Ile	His	Gln	Gly	Phe	Asn	Met	Gly	Phe	Leu	Val	Ala	Asn	Leu	Asp	Leu
							100		105			110			
Trp	Arg	Glu	Asn	Gly	Phe	Glu	Lys	Ile	Ala	Leu	Glu	Phe	Leu	Lys	Thr
							115		120			125			
Arg	Gly	Lys	Asp	Leu	Phe	Tyr	Pro	Glu	Gln	Cys	Leu	Ile	Asn	Met	Val
							130		135			140			
Phe	Leu	Glu	Arg	Ile	Leu	Glu	Leu	Pro	Ile	His	Tyr	Asn	Cys	Tyr	Ser
							145		150		155		160		
Asp	Phe	Phe	Lys	Glu	His	Tyr	Pro	Lys	Ser	Ile	Ile	Met	Leu	His	Phe
							165		170			175			
Ile	Lys	Tyr	Lys	Pro	Trp	Arg	Ser	Val	Ser	Ser	Leu	Asn	Gly	Arg	Leu
							180		185			190			
Ile	Cys	Tyr	Glu	Ala	Glu	Ala	Ser	Phe	Trp	Leu	Ala	Asn	Leu	Phe	Cys
							195		200			205			

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Thr Pro Phe Lys Asn Asp Phe Phe Lys Glu Arg Leu Glu Met Ala Lys  
 210                215                220  
 Asp Gln Gln Met Gln Ser Phe Lys Thr His Ile Arg Ser Lys Thr Ile  
 225                230                235                240  
 Arg Asp Tyr Phe Tyr Phe Arg Ile Lys Asn Ile Leu Lys Lys Val Phe  
 245                250                255  
 Glu Leu Ser

## (2) INFORMATION FOR SEQ ID NO:788:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...293

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:788

Leu Leu Leu Phe Ile Val Val Ile Thr Ser Leu Val Lys Asn Thr Ile  
 1                5                10                15  
 Pro Asn Ile Trp Leu Thr Lys Ile Leu Tyr Met Ala Ile Leu Cys  
 20                25                30  
 Ala Ile Ala His Ser Val Gly Unk Ile Leu Arg Trp Tyr Val Ser Gly  
 35                40                45  
 His Ser Pro Trp Ser Asn Ala Tyr Glu Ser Met Phe Tyr Ile Ala Trp  
 50                55                60  
 Ala Ser Val Ile Ala Gly Phe Val Leu Arg Unk Lys Leu Ala Leu Ser  
 65                70                75                80  
 Ala Ser Ser Phe Leu Ala Gly Ile Ala Leu Phe Val Ala His Leu Gly  
 85                90                95  
 Phe Met Asp Pro Gln Ile Gly Pro Leu Val Pro Val Leu Lys Ser Tyr  
 100                105                110  
 Trp Leu Asn Ile His Val Ser Val Ile Thr Ala Ser Tyr Gly Phe Leu  
 115                120                125  
 Gly Leu Cys Phe Val Leu Gly Ile Leu Ser Leu Val Leu Phe Ile Leu  
 130                135                140  
 Arg Lys Gln Gly Arg Phe Asn Leu Asp Lys Thr Ile Leu Ser Ile Ser  
 145                150                155                160  
 Ala Ile Asn Glu Met Ser Met Ile Leu Gly Leu Phe Met Leu Thr Ala  
 165                170                175  
 Gly Asn Phe Leu Gly Gly Val Trp Ala Asn Glu Ser Trp Gly Arg Tyr  
 180                185                190  
 Trp Gly Trp Asp Pro Lys Glu Thr Trp Ala Leu Ile Ser Ile Cys Val  
 195                200                205  
 Tyr Ala Leu Ile Leu His Leu Arg Phe Leu Gly Ser Gln Asn Trp Pro  
 210                215                220  
 Phe Ile Leu Ala Ser Ser Val Leu Gly Phe Tyr Ser Val Leu Met  
 225                230                235                240  
 Thr Leu Phe Trp Arg Glu Leu Leu Pro Phe Trp Leu Ala Gln Leu Cys  
 245                250                255  
 Arg Arg Unk Ser Phe Ala Asp Pro Tyr Phe Phe Ile Leu Phe Gly Ser  
 260                265                270  
 Asp Thr Phe Arg Ser Arg Ile Leu Ala Tyr Phe Lys Arg His Leu Ser

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275 Leu Pro Lys Leu Val 290	280	285
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## (2) INFORMATION FOR SEQ ID NO:788:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...293

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:788

Leu Leu Leu Phe Ile Val Val Ile Thr Ser Leu Val Lys Asn Thr Ile  
 1               5                           10                           15  
 Pro Asn Ile Trp Leu Thr Lys Ile Leu Tyr Met Ala Ile Leu Leu Cys  
                  20                           25                           30  
 Ala Ile Ala His Ser Val Gly Unk Ile Leu Arg Trp Tyr Val Ser Gly  
                  35                           40                           45  
 His Ser Pro Trp Ser Asn Ala Tyr Glu Ser Met Phe Tyr Ile Ala Trp  
                  50                           55                           60  
 Ala Ser Val Ile Ala Gly Phe Val Leu Arg Unk Lys Leu Ala Leu Ser  
                  65                           70                           75                           80  
 Ala Ser Ser Phe Leu Ala Gly Ile Ala Leu Phe Val Ala His Leu Gly  
                  85                           90                           95  
 Phe Met Asp Pro Gln Ile Gly Pro Leu Val Pro Val Leu Lys Ser Tyr  
                  100                          105                          110  
 Trp Leu Asn Ile His Val Ser Val Ile Thr Ala Ser Tyr Gly Phe Leu  
                  115                          120                          125  
 Gly Leu Cys Phe Val Leu Gly Ile Leu Ser Leu Val Leu Phe Ile Leu  
                  130                          135                          140  
 Arg Lys Gln Gly Arg Phe Asn Leu Asp Lys Thr Ile Leu Ser Ile Ser  
                  145                          150                          155                           160  
 Ala Ile Asn Glu Met Ser Met Ile Leu Gly Leu Phe Met Leu Thr Ala  
                  165                          170                           175  
 Gly Asn Phe Leu Gly Gly Val Trp Ala Asn Glu Ser Trp Gly Arg Tyr  
                  180                          185                          190  
 Trp Gly Trp Asp Pro Lys Glu Thr Trp Ala Leu Ile Ser Ile Cys Val  
                  195                          200                          205  
 Tyr Ala Leu Ile Leu His Leu Arg Phe Leu Gly Ser Gln Asn Trp Pro  
                  210                          215                          220  
 Phe Ile Leu Ala Ser Ser Val Leu Gly Phe Tyr Ser Val Leu Met  
                  225                          230                          235                           240  
 Thr Leu Phe Trp Arg Glu Leu Leu Pro Phe Trp Leu Ala Gln Leu Cys  
                  245                          250                           255  
 Arg Arg Unk Ser Phe Ala Asp Pro Tyr Phe Phe Ile Leu Phe Gly Ser  
                  260                          265                          270  
 Asp Thr Phe Arg Ser Arg Ile Leu Ala Tyr Phe Lys Arg His Leu Ser  
                  275                          280                           285  
 Leu Pro Lys Leu Val  
                  290

## (2) INFORMATION FOR SEQ ID NO:789:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789

Val	Ile	Val	Cys	Ser	Ala	Ala	Gly	Leu	Ser	His	Phe	Phe	Gly	Phe	Ser
1					5				10				15		
Met	Ser	Leu	Gly	Ala	Phe	Ile	Val	Gly	Met	Ala	Ile	Ser	Lys	Ser	Arg
					20				25				30		
Tyr	Lys	Ile	Asn	Val	Gln	Glu	Glu	Phe	Ala	Gln	Leu	Lys	Asn	Leu	Phe
					35			40				45			
Leu	Ala	Leu	Phe	Phe	Ile	Thr	Ile	Gly	Met	Gln	Ile	Asn	Val	Ser	Phe
					50			55			60				
Phe	Met	Glu	Lys	Phe	Phe	Val	Val	Ile	Phe	Leu	Leu	Ile	Leu	Val	Met
					65			70			75			80	
Ser	Phe	Lys	Thr	Phe	Ile	Ile	Tyr	Ala	Leu	Leu	Arg	Phe	Arg	Asp	
					85			90			95				
Ala	Lys	Thr	Ala	Ile	Lys	Thr	Ala	Leu	Ser	Leu	Ala	Gln	Ile	Gly	Glu
					100			105			110				
Phe	Ser	Phe	Val	Ile	Phe	Leu	Asn	Ser	Gly	Ser	His	Gln	Leu	Phe	Asn
					115			120			125				
Leu	Gln	Glu	Lys	Lys	Gly	Ile	Leu	Gly	Phe	Leu	His	Gln	Lys	Asn	Ile
					130			135			140				
Leu	Asn	Ile	Ala	Gln	Asn	Asp	Ile	His	Gln	Leu	Leu	Ile	Leu	Met	Val
					145			150			155			160	
Val	Phe	Ser	Met	Leu	Ala	Thr	Pro	Phe	Ile	Leu	Lys	Tyr	Leu	Glu	Ser
					165			170			175				
Ile	Ala	Gln	Phe	Ile	Leu	His	Gln	Lys	Ser	Gln	Glu	Asn	Glu	Pro	Ala
					180			185			190				
Lys	Lys														

## (2) INFORMATION FOR SEQ ID NO:790:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...132

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:790

Met Phe Tyr Leu Ile Asn Thr Gly Val Pro His Leu Val Gly Phe Val  
 1               5               10               15  
 Lys Asn Lys Gly Leu Leu Asn Ser Leu Asn Thr Leu Glu Leu Arg Ala  
 20              25              30  
 Leu Arg His Phe Asn Ala Asn Ile Asn Ile Ala Phe Ile Glu Asn  
 35              40              45  
 Lys Glu Thr Ile Phe Leu Gln Thr Tyr Glu Arg Gly Val Glu Asp Phe  
 50              55              60  
 Thr Leu Ala Cys Gly Thr Gly Met Ala Ala Val Phe Ile Ala Ala Arg  
 65              70              75              80  
 Leu Phe His Asn Thr Pro Lys Lys Ala Thr Leu Ile Pro Lys Ser Asn  
 85              90              95  
 Glu Phe Leu Glu Leu Ser Leu Lys Asn Asp Gly Ile Phe Tyr Lys Gly  
 100             105             110  
 Val Ala Arg Tyr Ile Gly Met Ser Val Leu Gly Met Gly Val Phe Lys  
 115             120             125  
 Asn Gly Cys Phe  
 130

## (2) INFORMATION FOR SEQ ID NO:791:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...213

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:791

Met Ile Lys Ala Ile Asp Ile Ser His Asp Phe Glu Lys Pro Leu Tyr  
 1               5               10               15  
 Asn Gly Val Asn Leu Arg Ile Lys Pro Lys Glu Ser Met Glu Ile Leu  
 20              25              30  
 Gly Val Ser Gly Ser Gly Lys Ser Thr Leu Ile Ser His Leu Ala Thr  
 35              40              45  
 Met Leu Lys Pro Asp Ser Gly Thr Val Ser Leu Leu Glu His Gln Asp  
 50              55              60  
 Ile Tyr Ala Leu Asn Ser Lys Lys Leu Leu Glu Leu Arg Arg Leu Lys  
 65              70              75              80  
 Val Gly Ile Val Phe Gln Ser His Tyr Leu Phe Lys Gly Phe Ser Ala  
 85              90              95  
 Leu Glu Asn Leu Gln Val Ala Ser Ile Leu Ala Lys Gln Glu Ile Asn  
 100             105             110  
 His Ser Leu Leu Glu Gln Leu Gly Ile Ala His Thr Leu Lys Gln Gly  
 115             120             125  
 Val Gly Glu Leu Ser Gly Gly Gln Gln Arg Leu Ser Ile Ala Arg  
 130             135             140  
 Val Leu Ser Lys Lys Pro Gln Ile Ile Ala Asp Glu Pro Thr Gly  
 145             150             155              160  
 Asn Leu Asp Thr Thr Ser Ala Asn Gln Val Ile Ser Met Leu Gln Asn  
 165             170             175

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Tyr Ile Thr Glu Asn Glu Gly Ala Leu Val Leu Ala Thr His Asp Glu  
 180                   185                   190  
 His Leu Ala Phe Thr Cys Ser Gin Val Tyr Arg Leu Glu Lys Glu Ser  
 195                   200                   205  
 Leu Ile Lys Glu Lys  
 210

## (2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 47 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...47

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792

Met Leu Asp Lys Arg Ile Lys Thr Leu Leu Phe Phe Gly Leu Asn  
 1               5                   10                   15  
 Met Val Cys Leu Ser Val Ser Phe Thr Asn Lys Pro His Leu Cys Phe  
 20               25                   30  
 Trp Phe Leu Val Leu Gly Cys Tyr Leu Val Tyr Glu Trp Gln Lys  
 35               40                   45

## (2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 142 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793

Val Glu Met Ile His Thr Gln Asp Tyr Ile Lys Met Glu Glu Ala Ala  
 1               5                   10                   15  
 Thr Glu Ala Ile Lys Arg Lys Glu Ser Ser Ile Tyr Leu Gly Met Asp  
 20               25                   30  
 Ile Leu Lys Asn Gly Ala Asp Ala Leu Ile Ser Ala Gly His Ser Gly  
 35               40                   45  
 Ala Thr Met Gly Leu Ala Thr Leu Arg Leu Gly Arg Ile Lys Gly Val  
 50               55                   60  
 Glu Arg Pro Ala Ile Cys Thr Leu Met Pro Ser Val Gly Lys Arg Pro

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65	70	75	80
Ser Val Leu Leu Asp Ala Gly Ala Asn Thr Asp Cys Lys Pro Glu Tyr			
85	90	95	
Leu Ile Asp Phe Ala Leu Met Gly Tyr Glu Tyr Ala Lys Ser Val Leu			
100	105	110	
His Tyr Asp Ser Pro Lys Val Gly Leu Leu Ser Asn Gly Glu Glu Asp			
115	120	125	
Ile Lys Gly Gly Ile Arg Ser Leu Lys Lys Arg Ile Lys Cys			
130	135	140	

## (2) INFORMATION FOR SEQ ID NO:793:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793

Val Glu Met Ile His Thr Gln Asp Tyr Ile Lys Met Glu Glu Ala Ala			
1	5	10	15
Thr Glu Ala Ile Lys Arg Lys Glu Ser Ser Ile Tyr Leu Gly Met Asp			
20	25	30	
Ile Leu Lys Asn Gly Ala Asp Ala Leu Ile Ser Ala Gly His Ser Gly			
35	40	45	
Ala Thr Met Gly Leu Ala Thr Leu Arg Leu Gly Arg Ile Lys Gly Val			
50	55	60	
Glu Arg Pro Ala Ile Cys Thr Leu Met Pro Ser Val Gly Lys Arg Pro			
65	70	75	80
Ser Val Leu Leu Asp Ala Gly Ala Asn Thr Asp Cys Lys Pro Glu Tyr			
85	90	95	
Leu Ile Asp Phe Ala Leu Met Gly Tyr Glu Tyr Ala Lys Ser Val Leu			
100	105	110	
His Tyr Asp Ser Pro Lys Val Gly Leu Leu Ser Asn Gly Glu Glu Asp			
115	120	125	
Ile Lys Gly Gly Ile Arg Ser Leu Lys Lys Arg Ile Lys Cys			
130	135	140	

## (2) INFORMATION FOR SEQ ID NO:794:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

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- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...69

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:794

Met	Lys	Thr	Ile	Lys	Asn	Gly	Ile	Met	Ile	Gly	Thr	Leu	Gly	Ala	Leu
1							5			10				15	
Leu	Leu	Ser	Gly	Cys	Ser	Ser	Phe	Asp	Ala	Gln	Arg	Phe	Ala	Cys	Leu
							20			25				30	
Pro	Lys	Asp	His	Ser	Ser	Lys	Asp	Ala	Ser	Thr	Lys	Lys	Glu	Ala	Gln
							35			40				45	
Tyr	Ile	Pro	Lys	Gly	Phe	Phe	Asp	Pro	Tyr	Ser	Ser	Asn	Leu	Asn	His
							50			55				60	
Trp	Asp	Ser	Thr	Phe											
							65								

## (2) INFORMATION FOR SEQ ID NO:795:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 144 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...144

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:795

Met	Leu	Glu	Ile	Lys	Asn	Leu	Asn	Cys	Val	Leu	Asn	Ser	His	Phe	Ser
1								5			10			15	
Leu	Gln	Asn	Ile	Asn	Ile	Ser	Leu	Ser	Tyr	Ser	Glu	Arg	Val	Ala	Ile
							20			25			30		
Val	Gly	Glu	Ser	Gly	Ser	Gly	Lys	Ser	Ser	Ile	Ala	Asn	Leu	Val	Met
							35			40			45		
Arg	Leu	Asn	Pro	Arg	Phe	Lys	Ser	His	Asn	Gly	Glu	Ile	Leu	Phe	Glu
							50			55			60		
Thr	Thr	Asn	Leu	Leu	Lys	Glu	Ser	Glu	Ala	Phe	Unk	Gln	His	Leu	Arg
							65			70			75		80
Gly	Asn	Ile	Ile	Ala	Tyr	Ile	Ala	Gln	Asp	Pro	Leu	Ser	Ser	Leu	Asn
							85			90			95		
Pro	Leu	His	Ile	Gly	Lys	Gln	Met	Ser	Glu	Ala	Tyr	Phe	Leu	His	
							100			105			110		
His	Lys	Asn	Ala	Ser	Gln	Val	Ser	Leu	Asn	Glu	Gln	Val	Leu	Asn	Val
							115			120			125		
Met	Lys	Gln	Val	Gln	Leu	Asp	Glu	Asn	Phe	Trp	Asn	Val	Ser	Leu	Met
							130			135			140		

## (2) INFORMATION FOR SEQ ID NO:795:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 144 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...144
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:795

Met	Leu	Glu	Ile	Lys	Asn	Leu	Asn	Cys	Val	Leu	Asn	Ser	His	Phe	Ser
1		5						10					15		
Leu	Gln	Asn	Ile	Asn	Ile	Ser	Leu	Ser	Tyr	Ser	Glu	Arg	Val	Ala	Ile
								20		25			30		
Val	Gly	Glu	Ser	Gly	Ser	Gly	Lys	Ser	Ser	Ile	Ala	Asn	Leu	Val	Met
							35		40			45			
Arg	Leu	Asn	Pro	Arg	Phe	Lys	Ser	His	Asn	Gly	Glu	Ile	Leu	Phe	Glu
	50					55				60					
Thr	Thr	Asn	Leu	Leu	Lys	Glu	Ser	Glu	Ala	Phe	Unk	Gln	His	Leu	Arg
	65				70				75			80			
Gly	Asn	Ile	Ile	Ala	Tyr	Ile	Ala	Gln	Asp	Pro	Leu	Ser	Ser	Leu	Asn
					85				90			95			
Pro	Leu	His	Ile	Gly	Lys	Gln	Met	Ser	Glu	Ala	Tyr	Phe	Leu	His	
	100					105				110					
His	Lys	Asn	Ala	Ser	Gln	Val	Ser	Leu	Asn	Glu	Gln	Val	Leu	Asn	Val
	115					120				125					
Met	Lys	Gln	Val	Gln	Leu	Asp	Glu	Asn	Phe	Trp	Asn	Val	Ser	Leu	Met
	130				135				140						

## (2) INFORMATION FOR SEQ ID NO:796:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 190 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...190
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:796

Met	Glu	Leu	Ile	Leu	Gly	Ser	Gln	Ser	Ser	Ala	Arg	Ala	Asn	Leu	Leu
1		5			10					15					
Lys	Glu	His	Gly	Ile	Lys	Phe	Glu	Gln	Lys	Ala	Leu	Tyr	Phe	Asp	Glu
				20		25			30						
Glu	Ser	Leu	Lys	Thr	Thr	Asp	Pro	Arg	Glu	Phe	Val	Tyr	Leu	Ala	Cys
				35		40			45						
Lys	Gly	Lys	Leu	Glu	Lys	Ala	Lys	Glu	Leu	Ala	Asn	Asn	Cys	Ala	
				50		55			60						
Ile	Val	Val	Ala	Asp	Ser	Val	Val	Ser	Val	Gly	Asn	Arg	Met	Gln	Arg
	65				70				75			80			
Lys	Ala	Lys	Asn	Lys	Arg	Glu	Ala	Leu	Glu	Phe	Leu	Lys	Arg	Gln	Asn
				85				90				95			

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Gly Asn Glu Ile Glu Val Leu Thr Cys Ser Ala Leu Ile Ser Pro Val  
 100 105 110  
 Leu Glu Trp Leu Asp Leu Ser Val Phe Arg Ala Arg Leu Lys Ala Phe  
 115 120 125  
 Asp Cys Ser Glu Ile Glu Lys Tyr Leu Glu Ser Gly Leu Trp Gln Gly  
 130 135 140  
 Ser Ala Gly Cys Val Arg Leu Glu Asp Phe His Lys Pro Tyr Ile Lys  
 145 150 155 160  
 Ser Ser Ser Lys Asn Leu Ser Val Gly Leu Gly Leu Asn Val Glu Gly  
 165 170 175  
 Leu Leu Gly Ala Leu Lys Leu Gly Val Lys Leu Ser Leu Leu  
 180 185 190

## (2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 83 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797

Met Asn Tyr Lys Val Ala Ser Ala Arg Asn Ile Ala Thr Leu Leu Phe  
 1 5 10 15  
 Leu Phe Phe Ser Gln Ser Glu Ala Phe Asp Leu Gly Lys Ile Ala Lys  
 20 25 30  
 Ile Lys Ala Gly Ala Glu Ser Phe Ser Lys Val Gly Phe Asn Asn Lys  
 35 40 45  
 Pro Ile Asn Unk Asn Lys Gly Ile Tyr Pro Thr Glu Thr Phe Met Thr  
 50 55 60  
 Ile Asn Gly Leu His Ala Gly Gly Phe Tyr Gly Ala Leu Ala Gln Lys  
 65 70 75 80  
 Arg Tyr Gly

## (2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 83 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...83

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:797

Met Asn Tyr Lys Val Ala Ser Ala Arg Asn Ile Ala Thr Leu Leu Phe  
 1 5 10 15  
 Leu Phe Phe Ser Gln Ser Glu Ala Phe Asp Leu Gly Lys Ile Ala Lys  
 20 25 30  
 Ile Lys Ala Gly Ala Glu Ser Phe Ser Lys Val Gly Phe Asn Asn Lys  
 35 40 45  
 Pro Ile Asn Unk Asn Lys Gly Ile Tyr Pro Thr Glu Thr Phe Met Thr  
 50 55 60  
 Ile Asn Gly Leu His Ala Gly Gly Phe Tyr Gly Ala Leu Ala Gln Lys  
 65 70 75 80  
 Arg Tyr Gly

## (2) INFORMATION FOR SEQ ID NO:798:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...135

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:798

Met Leu Ile Leu Gly His Pro Leu Ile Pro Ser Ala Arg Phe Val Phe  
 1 5 10 15  
 Ile Lys Asn Thr Asp Ala Ile His Ser Ser Ala Asn Asn Asp Ile Val  
 20 25 30  
 Cys Phe Glu Ala Asn Pro Lys Asn Leu Glu Leu Ala Gln Tyr Cys Cys  
 35 40 45  
 Glu Asn Gly Val His Phe Ser Val Ile Phe Leu Ser His Lys Ile Glu  
 50 55 60  
 Thr Asp Thr Phe Phe Leu Phe Asn Ala Phe Lys Pro Leu Tyr Cys Ile  
 65 70 75 80  
 Phe Lys Asp Ile Lys Gln Ala Ile Leu Ala Gln Gln His Ala Thr Asn  
 85 90 95  
 Tyr Leu Leu Asp Ser Lys Ile Leu Phe Ser Met Asp Phe Asn Asp Thr  
 100 105 110  
 Glu Ser Trp Glu Ile Cys Ala Lys Asn Gln Ile Asp Gly Val Ile Ser  
 115 120 125  
 Lys Asp Ser Leu Leu Lys  
 130 135

## (2) INFORMATION FOR SEQ ID NO:799:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799

Met	Lys	Lys	Arg	Leu	Asn	Ile	Gly	Leu	Val	Gly	Leu	Gly	Val	Gly	
1				5				10					15		
Ser	Thr	Val	Ala	Lys	Ile	Leu	Gln	Glu	Asn	Gln	Glu	Ile	Ile	Lys	Asp
				20			25					30			
Arg	Ala	Gly	Val	Glu	Ile	Lys	Ile	Lys	Lys	Ala	Val	Val	Arg	Asp	Val
				35			40				45				
Lys	Lys	His	Lys	Gly	Tyr	Ala	Phe	Glu	Ile	Ser	Asp	Asp	Leu	Glu	Ser
				50			55				60				
Val	Ile	Glu	Asp	Lys	Gly	Ile	Asp	Ile	Val	Val	Glu	Leu	Met	Gly	Gly
				65			70			75			80		
Val	Glu	Ala	Pro	Tyr	Leu	Leu	Ala	Lys	Lys	Thr	Leu	Ala	Lys	Gln	Lys
				85			90				95				
Ala	Phe	Val	Thr	Ala	Asn	Lys	Ala	Met	Leu	Ala	Tyr	His	Arg	Tyr	Glu
				100			105				110				
Leu	Glu	Gln	Ile	Ala	Lys	Asn	Thr	Pro	Ile	Gly	Phe	Glu	Ala	Ser	Val
				115			120				125				
Cys	Gly	Gly	Ile	Pro	Ile	Ile	Lys	Ala	Leu	Lys	Asp	Gly	Leu	Ser	Ala
				130			135				140				
Asn	His	Ile	Leu	Ser	Phe	Lys	Gly	Ile	Leu	Asn	Gly	Thr	Ser	Asn	Tyr
				145			150			155			160		
Ile	Leu	Ser	Gln	Met	Phe	Lys	Asn	Gln	Ala	Ser	Phe	Lys	Asp	Ala	Leu
				165			170				175				
Lys	Asp	Ala	Gln	His	Leu	Gly	Tyr	Ala	Glu	Leu	Asn	Pro	Glu	Phe	Asp
				180			185				190				
Ile	Lys	Gly	Ile	Asp	Ala	Ala	His	Lys	Leu	Ile	Leu	Ala	Ser	Leu	
				195			200				205				
Ala	Tyr	Gly	Ile	Asp	Ala	Lys	Leu	Glu	Ile	Leu	Ile	Glu	Gly	Ile	
				210			215				220				
Glu	Lys	Ile	Glu	Pro	Asp	Asp	Met	Glu	Phe	Ala	Lys	Glu	Phe	Gly	Tyr
				225			230			235			240		
Ser	Ile	Lys	Leu	Leu	Gly	Ile	Ala	Lys	Lys	His	Gln	Gly	Leu	His	
				245			250				255				

(2) INFORMATION FOR SEQ ID NO:800:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800

Met Gln Glu Lys Arg Leu Lys Ala Ile Gln Asn Lys Ile Ala Ser Trp  
 1 5 10 15  
 Ile Lys Glu Ile Glu Ser Gly Phe Ile Asp Ala Leu Phe Ser Lys Ile  
 20 25 30  
 Gly Pro Ser Lys Met Leu Arg Ser Lys Leu Met Leu Ala Leu Leu Asp  
 35 40 45  
 Glu Lys Thr Asp Ala Ile Leu Leu Asp Lys Ala Leu Asn Leu Cys Ala  
 50 55 60  
 Ile Val Glu Met Ile Gln Thr Ala Ser Leu Leu His Asp Asp Val Ile  
 65 70 75 80  
 Asp Lys Ala Thr Met Arg Arg Lys Leu Pro Ser Ile Asn Ala Leu Phe  
 85 90 95  
 Gly Asn Phe Asn Ala Val Met Leu Gly Asp Val Phe Tyr Ser Lys Ala  
 100 105 110  
 Phe Phe Glu Leu Ser Lys Met Gly Glu Ser Ile Ala Gln Ala Leu Ser  
 115 120 125  
 Asn Ala Val Leu Arg Leu Ser Arg Gly Glu Ile Glu Asp Val Phe Val  
 130 135 140  
 Gly Glu Cys Phe Asn Ser Asp Lys Gln Lys Tyr Trp Arg Ile Leu Glu  
 145 150 155 160  
 Asp Lys Thr Ala His Phe Ile Glu Ala Ser Leu Lys Ser Met Ala Ile  
 165 170 175  
 Leu Leu Asn Lys Asp Ala Lys Met Tyr Ala Asp Phe Gly Leu His Phe  
 180 185 190  
 Gly Met Ala Phe Gln Ile Ile Asp Asp Leu Leu Asp Ile Thr Gln Asp  
 195 200 205  
 Ala Asn Thr Leu Gly Lys Pro Asn Phe Ser Asp Phe Lys Glu Gly Lys  
 210 215 220  
 Thr Thr Leu Pro Tyr Leu Leu Tyr Glu Lys Leu Asn Gln His Glu  
 225 230 235 240  
 Gln Gly Phe

## (2) INFORMATION FOR SEQ ID NO:801:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 252 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801

Met Leu Gly Lys Lys Asn Glu Glu Val Leu Ile Asp Glu Asn Leu Val  
 1 5 10 15  
 Gly Gly Val Ile Ala Leu Asp Arg Leu Ala Lys Leu Asn Lys Ala Asn  
 20 25 30  
 Arg Thr Phe Lys Arg Ala Phe Tyr Leu Ser Met Val Leu Asn Val Ala  
 35 40 45  
 Ala Val Thr Ser Ile Val Met Met Pro Leu Lys Lys Thr Asp Ile  
 50 55 60  
 Phe Val Tyr Gly Ile Asp Arg Tyr Thr Gly Glu Phe Lys Ile Val Lys  
 65 70 75 80

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Arg	Ser	Asp	Ala	Arg	Gln	Ile	Val	Asn	Ser	Glu	Ala	Val	Val	Asp	Ser
				85				90						95	
Ala	Thr	Ser	Lys	Phe	Val	Ser	Leu	Leu	Phe	Gly	Tyr	Ser	Lys	Asn	Ser
				100				105					110		
Leu	Arg	Asp	Arg	Lys	Asp	Gln	Leu	Met	Gln	Tyr	Cys	Asp	Val	Ser	Phe
				115				120				125			
Gln	Thr	Gln	Ala	Met	Arg	Met	Phe	Asn	Glu	Asn	Ile	Arg	Gln	Phe	Val
				130				135			140				
Asp	Lys	Val	Arg	Ala	Glu	Ala	Ile	Ile	Ser	Ser	Asn	Ile	Gln	Arg	Glu
				145				150			155			160	
Lys	Val	Lys	Asn	Pro	Leu	Thr	Arg	Leu	Thr	Phe	Phe	Ile	Thr	Ile	
				165				170				175			
Lys	Ile	Thr	Pro	Asp	Thr	Met	Glu	Asn	Tyr	Glu	Tyr	Ile	Lys	Lys	
				180				185				190			
Gln	Val	Thr	Ile	Tyr	Tyr	Asp	Phe	Ala	Arg	Gly	Asn	Ser	Ser	Gln	Glu
				195				200				205			
Asn	Leu	Ile	Ile	Asn	Pro	Phe	Gly	Phe	Lys	Val	Phe	Asp	Ile	Gln	Ile
				210				215			220				
Thr	Asp	Leu	Gln	Asn	Gln	Thr	Val	Ser	Glu	Ile	Leu	Arg	Lys	Ile	
				225				230			235			240	
Lys	Glu	Val	Glu	Ser	Lys	Asn	Lys	Ala	Leu	Asn	Lys				
				245				250							

## (2) INFORMATION FOR SEQ ID NO:802:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 165 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802

Met	Arg	Ala	Ile	Ala	Ile	Val	Leu	Ala	Arg	Ser	Ser	Ser	Lys	Arg	Ile
1					5				10				15		
Lys	Asn	Lys	Asn	Met	Ile	Asp	Phe	Phe	Asn	Lys	Pro	Met	Leu	Ala	Tyr
					20				25			30			
Pro	Ile	Glu	Thr	Ala	Leu	Asn	Ser	Lys	Leu	Phe	Glu	Lys	Val	Phe	Ile
					35				40			45			
Ser	Ser	Asp	Ser	Met	Glu	Tyr	Val	Asn	Leu	Ala	Lys	Asn	Tyr	Gly	Ala
					50				55			60			
Ser	Phe	Leu	Asn	Leu	Arg	Pro	Lys	Asn	Leu	Ala	Asp	Asp	Arg	Ala	Thr
					65				70			75			80
Thr	Leu	Glu	Val	Met	Ala	Tyr	His	Met	Lys	Glu	Leu	Leu	Lys	Asp	
					85				90			95			
Glu	Asp	Ile	Ala	Cys	Cys	Leu	Tyr	Gly	Val	Ser	Val	Phe	Leu	Gln	Glu
					100				105			110			
Lys	His	Leu	Gln	Asn	Ala	Phe	Glu	Thr	Leu	Lys	Gln	Asn	Gln	Asn	Thr
					115				120			125			
Asp	Tyr	Val	Phe	Thr	Cys	Ser	Pro	Phe	Ser	Ala	Ser	Pro	Ile	Val	Leu
					130				135			140			
Leu	Ala	Leu	Lys	Thr	Ala	Phe	Lys	Trp	Leu	Leu	Lys	Ser	Ile	Gln	Thr
					145				150			155			160
Arg	Ala	Arg	Lys	Ile											

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## (2) INFORMATION FOR SEQ ID NO:803:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...171

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:803

Met	Ser	Asn	Gln	Ala	Ser	His	Leu	Asp	Asn	Phe	Met	Asn	Ala	Lys	Asn
1							5			10				15	
Pro	Lys	Ser	Phe	Phe	Asp	Asn	Lys	Gly	Asn	Thr	Lys	Phe	Ile	Ala	Ile
							20			25				30	
Thr	Ser	Gly	Lys	Gly	Gly	Val	Gly	Lys	Ser	Asn	Ile	Ser	Ala	Asn	Leu
						35			40				45		
Ala	Tyr	Ser	Leu	Tyr	Lys	Lys	Gly	Tyr	Lys	Val	Gly	Val	Phe	Asp	Ala
						50			55			60			
Asn	Ile	Gly	Leu	Ala	Asn	Leu	Asp	Val	Ile	Phe	Gly	Val	Lys	Thr	Gln
						65			70			75			80
Lys	Asn	Ile	Leu	His	Asp	Leu	Lys	Gly	Glu	Asp	Lys	Leu	Lys	Glu	Ile
						85			90			95			
Ile	Cys	Glu	Ile	Glu	Pro	Gly	Leu	Cys	Leu	Ile	Pro	Gly	Asp	Ser	Gly
						100			105			110			
Glu	Glu	Ile	Leu	Lys	Tyr	Ile	Ser	Glu	Ala	Glu	Asp	Phe	Asp	Ser	Phe
						115			120			125			
Leu	Asp	Glu	Glu	Gly	Val	Leu	Ser	Ala	Leu	Ile	Tyr	Ile	Leu	Ile	Asn
						130			135			140			
Thr	Phe	Ser	Lys	Asn	Leu	Gly	Pro	Leu	Ser	Gln	Thr	Phe	Leu	Asn	Phe
						145			150			155			160
Gln	Ser	Phe	Leu	Phe	Ile	Phe	Ile	Gln	Ser	Pro					
						165			170						

## (2) INFORMATION FOR SEQ ID NO:804:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...62

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:804

Met	Gln	His	Leu	Val	Leu	Ile	Gly	Phe	Met	Gly	Ser	Gly	Lys	Ser	Ser
1															15
Leu	Ala	Gln	Glu	Leu	Gly	Leu	Ala	Leu	Lys	Leu	Glu	Val	Leu	Asp	Thr
															30
Asp	Met	Ile	Ile	Ser	Glu	Arg	Val	Gly	Leu	Ser	Val	Arg	Gly	Ile	Phe
															45
Glu	Glu	Leu	Gly	Glu	Asp	Asn	Phe	Arg	Met	Phe	Glu	Lys	Ile		
50															60

## (2) INFORMATION FOR SEQ ID NO:805:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...199

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:805

Met	Ser	Ile	Lys	Glu	Asn	Leu	Glu	Gln	Val	Arg	Asn	Glu	Phe	Ser	
1															15
Asp	Glu	Lys	Leu	Leu	Glu	Gly	Ala	Phe	Arg	Leu	Glu	Lys	Phe	Phe	Lys
															30
Arg	Tyr	Lys	Trp	Val	Leu	Leu	Phe	Ile	Val	Val	Ala	Phe	Ile	Ala	Tyr
															45
Leu	Gly	Asp	Thr	Lys	Leu	Gln	Asp	Tyr	Lys	His	Glu	Gln	Thr	Arg	Glu
															50
Arg	Ile	Thr	Gln	Ile	Tyr	Asn	Glu	Val	Leu	Glu	Ser	Pro	Asn	Asn	Ile
															65
Ala	Leu	Gln	Lys	Arg	Leu	Lys	Glu	Val	Ala	Pro	Glu	Leu	Tyr	Asp	Leu
															85
Tyr	Gln	Phe	Ala	Arg	Ala	Ser	Glu	Arg	Asn	Asp	Ala	Asn	Glu	Phe	Lys
															100
Arg	Leu	Ser	Gln	Ser	Ser	Asn	Glu	Ile	Val	Lys	Ala	Phe	Ala	Lys	Tyr
															115
Ser	Tyr	Ala	Ser	Leu	Ser	Arg	Asp	Lys	Asn	Leu	Leu	Glu	Lys	Ser	Pro
															130
Ile	Leu	Lys	Glu	Met	Ser	Ala	Leu	Gln	Glu	Val	Asn	Leu	Tyr	Glu	
															145
Glu	Asn	Ser	Lys	Asp	Ala	Ile	Lys	Lys	Ala	His	Gln	Ser	Leu	Ser	Thr
															165
Ile	Pro	Leu	Ser	Ser	Ser	Leu	Tyr	Ala	Ile	Ile	Ser	Val	Leu	Lys	His
															180
Tyr	Gly	Met	Leu	Glu	Asp	Ile									195

## (2) INFORMATION FOR SEQ ID NO:806:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806

Met	Asp	Ala	Leu	Glu	Ile	Thr	Gln	Lys	Leu	Ile	Ser	Tyr	Pro	Thr	Ile
1					5				10					15	
Thr	Pro	Lys	Glu	Cys	Gly	Ile	Phe	Glu	Tyr	Ile	Lys	Ser	Leu	Phe	Pro
						20			25					30	
Ala	Phe	Lys	Thr	Leu	Glu	Cys	Glu	Lys	Asn	Gly	Val	Lys	Asn	Leu	Phe
						35			40				45		
Leu	Tyr	Arg	Ile	Phe	Asn	Pro	Leu	Lys	Lys	His	Ala	Glu	Lys	Glu	His
						50			55			60			
Ala	Lys	Glu	Lys	His	Val	Lys	Glu	Asn	Val	Unk	Pro	Leu	His	Phe	Cys
						65			70			75		80	
Unk	Ala	Gly	His	Ile	Unk	Val	Val	Pro	Pro	Gly	Unk	Unk	Unk	Unk	Unk
						85			90			95			
Asp	Ser	Phe	Unk	Unk	Ile	Ile	Lys	Glu	Gly	Phe	Leu	Tyr	Gly	Arg	Gly
						100			105			110			
Ala	Gln	Asp	Met	Lys	Gly	Gly	Val	Gly	Unk	Phe	Unk	Arg	Cys	Unk	Unk
						115			120			125			
Lys	Phe														
															130

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806

Met	Asp	Ala	Leu	Glu	Ile	Thr	Gln	Lys	Leu	Ile	Ser	Tyr	Pro	Thr	Ile
1					5				10				15		
Thr	Pro	Lys	Glu	Cys	Gly	Ile	Phe	Glu	Tyr	Ile	Lys	Ser	Leu	Phe	Pro
						20			25				30		
Ala	Phe	Lys	Thr	Leu	Glu	Cys	Glu	Lys	Asn	Gly	Val	Lys	Asn	Leu	Phe
						35			40			45			
Leu	Tyr	Arg	Ile	Phe	Asn	Pro	Leu	Lys	Lys	His	Ala	Glu	Lys	Glu	His
						50			55			60			
Ala	Lys	Glu	Lys	His	Val	Lys	Glu	Asn	Val	Unk	Pro	Leu	His	Phe	Cys
						65			70			75		80	

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Unk	Ala	Gly	His	Ile	Unk	Val	Val	Pro	Pro	Gly	Unk	Unk	Unk	Unk	
					85		90				95				
Asp	Ser	Phe	Unk	Unk	Ile	Ile	Lys	Glu	Gly	Phe	Leu	Tyr	Gly	Arg	Gly
					100		105				110				
Ala	Gln	Asp	Met	Lys	Gly	Gly	Val	Gly	Unk	Phe	Unk	Arg	Cys	Unk	Unk
					115		120				125				
Lys	Phe														
					130										

## (2) INFORMATION FOR SEQ ID NO:807:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...101

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:807

Val	His	Phe	Asn	Gln	Val	Val	Leu	Pro	Lys	Gly	Val	Gly	Ala	Ile	Leu
1					5			10					15		
Val	Ala	Pro	Lys	Gly	Pro	Gly	Ser	Ala	Leu	Arg	Glu	Glu	Tyr	Leu	Lys
					20			25			30				
Asn	Arg	Gly	Leu	Tyr	His	Leu	Ile	Ala	Ile	Glu	Gln	Glu	Ser	Ser	Ile
					35			40			45				
His	Asn	Ala	Lys	Ala	Val	Ala	Leu	Ser	Tyr	Ala	Lys	Ala	Met	Gly	Gly
					50			55			60				
Gly	Arg	Met	Gly	Val	Leu	Glu	Thr	Ser	Phe	Lys	Glu	Glu	Cys	Glu	Ser
					65			70			75			80	
Asp	Leu	Phe	Gly	Glu	Gln	Ala	Val	Leu	Cys	Gly	Gly	Leu	Glu	Val	Asp
					85			90			95				
Arg	Lys	Asn	Gly	Val											
				100											

## (2) INFORMATION FOR SEQ ID NO:808:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...80

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:808

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Met Lys Lys Phe Phe Ser Gln Ser Leu Leu Ala Leu Ile Ile Ser Met  
 1 5 10 15  
 Asn Ala Val Ser Gly Met Asp Gly Asn Gly Val Phe Leu Gly Ala Gly  
 20 25 30  
 Tyr Leu Gln Gly Gln Ala Gln Met His Ala Asp Ile Asn Ser Gln Lys  
 35 40 45  
 Gln Ala Thr Asn Ala Thr Ile Lys Gly Phe Asp Ala Leu Leu Gly Tyr  
 50 55 60  
 Gln Phe Phe Glu Lys His Phe Gly Leu Arg Leu Tyr Gly Val Phe  
 65 70 75 80

## (2) INFORMATION FOR SEQ ID NO:809:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...447

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:809

Met Leu Lys Lys Ile Phe Tyr Gly Phe Ile Val Leu Phe Leu Ile Ile  
 1 5 10 15  
 Val Gly Leu Leu Ala Val Leu Val Ala Gln Val Trp Val Thr Thr Asp  
 20 25 30  
 Lys Asp Ile Ala Lys Ile Lys Asp Tyr Arg Pro Ser Val Ala Ser Gln  
 35 40 45  
 Ile Leu Asp Arg Lys Gly Arg Leu Ile Ala Asn Ile Tyr Asp Lys Glu  
 50 55 60  
 Phe Arg Phe Tyr Ala Arg Phe Glu Glu Ile Pro Pro Arg Phe Val Glu  
 65 70 75 80  
 Ser Leu Leu Ala Val Glu Asp Thr Leu Phe Phe Glu His Gly Gly Ile  
 85 90 95  
 Asn Leu Asp Ala Val Met Arg Ala Met Ile Lys Asn Ala Lys Ser Gly  
 100 105 110  
 Arg Tyr Thr Glu Gly Gly Ser Thr Leu Thr Gln Gln Leu Val Lys Asn  
 115 120 125  
 Met Val Leu Thr Arg Glu Lys Thr Leu Thr Arg Lys Leu Lys Glu Ala  
 130 135 140  
 Ile Ile Ser Ile Arg Ile Glu Lys Val Leu Ser Lys Glu Glu Ile Leu  
 145 150 155 160  
 Glu Arg Tyr Leu Asn Gln Thr Phe Phe Gly His Gly Tyr Tyr Gly Val  
 165 170 175  
 Lys Thr Ala Ser Leu Gly Tyr Phe Lys Lys Pro Leu Asp Lys Leu Thr  
 180 185 190  
 Leu Lys Glu Ile Thr Met Leu Val Ala Leu Pro Arg Ala Pro Ser Phe  
 195 200 205  
 Tyr Asp Pro Thr Lys Asn Leu Glu Phe Ser Leu Ser Arg Ala Asn Asp  
 210 215 220  
 Ile Leu Arg Arg Leu Tyr Ser Leu Gly Unk Ile Ser Ser Asn Glu Leu  
 225 230 235 240  
 Lys Ser Ala Leu Asn Glu Val Pro Ile Val Tyr Asn Gln Thr Ser Thr  
 245 250 255

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Gln Asn Ile Ala Pro Tyr Val Val Asp Glu Val Leu Lys Gln Leu Asp  
 260 265 270  
 Gln Leu Asp Gly Leu Lys Thr Gln Gly Tyr Thr Ile Lys Leu Thr Ile  
 275 280 285  
 Asp Leu Asp Tyr Gln Arg Leu Ala Leu Glu Ser Leu Arg Phe Gly His  
 290 295 300  
 Gln Lys Ile Leu Glu Lys Ile Ala Lys Glu Lys Pro Lys Thr Asn Ala  
 305 310 315 320  
 Ser Asn Asp Lys Asp Asp Asn Leu Asn Ala Ser Met Ile Val Thr  
 325 330 335  
 Glu Thr Ser Thr Gly Lys Ile Leu Ala Leu Val Gly Gly Ile Asp Tyr  
 340 345 350  
 Lys Lys Ser Ala Phe Asn Arg Ala Thr Gln Ala Lys Arg Gln Phe Gly  
 355 360 365  
 Ser Ala Ile Lys Pro Phe Val Tyr Gln Ile Ala Phe Asp Asn Gly Tyr  
 370 375 380  
 Ser Thr Thr Ser Lys Ile Pro Asp Thr Ala Arg Asn Phe Glu Asn Gly  
 385 390 395 400  
 Asn Tyr Ser Lys Asn Ser Val Gln Asn His Ala Trp His Pro Ser Asn  
 405 410 415  
 Tyr Unk Arg Lys Phe Leu Gly Leu Val Thr Leu Gln Glu Ala Leu Ser  
 420 425 430  
 His Ser Leu Asn Leu Ala Thr Ile Asn Leu Ala Ile Ala Trp Leu  
 435 440 445

## (2) INFORMATION FOR SEQ ID NO:810:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...218

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:810

Met Asn Asp Thr Thr Glu His His Gly Ser Asn Pro Leu Asn Ala Pro  
 1 5 10 15  
 Pro Pro Ser Asn Ser Gln Ser Asn Asp Leu Leu Asn Leu Leu Asp Ser  
 20 25 30  
 Leu Tyr Pro Lys Gly Ser Leu Gly Glu Gln Arg Phe His Glu Ala Leu  
 35 40 45  
 Lys Asn Gln Glu Glu Leu Lys Asn Ile Leu Ile Glu Ile Glu Lys Leu  
 50 55 60  
 Pro Gln Glu Lys Arg Tyr Glu Leu Leu Met Gln Ile Gly Gln Ala Lys  
 65 70 75 80  
 Gln Arg Ile Met Glu Ala Tyr Ala His Ser Phe Leu Gly Tyr Ile Gly  
 85 90 95  
 Gly Leu Glu His Leu Leu Gly Leu Cys Met Gly Gly Ile Phe Val Leu  
 100 105 110  
 Phe Ala Ile Tyr Phe Val Phe Leu Arg Thr Ser Lys Asn Thr Glu Leu  
 115 120 125  
 Val Glu Ser Leu Lys Thr Lys Leu Lys Leu Gln Tyr Phe Tyr Tyr Ala  
 130 135 140  
 Phe Gly Val Gly Ala Val Leu Phe Phe Gly Leu Glu Thr Ile Arg Ser

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145	150	155	160												
Ile	Tyr	Glu	Leu	Tyr	Ile	Leu	Gly	Ile	Gly	Ser	Thr	Asn	Asp	Lys	Val
165								170						175	
Leu	Phe	Val	Leu	Lys	Asn	Ile	Cys	Phe	Ile	Gly	Met	Gly	Tyr	Leu	Ile
180								185					190		
Tyr	Lys	Val	Ile	Lys	Val	Ile	Gly	Ile	Lys	Asn	Phe	Ile	Asn	Gly	Leu
195								200					205		
Phe	Ala	Ser	Lys	Lys	Gln	Gly	Gly	Ala	Glu						
210						215									

## (2) INFORMATION FOR SEQ ID NO:811:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...192

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:811

Met	Met	Asp	Lys	Val	Gly	Phe	Lys	Ser	Gln	Gly	Ile	Phe	Val	Met	Asp	
1				5				10					15			
Ala	Ser	Lys	Arg	Asp	Gly	Arg	Leu	Asn	Ala	Tyr	Phe	Gly	Gly	Leu	Gly	
							20			25			30			
Lys	Asn	Lys	Arg	Val	Val	Val	Leu	Phe	Asp	Thr	Leu	Ile	Ser	Lys	Val	Gly
							35			40			45			
Thr	Glu	Unk	Leu	Leu	Ala	Ile	Leu	Gly	His	Glu	Leu	Gly	His	Phe	Lys	
							50			55			60			
Asn	Lys	Asp	Leu	Leu	Lys	Asn	Leu	Gly	Ile	Met	Gly	Gly	Leu	Leu	Ala	
							65			70			75		80	
Leu	Val	Phe	Ala	Leu	Ile	Ala	His	Leu	Pro	Pro	Leu	Val	Phe	Glu	Gly	
							85			90			95			
Phe	Asn	Val	Ser	Gln	Thr	Pro	Ala	Ser	Leu	Ile	Thr	Ile	Leu	Leu		
							100			105			110			
Phe	Leu	Pro	Val	Phe	Ser	Phe	Tyr	Ala	Met	Pro	Leu	Ile	Gly	Phe	Phe	
							115			120			125			
Ser	Arg	Lys	Asn	Glu	Tyr	Asn	Ala	Asp	Lys	Phe	Gly	Ala	Ser	Leu	Ser	
							130			135			140			
Ser	Lys	Glu	Thr	Leu	Ala	Lys	Ala	Leu	Val	Ser	Ile	Val	Asn	Glu	Asn	
							145			150			155		160	
Lys	Ala	Phe	Pro	Tyr	Ser	His	Pro	Phe	Tyr	Val	Phe	Leu	His	Phe	Thr	
							165			170			175			
His	Pro	Pro	Leu	Leu	Glu	Arg	Leu	Lys	Ala	Leu	Asp	Tyr	Glu	Ile	Glu	
							180			185			190			

## (2) INFORMATION FOR SEQ ID NO:812:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812

Met	Ile	Leu	Ser	Ile	Glu	Ser	Ser	Cys	Asp	Asp	Ser	Ser	Leu	Ala	Leu
1		5					10						15		
Thr	Arg	Ile	Glu	Asp	Ala	Lys	Leu	Ile	Ala	His	Phe	Lys	Ile	Ser	Gln
						20			25			30			
Glu	Lys	His	His	Ser	Ser	Tyr	Gly	Gly	Val	Val	Pro	Glu	Ile	Ala	Ser
						35			40			45			
Arg	Leu	His	Ala	Glu	Asn	Leu	Pro	Leu	Leu	Leu	Glu	Arg	Val	Lys	Ile
						50			55			60			
Ser	Leu	Asn	Lys	Asp	Phe	Ser	Lys	Ile	Lys	Ala	Ile	Ala	Ile	Thr	Asn
						65			70			75			80
Gln	Pro	Gly	Leu	Ser	Val	Thr	Leu	Ile	Glu	Gly	Leu	Met	Met	Ala	Lys
						85			90			95			
Ala	Leu	Ser	Leu	Ser	Leu	Asn	Leu	Pro	Leu	Ile	Leu	Glu	Asp	His	Leu
						100			105			110			
Arg	Gly	His	Val	Tyr	Ser	Leu	Phe	Ile	Asn	Glu	Lys	Gln	Thr	Arg	Met
						115			120			125			
Pro	Leu	Ser	Val	Leu	Leu	Val	Ser	Gly	Gly	His	Ser	Leu	Ile	Leu	Glu
						130			135			140			
Ala	Arg	Asp	Tyr	Glu	Asp	Ile	Lys	Ile	Val	Ala	Thr	Ser	Leu	Asp	Asp
						145			150			155			160
Ser	Phe	Gly	Glu	Ser	Phe	Asp	Lys	Val	Ser	Lys	Met	Leu	Asp	Leu	Gly
						165			170			175			
Tyr	Pro	Gly	Gly	Pro	Ile	Val	Glu	Lys	Leu	Ala	Leu	Asp	Tyr	Ala	His
						180			185			190			
Pro	Asn	Glu	Pro	Leu	Met	Phe	Pro	Ile	Pro	Leu	Lys	Asn	Ser	Pro	Asn
						195			200			205			
Leu	Ala	Phe	Ser	Phe	Ser	Gly	Leu	Lys	Asn	Ala	Val	Arg	Leu	Glu	Val
						210			215			220			
Glu	Lys	Asn	Ala	His	Asn	Leu	Asn	Asp	Glu	Val	Lys	Gln	Lys	Ile	Gly
						225			230			235			240
Tyr	His	Phe	Gln	Ser	Ala	Ala	Ile	Glu	His	Leu	Ile	Gln	Gln	Thr	Lys
						245			250			255			
Arg	Tyr	Phe	Lys	Ile	Lys	Arg	Pro	Lys	Ile	Phe	Gly	Ile	Val	Gly	Gly
						260			265			270			
Ala	Ser	Gln	Asn	Leu	Ala	Leu	Arg	Lys	Ala	Phe	Glu	Asp	Leu	Cys	Ala
						275			280			285			
Glu	Phe	Asp	Cys	Glu	Leu	Val	Leu	Ala	Pro	Leu	Glu	Phe	Cys	Ser	Asp
						290			295			300			
Asn	Ala	Ala	Met	Ile	Gly	Arg	Ser	Ser	Leu	Glu	Ala	Tyr	Gln	Lys	Lys
						305			310			315			320
Arg	Phe	Ile	Pro	Leu	Glu	Lys	Ala	Asp	Ile	Ser	Pro	Arg	Thr	Leu	Leu
						325			330			335			
Lys	Asn	Phe	Glu												
						340									

(2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear**SUBSTITUTE SHEET (RULE 26)**

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812

Met	Ile	Leu	Ser	Ile	Glu	Ser	Ser	Cys	Asp	Asp	Ser	Ser	Leu	Ala	Leu
1				5				10					15		
Thr	Arg	Ile	Glu	Asp	Ala	Lys	Leu	Ile	Ala	Mis	Phe	Lys	Ile	Ser	Gln
						20		25				30			
Glu	Lys	His	His	Ser	Ser	Tyr	Gly	Gly	Val	Val	Pro	Glu	Ile	Ala	Ser
				35			40				45				
Arg	Leu	His	Ala	Glu	Asn	Leu	Pro	Leu	Leu	Glu	Arg	Val	Lys	Ile	
	50				55			60							
Ser	Leu	Asn	Lys	Asp	Phe	Ser	Lys	Ile	Lys	Ala	Ile	Ala	Ile	Thr	Asn
65					70			75				80			
Gln	Pro	Gly	Leu	Ser	Val	Thr	Leu	Ile	Glu	Gly	Leu	Met	Met	Ala	Lys
				85			90				95				
Ala	Leu	Ser	Leu	Ser	Leu	Asn	Leu	Pro	Leu	Ile	Glu	Asp	His	Leu	
	100				105			110							
Arg	Gly	His	Val	Tyr	Ser	Leu	Phe	Ile	Asn	Glu	Lys	Gln	Thr	Arg	Met
	115				120			125							
Pro	Leu	Ser	Val	Leu	Leu	Val	Ser	Gly	Gly	Mis	Ser	Leu	Ile	Leu	Glu
	130				135			140							
Ala	Arg	Asp	Tyr	Glu	Asp	Ile	Lys	Ile	Val	Ala	Thr	Ser	Leu	Asp	Asp
145					150			155				160			
Ser	Phe	Gly	Glu	Ser	Phe	Asp	Lys	Val	Ser	Lys	Met	Leu	Asp	Leu	Gly
	165				170			175							
Tyr	Pro	Gly	Gly	Pro	Ile	Val	Glu	Lys	Leu	Ala	Leu	Asp	Tyr	Ala	His
	180				185			190							
Pro	Asn	Glu	Pro	Leu	Met	Phe	Pro	Ile	Pro	Leu	Lys	Asn	Ser	Pro	Asn
	195				200			205							
Leu	Ala	Phe	Ser	Phe	Ser	Gly	Leu	Lys	Asn	Ala	Val	Arg	Leu	Glu	Val
210					215			220							
Glu	Lys	Asn	Ala	His	Asn	Leu	Asn	Asp	Glu	Val	Lys	Gln	Lys	Ile	Gly
225					230			235				240			
Tyr	His	Phe	Gln	Ser	Ala	Ala	Ile	Glu	His	Leu	Ile	Gln	Gln	Thr	Lys
	245				250			255							
Arg	Tyr	Phe	Lys	Ile	Lys	Arg	Pro	Lys	Ile	Phe	Gly	Ile	Val	Gly	Gly
	260				265			270							
Ala	Ser	Gln	Asn	Leu	Ala	Leu	Arg	Lys	Ala	Phe	Glu	Asp	Leu	Cys	Ala
275					280			285							
Glu	Phe	Asp	Cys	Glu	Leu	Val	Leu	Ala	Pro	Leu	Glu	Phe	Cys	Ser	Asp
290					295			300							
Asn	Ala	Ala	Met	Ile	Gly	Arg	Ser	Ser	Leu	Glu	Ala	Tyr	Gln	Lys	Lys
305					310			315				320			
Arg	Phe	Ile	Pro	Leu	Glu	Lys	Ala	Asp	Ile	Ser	Pro	Arg	Thr	Leu	Leu
	325				330			335							
Lys	Asn	Phe	Glu												
	340														

(2) INFORMATION FOR SEQ ID NO:813:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear**SUBSTITUTE SHEET (RULE 26)**

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813

Met Asn Ile Tyr Gln Lys Asn Leu Gln Ala Leu Phe Lys Asp Pro  
 1 5 10 15  
 Leu Leu Phe Ala Lys Leu Lys Ala Ile Lys Glu Asn Lys Lys Tyr Glu  
 20 25 30  
 Val Phe Leu Gly Asn Asp Ser Ala Asn Phe Asn Leu Leu Asp Lys Glu  
 35 40 45  
 Thr Asn Thr Pro Leu Phe Glu Lys Ser Pro Leu Asp Ser Ser Leu Glu  
 50 55 60  
 Leu Tyr Lys Asn Ser Glu Ile His Met Leu Tyr Pro Tyr Leu Tyr Tyr  
 65 70 75 80  
 Phe Gly Leu Gly Asn Gly Val Phe Tyr Arg Leu Leu Leu Gly Asn Glu  
 85 90 95  
 Asn Leu Lys Arg Leu Val Val Ile Glu Pro Glu Ile Glu Val Ile Phe  
 100 105 110  
 Ile Val Leu Asn Leu Leu Asp Phe Ser Thr Glu Ile Leu Glu Asn Arg  
 115 120 125  
 Leu Ile Leu Leu His Ala Ser Phe Cys Asn Tyr Asn Met Ile Ala Ser  
 130 135 140  
 Leu Phe Asp Met Asp Lys Lys Ser Arg Leu Tyr Ala Arg Met Tyr Asp  
 145 150 155 160  
 Leu Lys Leu Phe Asn Ala Tyr Tyr Glu Arg Tyr Ser His Gln Met Ile  
 165 170 175  
 Glu Ile Asn Gln His Phe Thr Arg Ala Leu Glu His Gly Ala Ile Ser  
 180 185 190  
 Val Gly Asn Asp Ala Lys Ala His Ser  
 195 200

(2) INFORMATION FOR SEQ ID NO:814:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814

Met Lys Lys Ile Ile Leu Ala Cys Leu Val Ala Phe Val Gly Ala Asn  
 1 5 10 15  
 Leu Ser Ala Glu Pro Lys Trp Tyr Ser Lys Ala Tyr Asn Lys Thr Asn

677

20	25	30
Ala Gln Lys Gly Tyr Leu Tyr Gly Ser Gly Ser Ala Thr Ser Lys Glu		
35	40	45
Ala Ser Lys Gln Lys Ala Leu Ala Asp Leu Val Ala Ser Ile Ser Val		
50	55	60
Val Val Asn Ser Gln Ile His Ile Gln Lys Ser Arg Val Asp Asn Lys		
65	70	75
Leu Lys Ser Ser Asp Ser Gln Thr Ile Asn Leu Lys Thr Asp Asp Leu		
85	90	95
Glu Leu Asn Asn Val Glu Ile Val Asn Gln Glu Ala Gln Lys Gly Ile		
100	105	110
Tyr Tyr Thr Arg Val Arg Asn Gln Ser Lys Leu Val Phe Ala Gly Phe		
115	120	125
Lys Gly		
130		

## (2) INFORMATION FOR SEQ ID NO:815:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...144

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:815

Met Lys Ile Gln Thr Ile Ser Thr Leu Val Leu Thr Ile Ile Met Val		
1	5	10
Ile Gln Lys Met Ile Val Gly Lys Ile Ser Pro His Lys Thr Ala Glu		
20	25	30
Glu Phe Thr Asn Leu Met Leu Asn Met Ile Ala Val Leu Asp Ser Gln		
35	40	45
Ser Trp Gly Asp Ala Ile Leu Asn Ala Pro Phe Glu Phe Thr Asn Ser		
50	55	60
Pro Thr Asp Cys Asp Asn Asp Pro Ser Lys Cys Val Asn Pro Gly Thr		
65	70	75
Asn Gly Leu Val Asn Ser Lys Val Asp Gln Lys Tyr Val Leu Asn Lys		
85	90	95
Gln Asp Ile Val Asn Lys Phe Lys Asn Lys Ala Asp Leu Asp Val Ile		
100	105	110
Val Leu Lys Asp Ser Gly Val Val Gly Unk Unk Asn Gly Tyr Gly Asn		
115	120	125
Asp Gly Glu Tyr Gly Thr Leu Gly Val Unk Ala Tyr Ala Leu Gly Ser		
130	135	140

## (2) INFORMATION FOR SEQ ID NO:816:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

**(ix) FEATURE:**

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817

```

Met Lys Asn Phe Ser Pro Leu Tyr Cys Leu Lys Unk Leu Lys Lys Arg
1      5          10          15
His Leu Ile Ala Leu Ser Leu Pro Leu Leu Ser Tyr Ala Asn Gly Phe
20     25          30
Lys Ile Gln Glu Gln Ser Leu Asn Gly Thr Ala Leu Gly Ser Ala Tyr
35     40          45
Val Ala Gly Ala Arg Gly Ala Asp Ala Ser Phe Tyr Asn Pro Ala Asn
50     55          60
Met Gly Phe Thr Asn Asp Trp Gly Glu Asn Arg Ser Glu Phe Glu Met
65     70          75          80
Thr Thr Thr Val Ile Asn Ile Pro Thr Phe Ser Phe Lys Val Pro Thr
85     90          95
Thr Asn Gln Unk Leu Tyr Ser Val Thr Ser Leu Glu Ile Asp Lys Ser
100    105         110
Gln Gln Asn Ile Leu Gly Ile Ile Asn Thr Ile Gly Leu Gly Asn Ile
115    120         125
Leu Lys Ala Leu Gly Asn Thr Ala Ala Thr Asn Gly Leu Ser Gln Ala
130    135         140
Ile Asn Arg Val Gln Gly Leu Met Asn Leu Thr Asn Gln Lys Val Val
145    150         155         160
Thr Leu Ala Ser

```

(2) INFORMATION FOR SEQ ID NO:818:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818

```

Met Cys Leu Ala Ile Pro Ser Lys Val Ile Ala Ile Asn Asp Asn Val
1      5          10          15
Ala Leu Leu Glu Thr Leu Gly Val Gln Arg Glu Ala Ser Leu Asp Leu
20     25          30
Met Gly Glu Ser Val Lys Val Gly Asp Tyr Val Leu Leu His Ile Gly
35     40          45
Tyr Val Met Ser Lys Asp
50

```

(2) INFORMATION FOR SEQ ID NO:819:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 202 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819

Met	Lys	Tyr	Leu	Trp	Leu	Phe	Leu	Ile	Tyr	Ala	Ile	Gly	Leu	Phe	Ala
1									5					10	
															15
Thr	Asp	Lys	Thr	Leu	Asp	Ile	Ile	Lys	Thr	Ile	Gln	Lys	Leu	Pro	Lys
									20					25	
															30
Ile	Glu	Val	Arg	Tyr	Ser	Ile	Asp	Asn	Asp	Ala	Asn	Tyr	Ala	Leu	Lys
															35
															40
Leu	His	Glu	Val	Leu	Ala	Asn	Asp	Leu	Lys	Thr	Ser	Gln	His	Phe	Asp
															50
															55
Val	Ser	Gln	Asn	Lys	Glu	Gln	Gly	Ala	Ile	Asn	Tyr	Ala	Glu	Leu	Lys
									65					70	
															75
Asp	Lys	Lys	Val	His	Leu	Val	Ala	Leu	Val	Ser	Val	Ala	Val	Glu	Asn
															85
															90
Gly	Asn	Lys	Ile	Ser	Arg	Leu	Lys	Leu	Tyr	Asp	Val	Asp	Thr	Gly	Thr
									100					105	
															110
Leu	Lys	Lys	Thr	Phe	Asp	Tyr	Pro	Ile	Val	Ser	Leu	Asp	Leu	Tyr	Pro
								115						120	
															125
Phe	Ala	Ala	His	Asn	Met	Ala	Ile	Val	Val	Asn	Asp	Tyr	Leu	Lys	Ala
								130						135	
															140
Pro	Ser	Ile	Ala	Trp	Met	Lys	Arg	Leu	Ile	Val	Phe	Ser	Lys	Tyr	Ile
								145						150	
															155
Gly	Pro	Gly	Ile	Thr	Asn	Ile	Ala	Leu	Ala	Asn	Tyr	Thr	Met	Arg	Tyr
								165						170	
															175
Gln	Lys	Glu	Ile	Ile	Lys	Asn	Asn	Arg	Leu	Asn	Ile	Phe	Pro	Lys	Trp
								180						185	
															190
Ala	Asn	Ala	Glu	Gln	Thr	Glu	Phe	Tyr	Tyr						
								195						200	

(2) INFORMATION FOR SEQ ID NO:820:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 168 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820

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Met Leu Ser Ser Asn Asp Leu Phe Met Val Val Leu Gly Ala Ile Leu  
 1 5 10 15  
 Leu Val Leu Val Cys Leu Val Gly Tyr Leu Tyr Leu Lys Glu Lys Glu  
 20 25 30  
 Phe Tyr His Lys Met Arg Arg Leu Glu Lys Thr Leu Asp Glu Ser Tyr  
 35 40 45  
 Gln Glu Asn Tyr Leu Tyr Ser Lys Arg Leu Arg Glu Leu Glu Gly Arg  
 50 55 60  
 Leu Glu Gly Leu Ser Leu Glu Lys Ser Ala Lys Glu Asp Ser Ser Leu  
 65 70 75 80  
 Lys Thr Thr Leu Ser His Leu Tyr Asn Gln Leu Gln Glu Ile Gln Lys  
 85 90 95  
 Ser Met Asp Lys Glu Arg Asp Tyr Leu Glu Glu Lys Ile Ile Unk Unk  
 100 105 110  
 Lys Thr Unk Lys Thr Trp Gly Ile Met Pro Leu Ala Met Lys Ser  
 115 120 125  
 Thr Glu Lys Gln Val Leu Lys Met Tyr Gln Glu Gly Tyr Ser Val Asp  
 130 135 140  
 Ser Ile Ser Lys Glu Phe Lys Val Ser Lys Gly Glu Val Glu Phe Ile  
 145 150 155 160  
 Leu Asn Met Ala Gly Leu Lys Trp  
 165

## (2) INFORMATION FOR SEQ ID NO:820:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...168

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:820

Met Leu Ser Ser Asn Asp Leu Phe Met Val Val Leu Gly Ala Ile Leu  
 1 5 10 15  
 Leu Val Leu Val Cys Leu Val Gly Tyr Leu Tyr Leu Lys Glu Lys Glu  
 20 25 30  
 Phe Tyr His Lys Met Arg Arg Leu Glu Lys Thr Leu Asp Glu Ser Tyr  
 35 40 45  
 Gln Glu Asn Tyr Leu Tyr Ser Lys Arg Leu Arg Glu Leu Glu Gly Arg  
 50 55 60  
 Leu Glu Gly Leu Ser Leu Glu Lys Ser Ala Lys Glu Asp Ser Ser Leu  
 65 70 75 80  
 Lys Thr Thr Leu Ser His Leu Tyr Asn Gln Leu Gln Glu Ile Gln Lys  
 85 90 95  
 Ser Met Asp Lys Glu Arg Asp Tyr Leu Glu Glu Lys Ile Ile Unk Unk  
 100 105 110  
 Lys Thr Unk Lys Thr Trp Gly Ile Met Pro Leu Ala Met Lys Ser  
 115 120 125  
 Thr Glu Lys Gln Val Leu Lys Met Tyr Gln Glu Gly Tyr Ser Val Asp  
 130 135 140  
 Ser Ile Ser Lys Glu Phe Lys Val Ser Lys Gly Glu Val Glu Phe Ile  
 145 150 155 160

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Leu Asn Met Ala Gly Leu Lys Trp  
165

## (2) INFORMATION FOR SEQ ID NO:821:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...186

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:821

Val	Val	Ser	Gly	Val	Val	Ile	Ile	Ile	Val	Phe	Phe	Val	Pro	Ile	Leu
1						5			10					15	
Thr	Leu	Gln	Gly	Leu	Glu	Gly	Lys	Met	Phe	Arg	Pro	Leu	Ala	Gln	Ser
						20			25					30	
Ile	Val	Tyr	Ala	Leu	Leu	Gly	Thr	Leu	Val	Leu	Ser	Ile	Thr	Ile	Ile
						35			40					45	
Pro	Val	Val	Ser	Ser	Leu	Val	Leu	Lys	Ala	Thr	Pro	His	Ser	Glu	Thr
						50			55					60	
Phe	Leu	Thr	Arg	Phe	Leu	Asn	Arg	Ile	Tyr	Ala	Pro	Leu	Leu	Glu	Phe
						65			70					75	
Phe	Val	His	Asn	Pro	Lys	Lys	Val	Ile	Leu	Gly	Ala	Phe	Val	Phe	Leu
						85			90					95	
Ile	Ala	Ser	Leu	Ser	Leu	Phe	Pro	Phe	Val	Gly	Lys	Asn	Phe	Met	Pro
						100			105					110	
Ala	Leu	Asp	Glu	Gly	Asp	Val	Val	Leu	Ser	Val	Glu	Thr	Thr	Pro	Ser
						115			120					125	
Ile	Ser	Leu	Asp	Gln	Ser	Lys	Asp	Leu	Met	Leu	Asn	Ile	Glu	Ser	Ala
						130			135					140	
Ile	Lys	Lys	His	Val	Lys	Glu	Val	Lys	Ser	Ile	Val	Ala	Arg	Thr	Gly
						145			150					155	
Ser	Asp	Glu	Leu	Gly	Leu	Asp	Leu	Gly	Gly	Leu	Asn	Gln	Thr	Asp	Thr
						165			170					175	
Phe	Ile	Ser	Phe	Ile	Pro	Lys	Lys	Glu	Trp						
						180			185						

## (2) INFORMATION FOR SEQ ID NO:822:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

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(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822

Val Gly Tyr Ile Pro Unk Glu Lys Ile Val Gly Ile Ser Ala Ile Ala  
 1 5 10 15  
 Lys Leu Ile Glu Ile Tyr Ser Lys Arg Leu Gln Ile Gln Glu Arg Leu  
 20 25 30  
 Thr Thr Gln Ile Ala Glu Thr Phe Asp Glu Ile Ile Glu Pro Arg Gly  
 35 40 45  
 Val Ile Val Val Cys Glu Ala Lys Pro Leu Val His Glu His Ala Arg  
 50 55 60  
 Gly Ala Lys Ala Lys Cys Asp His  
 65 70

(2) INFORMATION FOR SEQ ID NO:823:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 121 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823

Leu Asp Pro Phe Ser His Lys Glu Asn Phe Leu Ala Val Glu Thr Phe  
 1 5 10 15  
 Lys Met Leu Gly Lys Thr Glu Ser Lys Asp Asn Leu Asn Trp Met Ile  
 20 25 30  
 Ala Leu Ile Ile Glu Lys Asp Lys Val Tyr Glu Gln Val Gly Ser Val  
 35 40 45  
 Arg Phe Val Val Val Ala Ser Ala Ile Met Val Leu Ala Leu Ile  
 50 55 60  
 Ile Ala Ile Thr Leu Leu Met Arg Ala Ile Val Ser Asn Arg Leu Glu  
 65 70 75 80  
 Val Val Ser Ser Thr Leu Ser His Phe Phe Lys Leu Leu Asn Asn Gln  
 85 90 95  
 Unk His Ser Ser Unk Unk Lys Leu Val Unk Ala Arg Ser Asn Asp Glu  
 100 105 110  
 Leu Gly Arg Unk Gln Thr Unk Asp Unk  
 115 120

(2) INFORMATION FOR SEQ ID NO:823:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 121 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823

Leu Asp Pro Phe Ser His Lys Glu Asn Phe Leu Ala Val Glu Thr Phe  
1 5 10 15  
Lys Met Leu Gly Lys Thr Glu Ser Lys Asp Asn Leu Asn Trp Met Ile  
20 25 30  
Ala Leu Ile Ile Glu Lys Asp Lys Val Tyr Glu Gln Val Gly Ser Val  
35 40 45  
Arg Phe Val Val Val Ala Ser Ala Ile Met Val Leu Ala Leu Ile  
50 55 60  
Ile Ala Ile Thr Leu Leu Met Arg Ala Ile Val Ser Asn Arg Leu Glu  
65 70 75 80  
Val Val Ser Ser Thr Leu Ser His Phe Phe Lys Leu Leu Asn Asn Gln  
85 90 95  
Unk His Ser Ser Unk Unk Lys Leu Val Unk Ala Arg Ser Asn Asp Glu  
100 105 110  
Leu Gly Arg Unk Gln Thr Unk Asp Unk  
115 120

(2) INFORMATION FOR SEQ ID NO:824:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824

Val Ala Leu Val Phe Asp Ser Leu Ile Glu Asn Lys Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 99 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Helicobacter pylori

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## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...99

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:825

Met	Lys	Lys	Ile	Gly	Leu	Ser	Leu	Cys	Leu	Val	Leu	Ser	Leu	Gly	Phe
1					5					10					15
Leu	Lys	Ala	His	Glu	Val	Ser	Ala	Glu	Glu	Ile	Ala	Asp	Ile	Phe	Tyr
					20				25					30	
Lys	Leu	Asn	Ala	Lys	Glu	Pro	Lys	Met	Lys	Ile	Asn	His	Thr	Lys	Gly
					35				40				45		
Phe	Cys	Ala	Lys	Gly	Val	Phe	Leu	Pro	Asn	Pro	Gln	Ala	Arg	Glu	Asp
					50				55			60			
Leu	Glu	Val	Pro	Leu	Leu	Asn	Glu	Lys	Glu	Ile	Pro	Ala	Ser	Val	Arg
					65				70		75		80		
Tyr	Ser	Leu	Gly	Gly	Val	Val	Asp	Trp	Thr	Ile	Lys	Ala	Arg	Leu	Gly
					85				90			95			
Glu	Trp	Arg													

## (2) INFORMATION FOR SEQ ID NO:826:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...71

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:826

Val	Ile	Lys	Pro	His	Ser	Val	Gly	Leu	Val	Arg	Ile	Gly	Ile	Cys	Leu
1						5				10				15	
Ser	Leu	Glu	Val	Gly	Tyr	Glu	Leu	Gln	Val	Arg	Thr	Arg	Ser	Gly	Leu
					20				25			30			
Ala	Leu	Asn	His	Gln	Val	Met	Val	Leu	Asn	Unk	Pro	Gly	Thr	Val	Asp
					35				40			45			
Asn	Asp	Tyr	Arg	Gly	Glu	Ile	Lys	Val	Ile	Leu	Ala	Asn	Leu	Ser	Asp
					50				55			60			
Lys	Asp	Phe	Lys	Val	Gln	Val									
					65				70						

## (2) INFORMATION FOR SEQ ID NO:827:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827

```

Met Glu Phe Tyr Gln Val Tyr Asp Pro Leu Gly His Ile Trp Leu Ser
1           5           10          15
Ala Leu Val Ala Leu Ser Pro Ile Ala Leu Phe Phe Ile Ser Leu Ile
20          25          30
Val Phe Lys Leu Lys Gly Tyr Ser Ala Gly Phe Leu Ser Leu Ala Leu
35          40          45
Ser Ile Leu Ile Ala Leu Phe Val Tyr Lys Met Pro Val Gln Met Val
50          55          60
Ser Ala Ser Phe Phe Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile Ala
65          70          75          80
Trp Ile Val Ile Ala Ala Ile Phe Leu Tyr Asn Leu Ser Val Lys Ser
85          90          95
Gly Tyr Phe Glu Ile Leu Lys Glu Ser Ile Leu Ser Leu Thr Pro Asp
100         105         110
His Arg Ile Leu Val Ile Leu Ile Gly Phe Cys Phe Gly Ser Phe Leu
115         120         125
Unk Gly Ala Unk Gly Phe Gly Pro Val Ala Ile Thr Ala Ala Ile
130         135         140
Leu Val Ala Leu Gly
145

```

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 149 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827

```

Met Glu Phe Tyr Gln Val Tyr Asp Pro Leu Gly His Ile Trp Leu Ser
1           5           10          15
Ala Leu Val Ala Leu Ser Pro Ile Ala Leu Phe Phe Ile Ser Leu Ile
20          25          30
Val Phe Lys Leu Lys Gly Tyr Ser Ala Gly Phe Leu Ser Leu Ala Leu
35          40          45
Ser Ile Leu Ile Ala Leu Phe Val Tyr Lys Met Pro Val Gln Met Val
50          55          60
Ser Ala Ser Phe Phe Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile Ala
65          70          75          80
Trp Ile Val Ile Ala Ala Ile Phe Leu Tyr Asn Leu Ser Val Lys Ser
85          90          95
Gly Tyr Phe Glu Ile Leu Lys Glu Ser Ile Leu Ser Leu Thr Pro Asp

```

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100	105	110
His Arg Ile Leu Val Ile Leu Ile	Gly Phe Cys Phe Gly Ser Phe Leu	
115	120	125
Unk Gly Ala Unk Gly Phe Gly Gly Pro Val Ala Ile Thr Ala Ala Ile		
130	135	140
Leu Val Ala Leu Gly		
145		

## (2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 255 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828

Met Glu Ile Ile Leu Leu Ile Val Ala Ala Val Val Leu Phe Tyr Phe			
1	5	10	15
Tyr Asn Thr Leu Lys Glu Tyr Leu Lys Asn Pro Leu Asn Pro Lys Thr			
20	25	30	
Lys Thr Glu Glu Tyr Asp Leu Lys Asn Asp Pro Tyr Leu Leu Val Gln			
35	40	45	
Ser Ser Pro Leu Asp Lys Phe Lys Gln Thr Gln Ile Gly Ala Tyr Met			
50	55	60	
Arg Leu Leu Lys Phe Leu Asp Ile Gln Lys Asn Ala Leu Asp Asn Ala			
65	70	75	80
Leu Arg Thr Leu Phe Ile His Glu Leu Glu Gln Pro Leu Asn Ser Glu			
85	90	95	
Gln Gln Asn Leu Ala Lys Glu Leu Leu Asn Glu Pro Val Asp Lys Lys			
100	105	110	
Glu Asn Phe Glu Ser Leu Cys Gln Glu Ile Ala Asp His Thr His Gly			
115	120	125	
Glu Tyr Thr Lys Arg Leu Lys Leu Val Glu Phe Leu Met Leu Leu Ala			
130	135	140	
Tyr Ala Asp Gly Ile Leu Asp Ser Lys Glu Lys Glu Leu Phe Leu Asp			
145	150	155	160
Val Gly Ala Phe Leu Gln Ile Asp Asn Gln Asp Phe Asn Glu Leu Tyr			
165	170	175	
Asp Asn Phe Glu His Phe Asn Ser Ile Glu Ile Pro Met Ser Leu Glu			
180	185	190	
Glu Ala Lys Asn Leu Phe Glu Ile Gln Thr His Thr Met Gln Asp			
195	200	205	
Leu Glu Lys Lys Ala Leu Asp Leu Ser Ala Pro Tyr Tyr His Lys Met			
210	215	220	
Asn Asp Asn Lys Arg Tyr Ser Glu Gln Asp Phe Ile Ser Leu Lys Lys			
225	230	235	240
Ile Ala Leu Ala Ser Gln Leu Leu Glu Asn Asp Leu Lys Asp Ser			
245	250	255	

## (2) INFORMATION FOR SEQ ID NO:829:

688

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 106 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...106
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:829

Met	Glu	Val	Glu	His	Gly	Lys	Ile	Glu	Thr	Thr	Leu	Ser	Leu	Gly	Ala
1	5							10						15	
Ser	His	Leu	Glu	Val	Ile	Lys	Met	Met	Leu	Leu	Glu	Ser	Leu	Pro	Ser
					20				25					30	
Leu	Val	Asn	Asn	Ile	Thr	Ile	Thr	Leu	Ile	Ser	Leu	Ile	Gly	Tyr	Ser
		35				40						45			
Ala	Lys	Ala	Gly	Ala	Leu	Gly	Ala	Gly	Gly	Leu	Gly	Asp	Leu	Ala	Ile
	50				55					60					
Arg	Ile	Gly	Tyr	Gln	Ser	Tyr	Arg	Gly	Asp	Val	Leu	Phe	Tyr	Ala	Val
	65			70			75					80			
Val	Val	Ile	Ile	Val	Leu	Val	Gln	Ile	Ile	Gln	Ser	Ala	Gly	Asp	Tyr
		85				90					95				
Val	Val	Lys	Arg	Leu	Arg	Lys	Asn	Lys	Tyr						
		100				105									

## (2) INFORMATION FOR SEQ ID NO:830:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 527 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...527
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:830

Met	Asn	Glu	Ile	Asp	Lys	Ser	Val	Asp	Ile	Gly	Phe	Leu	Arg	Ile	Leu
1	5							10					15		
Asp	Val	Ile	Lys	Lys	Val	Lys	Thr	Pro	Lys	Gly	Gly	Ile	Glu	Val	Leu
			20				25					30			
Arg	Thr	Leu	Ile	Asp	Phe	Thr	Pro	Lys	Ile	Glu	Asn	Ala	Leu	Asn	Leu
	35				40					45					
Ala	Thr	Lys	Ser	His	Lys	Gly	Gln	Tyr	Arg	Lys	Ser	Gly	Glu	Pro	Tyr
	50			55			60								
Ile	Val	His	Pro	Ile	Cys	Val	Ala	Ser	Val	Val	Ala	Phe	Cys	Gly	Gly
	65			70			75					80			
Asp	Glu	Ala	Met	Val	Cys	Ala	Leu	Leu	His	Asp	Val	Val	Glu	Asp	

**SUBSTITUTE SHEET (RULE 26)**

85	90	95
Thr Pro Cys Glu Ile Glu Thr Ile Glu Arg Glu Phe Gly Gln Asp Val		
100	105	110
Ala Asn Leu Val Asp Ala Leu Thr Lys Ile Thr Glu Ile Arg Lys Glu		
115	120	125
Glu Leu Gly Val Ser Ser Gln Asp Pro Arg Met Val Val Ser Ala Leu		
130	135	140
Thr Phe Arg Lys Ile Leu Ile Ser Ala Ile Gln Asp Pro Arg Ala Leu		
145	150	155
Val Val Lys Ile Ser Asp Arg Leu His Asn Met Leu Thr Leu Asp Ala		
165	170	175
Leu Pro His Asp Lys Gln Val Arg Ile Ser Lys Glu Thr Leu Ala Val		
180	185	190
Tyr Ala Pro Ile Ala Ser Arg Leu Gly Met Ser Ser Ile Lys Asn Glu		
195	200	205
Leu Glu Asp Lys Ser Phe Tyr Tyr Ile Tyr Pro Glu Glu Tyr Lys Asn		
210	215	220
Ile Lys Glu Tyr Leu His Lys Asn Lys Gln Ser Leu Leu Leu Lys Leu		
225	230	235
Asn Ala Phe Ala Ser Lys Leu Glu Lys Lys Leu Phe Asp Ser Gly Phe		
245	250	255
Ser His Ser Asp Phe Lys Leu Val Thr Arg Val Lys Arg Pro Tyr Ser		
260	265	270
Ile Tyr Leu Lys Met Gln Arg Lys Gly Ala Val Asn Ile Asp Glu Ile		
275	280	285
Leu Asp Leu Leu Ala Ile Arg Ile Leu Leu Lys Asn Pro Ile Asp Cys		
290	295	300
Tyr Lys Val Leu Gly Ile Ile His Leu Asn Phe Lys Pro Ile Val Ser		
305	310	315
Arg Phe Lys Asp Tyr Ile Ala Leu Pro Lys Glu Asn Gly Tyr Lys Thr		
325	330	335
Ile His Thr Thr Ile Phe Asp Glu Ser Ser Val Tyr Glu Val Gln Ile		
340	345	350
Arg Thr Phe Asp Met His Met Gly Ala Glu Tyr Gly Asn Ser Ala His		
355	360	365
Trp Lys Tyr Lys Ala Gly Gly Val Asp His Glu Glu His His Glu Gly		
370	375	380
Met Arg Trp Leu Gln Asn Phe Lys Tyr His Asp Ser Asp Leu Lys Asn		
385	390	395
Asp Pro Lys Glu Phe Tyr Glu Leu Ala Lys Asn Asp Leu Tyr Arg Glu		
405	410	415
Asp Ile Val Val Phe Ser Pro His Gly Asp Thr Tyr Thr Leu Pro Val		
420	425	430
Gly Ala Ile Ala Leu Asp Phe Ala Tyr Met Val His Ser Asp Leu Gly		
435	440	445
Asp Lys Ala Thr Asp Ala Tyr Ile Asn Ser Lys Lys Ala Leu Leu Asn		
450	455	460
Gln Glu Leu Arg Ser Gly Asp Val Val Lys Ile Ile Lys Gly Asp Lys		
465	470	475
Val Ile Pro Arg Phe Ile Trp Met Asp Gln Leu Lys Thr Ser Lys Ala		
485	490	495
Lys Asn His Leu Arg Ile Gln Arg Arg Asn Arg Leu Lys Glu Ile Asp		
500	505	510
Thr Lys Ser Met Ile Asn Ile Leu Ala Thr Phe Phe Trp Ala Leu		
515	520	525

## (2) INFORMATION FOR SEQ ID NO:831:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 124 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

690

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831

Val	Val	Val	Val	Glu	Asn	Ile	Lys	Asp	Ala	Val	Pro	Leu	Ala	Gln	Ser
1				5				10						15	
Leu	Ile	Unk	Gly	Gly	Ile	Pro	Ile	Ile	Glu	Val	Thr	Leu	Arg	Ser	Asn
					20				25					30	
Cys	Ala	Leu	Glu	Ala	Ile	Glu	Leu	Ile	Ala	Lys	Asn	Val	Pro	Lys	Met
					35				40					45	
Arg	Val	Gly	Ala	Gly	Thr	Ile	Leu	Asn	Leu	Thr	Gln	Leu	Glu	Gln	Ala
					50				55					60	
Gln	Asn	Arg	Gly	Ala	Glu	Phe	Leu	Ile	Ser	Pro	Gly	Leu	Thr	Ile	Lys
					65				70					80	
Leu	Leu	Glu	His	Ala	Lys	Lys	Asp	Met	Pro	Leu	Ile	Pro	Gly	Val	
					85				90					95	
Ser	Ser	Ser	Ser	Glu	Val	Met	Gln	Ala	Leu	Glu	Leu	Gly	Tyr	Asn	Ala
					100				105					110	
Leu	Lys	Phe	Phe	Pro	Ala	Glu	Tyr	Cys	Gly	Gly	Arg				
					115				120						

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832

Val	Glu	Lys	Ile	Lys	Pro	Tyr	Ala	Pro	Lys	Asp	Ser	Pro	Leu	Ile	Asp
1					5				10					15	
Tyr	Ser	Ser	Leu	Val	Arg	Asn	Val	Gln	Ser	Thr	Leu	Lys	Gly	Thr	Ser
					20				25					30	
Phe	Glu	Thr	Leu	Ile	Asn	Gly	Val	Trp	Glu	Ser	Phe	Glu	Thr	Lys	Val
					35				40					45	
Leu	Gly	Glu	Phe	Asn	Ala	Tyr	Asn	Ile	Ala	Ser	Ala	Ile	Leu	Thr	Ala
					50				55					60	
Lys	His	Leu	Gly	Leu	Glu	Thr	Glu	Arg	Ile	Lys	Arg	Leu	Val	Phe	Glu
					65				70					80	
Leu	Lys	Pro	Ile	Asn	His	Arg	Leu	Gln	Leu	Glu	Ala	Asn	Gln	Lys	
					85				90					95	
Ile	Ile	Ile	Asp	Asp	Asn	Phe	Asn	Leu	Lys	Gly	Met				
					100				105					110	

## (2) INFORMATION FOR SEQ ID NO:833:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833

Met Lys Arg Ile Leu Val Ser Leu Ala Val Leu Ser His Ser Ala His  
 1 5 10 15  
 Ala Val Lys Thr His Asn Leu Glu Arg Val Glu Ala Ser Gly Val Ala  
 20 25 30  
 Asn Asp Lys Glu Ala Pro Leu Ser Trp Arg Ser Lys Glu Val Arg Asn  
 35 40 45  
 Tyr Met Gly Ser Arg Thr Val Ile Ser Asn Lys Gln Leu Thr Lys Ser  
 50 55 60  
 Ala Asn Gln Ser Ile Glu Glu Ala Leu Gln Asn Val Pro Gly Val His  
 65 70 75 80  
 Ile Arg Asn Ser Thr Gly Ile Gly Ala Val Pro Ser Ile Ser Ile Arg  
 85 90 95  
 Gly Phe Gly Ala Gly Gly Pro Gly His Ser Asn Thr Gly Met Ile Leu  
 100 105 110  
 Val Asn Gly Ile Pro Ile Tyr Val Ala Pro Tyr Val Glu Ile Gly Thr  
 115 120 125  
 Val Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile Ser Val Thr  
 130 135 140  
 Lys Gly Gly Glu Ser Val Arg Tyr Gly Pro Asn Ala Phe Gly Gly Val  
 145 150 155 160  
 Ile Asn Ile Ile Thr Lys Gly Ile Pro Thr Asn Trp Glu Ser Gln Val  
 165 170 175  
 Ser Glu Arg Thr Thr Phe Trp Gly Lys Ser Glu Asn Gly Gly Phe Phe  
 180 185 190  
 Asn Gln Asn Ser Lys Asn Ile Asp Lys Ser Leu Val Asn Asn Met Leu  
 195 200 205  
 Phe Asn Thr Tyr Leu Arg Thr Gly Gly Met Met Asn Lys His Phe Gly  
 210 215 220  
 Ile Gln Ala Gln Val Asn Trp Leu Lys Gly Gln Gly Phe Arg Tyr Asn  
 225 230 235 240  
 Ser Pro Thr Asp Ile Gln Asn Tyr Met Leu Asp Ser Leu Tyr Gln Ile  
 245 250 255  
 Asn Asp Ser Asn Lys Ile Thr Ala Phe Phe Gln Tyr Ser Tyr Phe  
 260 265 270  
 Leu Thr Asp Pro Gly Ser Leu Gly Ile Ala Ala Tyr Asn Gln Asn Arg  
 275 280 285  
 Phe Gln Asn Asn Arg Pro Asn Asn Asp Lys Ser Gly Arg Ala Lys Arg  
 290 295 300  
 Trp Gly Ala Val Tyr Gln Asn Phe Phe Gly Asp Thr Asp Arg Val Gly  
 305 310 315 320  
 Gly Gly Phe His Phe  
 325

692

## (2) INFORMATION FOR SEQ ID NO:833:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...325

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:833

Met Lys Arg Ile Leu Val Ser Leu Ala Val Leu Ser His Ser Ala His  
 1 5 10 15  
 Ala Val Lys Thr His Asn Leu Glu Arg Val Glu Ala Ser Gly Val Ala  
 20 25 30  
 Asn Asp Lys Glu Ala Pro Leu Ser Trp Arg Ser Lys Glu Val Arg Asn  
 35 40 45  
 Tyr Met Gly Ser Arg Thr Val Ile Ser Asn Lys Gln Leu Thr Lys Ser  
 50 55 60  
 Ala Asn Gln Ser Ile Glu Glu Ala Leu Gln Asn Val Pro Gly Val His  
 65 70 75 80  
 Ile Arg Asn Ser Thr Gly Ile Gly Ala Val Pro Ser Ile Ser Ile Arg  
 85 90 95  
 Gly Phe Gly Ala Gly Gly Pro Gly His Ser Asn Thr Gly Met Ile Leu  
 100 105 110  
 Val Asn Gly Ile Pro Ile Tyr Val Ala Pro Tyr Val Glu Ile Gly Thr  
 115 120 125  
 Val Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile Ser Val Thr  
 130 135 140  
 Lys Gly Gly Glu Ser Val Arg Tyr Gly Pro Asn Ala Phe Gly Gly Val  
 145 150 155 160  
 Ile Asn Ile Ile Thr Lys Gly Ile Pro Thr Asn Trp Glu Ser Gln Val  
 165 170 175  
 Ser Glu Arg Thr Thr Phe Trp Gly Lys Ser Glu Asn Gly Gly Phe Phe  
 180 185 190  
 Asn Gln Asn Ser Lys Asn Ile Asp Lys Ser Leu Val Asn Asn Met Leu  
 195 200 205  
 Phe Asn Thr Tyr Leu Arg Thr Gly Gly Met Met Asn Lys His Phe Gly  
 210 215 220  
 Ile Gln Ala Gln Val Asn Trp Leu Lys Gly Gln Gly Phe Arg Tyr Asn  
 225 230 235 240  
 Ser Pro Thr Asp Ile Gln Asn Tyr Met Leu Asp Ser Leu Tyr Gln Ile  
 245 250 255  
 Asn Asp Ser Asn Lys Ile Thr Ala Phe Phe Gln Tyr Tyr Ser Tyr Phe  
 260 265 270  
 Leu Thr Asp Pro Gly Ser Leu Gly Ile Ala Ala Tyr Asn Gln Asn Arg  
 275 280 285  
 Phe Gln Asn Asn Arg Pro Asn Asn Asp Lys Ser Gly Arg Ala Lys Arg  
 290 295 300  
 Trp Gly Ala Val Tyr Gln Asn Phe Phe Gly Asp Thr Asp Arg Val Gly  
 305 310 315 320  
 Gly Gly Phe His Phe  
 325

## (2) INFORMATION FOR SEQ ID NO:834:

**SUBSTITUTE SHEET (RULE 26)**

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 252 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834

Leu	Arg	Ser	Ile	Ser	Arg	Ile	Lys	Met	Leu	Ser	Val	Tyr	Glu	Lys	Gly
1	5						10						15		
Asn	Ala	Leu	Asp	Lys	Arg	Val	Leu	Glu	Glu	Trp	Leu	Leu	Ser	Glu	Asp
	20					25							30		
Ile	Leu	Met	Glu	Asn	Ala	Ala	Met	Ala	Leu	Glu	Arg	Ala	Val	Leu	Gln
	35					40					45				
Asn	Ala	Ser	Leu	Gly	Ala	Lys	Val	Ile	Ile	Leu	Cys	Gly	Ser	Gly	Asp
	50					55					60				
Asn	Gly	Gly	Asp	Gly	Tyr	Thr	Leu	Ala	Arg	Arg	Leu	Val	Gly	Arg	Phe
	65					70			75				80		
Lys	Thr	Leu	Val	Phe	Glu	Met	Lys	Leu	Ala	Lys	Ser	Pro	Met	Cys	Gln
	85						90					95			
Leu	Gln	Lys	Glu	Arg	Ala	Lys	Lys	Val	Gly	Val	Val	Ile	Lys	Ala	Trp
	100					105			110						
Glu	Glu	Lys	Asn	Glu	Asp	Leu	Glu	Cys	Asp	Val	Leu	Val	Asp	Cys	Val
	115					120			125						
Val	Gly	Ser	Ala	Phe	Lys	Gly	Gly	Leu	Glu	Pro	Phe	Leu	Asp	Phe	Glu
	130					135			140						
Ser	Leu	Ser	Gln	Lys	Ala	Arg	Phe	Lys	Ile	Ala	Cys	Asp	Ile	Pro	Ser
	145					150			155				160		
Gly	Ile	Asp	Ser	Lys	Gly	Arg	Val	Asp	Lys	Arg	Ala	Phe	Lys	Unk	Gly
	165					170			175						
Tyr	Arg	Leu	Ser	Ala	Trp	Ala	Leu	Phe	Lys	Ser	Cys	Leu	Leu	Ser	Unk
	180					185			190						
Lys	Unk	Lys	Unk	Tyr	Ile	Unk	Unk	Leu	Lys	Unk	Unk	His	Leu	Unk	Val
	195					200			205						
Phe	Asn	Gln	Ile	Tyr	Glu	Ile	Pro	Thr	Unk	Thr	Phe	Leu	Leu	Glu	Lys
	210					215			220						
Unk	Asp	Leu	Lys	Leu	Pro	Leu	Arg	Asp	Arg	Lys	Lys	Arg	Ser	Gln	Arg
	225					230			235				240		
Arg	Leu	Arg	Ala	Cys	Ala	Cys	Ala	Phe	Gly	Gln	Ala				
	245					250									

(2) INFORMATION FOR SEQ ID NO:834:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 252 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

694

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834

Leu	Arg	Ser	Ile	Ser	Arg	Ile	Lys	Met	Leu	Ser	Val	Tyr	Glu	Lys	Gly
1						5						10		15	
Asn	Ala	Leu	Asp	Lys	Arg	Val	Leu	Glu	Glu	Trp	Leu	Leu	Ser	Glu	Asp
						20						25		30	
Ile	Leu	Met	Glu	Asn	Ala	Ala	Met	Ala	Leu	Glu	Arg	Ala	Val	Leu	Gln
						35						40		45	
Asn	Ala	Ser	Leu	Gly	Ala	Lys	Val	Ile	Ile	Leu	Cys	Gly	Ser	Gly	Asp
						50						55		60	
Asn	Gly	Gly	Asp	Gly	Gly	Tyr	Thr	Leu	Ala	Arg	Arg	Leu	Val	Gly	Phe
						65						70		75	
Lys	Thr	Leu	Val	Phe	Glu	Met	Lys	Leu	Ala	Lys	Ser	Pro	Met	Cys	Gln
						85						85		90	
Leu	Gln	Lys	Glu	Arg	Ala	Lys	Lys	Val	Gly	Val	Val	Ile	Lys	Ala	Trp
						100						105		110	
Glu	Glu	Lys	Asn	Glu	Asp	Leu	Glu	Cys	Asp	Val	Leu	Val	Asp	Cys	Val
						115						120		125	
Val	Gly	Ser	Ala	Phe	Lys	Gly	Gly	Leu	Glu	Pro	Phe	Leu	Asp	Phe	Glu
						130						135		140	
Ser	Leu	Ser	Gln	Lys	Ala	Arg	Phe	Lys	Ile	Ala	Cys	Asp	Ile	Pro	Ser
						145						150		155	
Gly	Ile	Asp	Ser	Lys	Gly	Arg	Val	Asp	Lys	Arg	Ala	Phe	Lys	Unk	Gly
						165						170		175	
Tyr	Arg	Leu	Ser	Ala	Trp	Ala	Leu	Phe	Lys	Ser	Cys	Leu	Leu	Ser	Unk
						180						185		190	
Lys	Unk	Lys	Unk	Tyr	Ile	Unk	Unk	Leu	Lys	Unk	Unk	His	Leu	Unk	Val
						195						200		205	
Phe	Asn	Gln	Ile	Tyr	Glu	Ile	Pro	Thr	Unk	Thr	Phe	Leu	Leu	Glu	Lys
						210						215		220	
Unk	Asp	Leu	Lys	Leu	Pro	Leu	Arg	Asp	Arg	Lys	Lys	Arg	Ser	Gln	Arg
						225						230		235	
Arg	Leu	Arg	Ala	Cys	Ala	Cys	Ala	Phe	Gly	Gln	Ala				
						245						250			

(2) INFORMATION FOR SEQ ID NO:835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835

Met	Ser	Asn	Gln	Glu	Tyr	Thr	Phe	Gln	Thr	Glu	Ile	Asn	Gln	Leu	Leu
1						5						10		15	
Asp	Leu	Met	Ile	His	Ser	Leu	Tyr	Ser	Asn	Lys	Glu	Ile	Phe	Leu	Arg

**SUBSTITUTE SHEET (RULE 26)**

20	25	30	
Glu Leu Ile Ser Asn Ala Ser Asp Ala	Leu Asp Lys Leu Asn Tyr	Leu	
35	40	45	
Met Leu Thr Asp Glu Lys Leu Lys Gly	Leu Asn Thr Thr Pro	Ser Ile	
50	55	60	
His Leu Ser Phe Asp Ser Gln Lys Lys	Thr Leu Thr Ile Lys	Asp Asn	
65	70	75	80
Gly Ile Gly Met Asp Lys Ser Asp	Leu Ile Glu His	Leu Gly Thr Ile	
85	90	95	
Ala Lys Ser Gly Thr Lys Ser Phe	Leu Ser Ala Leu Ser	Gly Asp Lys	
100	105	110	
Lys Lys Asp Ser Ala Leu Ile Gly	Gln Phe Gly Val	Gly Phe Tyr Ser	
115	120	125	
Ala Phe Met Val Ala Ser Lys Ile Val Val	Gln Thr Lys	Lys Val Thr	
130	135	140	
Ser His Gln Ala Tyr Ala Trp Val	Ser Asp Gly Lys	Gly Lys Phe Glu	
145	150	155	160
Ile Ser Glu Cys Val Lys Glu Glu	Gln Gly Thr Glu Ile	Thr Leu Phe	
165	170	175	
Leu Lys Glu Glu Asp Ser His Phe	Ala Ser Arg Trp Glu	Ile Asp Ser	
180	185	190	
Val Val Lys Lys Tyr Ser Glu His	Ile Pro Phe Pro	Ile Phe Leu Thr	
195	200	205	
Tyr Thr Asp Thr Lys Phe Glu	Gly Glu Gly Asp	Asn Lys Lys Glu Val	
210	215	220	
Lys Glu Glu Lys Cys Asp Gln Ile Asn	Gln Ala Ser Ala	Leu Trp Lys	
225	230	235	240
Met Asn Lys Ser Glu Leu Lys Glu	Lys Asp Tyr Lys	Asp Phe Tyr Gln	
245	250	255	
Ser Phe Ala His Asp Asn Ser Glu	Pro Leu Ser Tyr Ile	His Asn Lys	
260	265	270	
Val Glu Gly Ser Leu Glu	Tyr Thr Leu Phe	Tyr Ile Pro Ser Lys	
275	280	285	
Ala Pro Phe Asp Leu Phe Arg Val	Asp Tyr Lys Ser	Gly Val Lys Leu	
290	295	300	
Tyr Val Lys Arg Val Phe Ile	Thr Asp Asp	Lys Glu Leu Leu Pro	
305	310	315	320
Ser Tyr Leu Arg Phe Val Lys	Gly Val Ile Asp Ser	Glu Asp Leu Pro	
325	330	335	
Leu Asn Val Ser Arg Glu Ile Leu	Gln Gln Asn Lys	Ile Leu Ala Asn	
340	345	350	
Ile Arg Ser Ala Ser Val Lys	Lys Ile Leu Ser	Glu Ile Glu Arg Leu	
355	360	365	
Ser Lys Asp Asn Lys Asn Tyr	His Lys Phe Tyr	Glu Pro Phe Gly Lys	
370	375	380	
Val Leu Lys Glu Gly	Leu Tyr Asp Phe	Glu Asn Lys Glu Lys Leu	
385	390	395	400
Leu Glu Leu Leu Arg Phe Tyr	Ser Lys Asp Gly	Glu Trp Ile Ser	
405	410	415	
Leu Lys Glu Tyr Lys Glu Asn	Leu Lys Glu Asn	Gln Lys Ser Ile Tyr	
420	425	430	
Tyr Leu Leu Gly Glu Asn	Leu Asp Leu	Leu Lys Ala Ser Pro Leu Leu	
435	440	445	
Glu Lys Tyr Ala Gln Lys	Gly Tyr Asp Val	Leu Leu Leu Ser Asp Glu	
450	455	460	
Ile Asp Ala Phe Val Met	Pro Gly Val Asn	Glu Tyr Asp Lys Thr Pro	
465	470	475	480
Phe Arg Asp Ala Ser His	Ser Glu Ser	Leu Lys Glu Leu Gly Leu Ala	
485	490	495	
Glu Ile His Asp Glu Val Lys	Asp Gln Phe Lys	Asp Leu Ile Lys Ala	
500	505	510	
Phe Glu Glu Asn Leu Lys Asp	Glu Ile Lys Gly	Val Glu Leu Ser Gly	
515	520	525	
His Leu Thr Ser Ala Val Ala	Leu Ile Glu Asp	Glu Pro Asn Ala Met	
530	535	540	

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Met Ala Asn Trp Met Arg Gln Met Gly Gln Ser Val Pro Glu Ser Lys			
545	550	555	560
Lys Thr Leu Glu Leu Asn Pro Asn His Ala Ile Leu Gln Lys Leu Leu			
565	570	575	
Lys Cys Glu Asp Lys Glu Gln Leu Ser Ala Phe Ile Trp Leu Leu Tyr			
580	585	590	
Asp Gly Arg Ser Phe			
595			

## (2) INFORMATION FOR SEQ ID NO:836:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836

Val Asn Leu Gly Ala Tyr Tyr Thr Pro Pro Tyr Leu Val Asp Cys Ala			
1	5	10	15
Tyr Lys Leu Leu Lys Lys His Val Gly Ile Glu Asn Tyr Thr Leu Leu			
20	25	30	
Asp Thr Ala Cys Gly Asn Lys Glu Phe Leu Lys Leu His His Pro Lys			
35	40	45	
Lys Ile Gly Ala Asp Ile Asp Pro Lys Cys Asp Ala Leu Ile Ile Asn			
50	55	60	
Ala Leu Ala Asn Pro Lys Arg Glu Asn Tyr Gly Ile Ser Gln Asp Glu			
65	70	75	80
Pro Leu Ile Ile Val Gly Asn Pro Pro Tyr Asn Asp Arg Thr Ser Phe			
85	90	95	
Ile Lys Gln Asp Ile Lys Asn Lys Asp Phe Ile Phe Glu Ile Asp Asn			
100	105	110	
Asp Leu Lys Ser Arg Asp Leu Gly Ile Ser Phe Leu Lys Ser Phe Ala			
115	120	125	
Ile Leu Lys Pro Ala Phe Ile Cys Val Leu His Pro Leu Ser Tyr Leu			
130	135	140	
Ile Lys Glu Ala Asn Phe Lys Gln Phe Lys Ala Ile			
145	150	155	

## (2) INFORMATION FOR SEQ ID NO:837:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

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## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...157

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:837

Met Lys Ser Ile Leu Leu Phe Ile Ile Phe Val Val Cys Gln Leu Glu  
 1 5 10 15  
 Gly Lys Lys Phe Ser Gln Asp Asn Phe Lys Val Asp Tyr Asn Tyr Tyr  
 20 25 30  
 Leu Arg Lys Gln Asp Leu His Ile Ile Lys Thr Gln Asn Asp Leu Ser  
 35 40 45  
 Asn Ala Trp Tyr Leu Pro Pro Gln Lys Ala Pro Lys Glu His Ser Trp  
 50 55 60  
 Val Asp Phe Ala Lys Lys Tyr Leu Asn Met Met Asp Tyr Leu Gly Thr  
 65 70 75 80  
 Tyr Phe Leu Pro Phe Tyr His Ser Phe Thr Pro Ile Phe Gln Trp Tyr  
 85 90 95  
 His Pro Asn Ile Asn Pro Tyr Lys Arg Asn Glu Phe Lys Phe Gln Ile  
 100 105 110  
 Ser Phe Arg Val Pro Val Phe Arg His Ile Leu Trp Thr Lys Gly Thr  
 115 120 125  
 Leu Tyr Leu Asp Tyr Thr Gln Thr Asn Trp Phe Gln Ile Tyr Asn Asp  
 130 135 140  
 Pro Gln Ser Ala Pro Met Arg Met Ile Lys Phe His Ala  
 145 150 155

## (2) INFORMATION FOR SEQ ID NO:838:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (iii) MOLECULE TYPE: protein

## (viii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...191

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:838

Met Gly Leu Met Gly Val Ser Gln Gly Leu Pro Asn Thr Thr Ser Lys  
 1 5 10 15  
 Phe Gly Ile Glu Phe Asp Ser Leu Ala Asp Val Val Ala Phe Gly Val  
 20 25 30  
 Ala Pro Ser Leu Ile Thr Tyr Phe Tyr Val Gly Tyr Asn Phe Gly Arg  
 35 40 45  
 Ile Gly Met Ala Val Ser Ala Leu Phe Val Ile Phe Gly Ala Ile Arg  
 50 55 60  
 Leu Ala Arg Phe Asn Ile Ser Thr Asn Thr Ser Asp Pro Tyr Ser Phe  
 65 70 75 80  
 Ile Gly Ile Pro Ile Pro Ala Ala Val Leu Val Val Leu Cys Val  
 85 90 95  
 Leu Leu Asp Asn Lys Tyr His Phe Leu Glu Gly Asn Thr Glu Lys Leu  
 100 105 110  
 Phe Leu Gly Phe Ile Val Leu Leu Gly Val Leu Met Val Ser Asn Ile  
 115 120 125

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Arg	Tyr	Pro	Asn	Phe	Lys	Lys	Val	Lys	Trp	Asn	Leu	Lys	Leu	Phe	Ile
130				135						140					
Leu	Val	Leu	Ile	Phe	Leu	Ser	Leu	Val	Phe	Val	Arg	Pro	Leu	Glu	Ala
145					150					155			160		
Leu	Ser	Val	Phe	Met	Gly	Leu	Tyr	Leu	Ile	Tyr	Gly	Ile	Ile	Arg	Trp
				165					170			175			
Ile	Phe	Leu	Met	Val	Lys	Ile	Thr	Phe	Asn	Lys	Asn	Lys	Ser	Ala	
				180				185			190				

## (2) INFORMATION FOR SEQ ID NO:839:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839

Met	Ile	Gly	Val	Tyr	Pro	Asn	Tyr	Ser	Lys	Lys	Gln	Leu	Lys	Arg	Pro
1				5					10					15	
Leu	Val	Ile	Phe	Val	Ser	Arg	Glu	Leu	Ala	Leu	Ala	Asn	Gly	Ile	Leu
					20			25				30			
Thr	Asp	Ala	Tyr	Asp	Ile	Glu	Ala	Asn	Leu	Tyr	Met	Asn	Ala	Arg	Ile
					35			40			45				
Val	Met	Unk	Asn	Asn	Lys	Arg	Lys	His	Tyr	Glu	Gln	Arg	Val	Asn	Leu
					50			55			60				
His	Phe	Unk	Arg	Ser	Leu	Gly	Unk	Val	Phe	Asp	His	Arg	Ser	Asn	His
					65			70			75			80	
Val	Leu	Cys	Asp	Glu	Lys	Asp	Leu	Leu	Arg						
					85						90				

## (2) INFORMATION FOR SEQ ID NO:840:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840

Val Lys Ile Thr Ile Met Ile Lys Asp Phe Asn His Tyr Cys Arg Lys

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1	5	10	15												
Ile	Thr	Gly	Phe	Val	Lys	Ile	Pro	Thr	Lys	Lys	Gln	Gly	Ala	Lys	
20	25	30													
Lys	Met	Lys	Lys	Ala	Gly	Phe	Leu	Phe	Leu	Ala	Ala	Met	Ala	Ile	Ile
35	40	45													
Val	Val	Ser	Leu	Asn	Ala	Lys	Asp	Pro	Asn	Val	Leu	Arg	Lys	Ile	Val
50	55	60													
Phe	Glu	Lys	Cys	Leu	Pro	Asn	Tyr	Glu	Lys	Asn	Gln	Asn	Pro	Ser	Pro
65	70	75	80												
Cys	Ile	Glu	Val	Lys	Pro	Asp	Ala	Gly	Tyr	Val	Val	Leu	Lys	Asp	Ile
85	90	95													
Asn	Gly	Pro	Leu	Gln	Tyr	Leu	Leu	Met	Pro	Thr	Thr	His	Ile	Ser	Gly
100	105	110													
Ile	Glu	Asn	Pro	Leu	Leu	Leu	Asp	Pro	Ser	Thr	Pro	Asn	Phe	Phe	Tyr
115	120	125													
Leu	Ser	Trp	Gln	Ala	Arg	Asp	Phe	Met	Ser	Unk	Lys	Tyr	Gly	Lys	Pro
130	135	140													
Ile	Pro	Asp	Tyr	Ala	Ile	Ser	Leu	Thr	Ile	Asn	Ser	Lys	Lys	Gly	Arg
145	150	155	160												
Ser	Gln	Asn	His	Phe	His	Ile	His	Ile	Ser	Cys	Ile	Ser	Leu	Asp	Val
165	170	175													
Arg	Lys	Gln	Leu	Asp	Asn	Asn	Leu	Lys	Asn	Ile	Asn	Ser	Arg	Trp	Ser
180	185	190													
Pro	Leu	Ser	Gly	Gly	Leu	Asn	Gly	His	Lys	Tyr	Leu	Ala	Arg	Arg	Val
195	200	205													
Thr	Glu	Ser	Glu	Leu	Ala	Gln	Lys	Ser	Pro	Phe	Val	Met	Leu	Ala	Lys
210	215	220													
Glu	Val	Pro	Asn	Ala	His	Lys	Arg	Met	Gly	Asp	Tyr	Gly	Leu	Ala	Val
225	230	235	240												
Val	Gln	Gln	Ser	Asp	Asn	Ser	Phe	Val	Leu	Leu	Ala	Thr	Gln	Phe	Asn
245	250	255													
Pro	Leu	Thr	Leu	Asn	Arg	Ala	Ser	Ala	Glu	Glu	Ile	Gln	Asp	His	Glu
260	265	270													
Cys	Ala	Ile	Leu	Arg											
275															

## (2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841

Val	Leu	Thr	Ser	Gly	Asp	Met	Ile	Thr	Cys	Pro	Tyr	Cys	Gly	Arg	Ile
1	5	10	15												
Leu	Tyr	Ala	Glu	Ser	Thr	His	Glu	Ser	Asn	Ala	Gln	Pro	Pro	Lys	Glu
20	25	30													
Ser	Gln	Pro	Lys	Glu	Ser	Gln	Glu	Glu	Ser	Gln	Glu	Glu	Ser	Gln	Glu
35	40	45													
Glu	Ser	Gln	Glu	Ala	Val	Arg	Leu	Ile	Val						
50	55														

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## (2) INFORMATION FOR SEQ ID NO:842:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...138

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:842

Met	Ala	Leu	Asp	Lys	Arg	Ile	Trp	Met	His	Phe	Asp	Leu	Leu	Pro	Phe
1								5		10					15
Val	Phe	Ile	Ile	Pro	Leu	Leu	Val	Val	Ser	Phe	Leu	Leu	Ile	Phe	Glu
								20		25					30
Ser	Ser	Ala	Val	Leu	Ser	Leu	Lys	Gln	Gly	Val	Tyr	Tyr	Ala	Ile	Gly
							35		40						45
Phe	Leu	Leu	Phe	Trp	Val	Val	Phe	Phe	Ile	Pro	Phe	Arg	Lys	Leu	Asp
							50		55						60
Arg	Trp	Leu	Phe	Ala	Leu	Tyr	Trp	Ala	Cys	Val	Ile	Leu	Leu	Ala	Leu
							65		70						80
Val	Asp	Phe	Met	Gly	Ser	Ser	Lys	Leu	Gly	Ala	Gln	Arg	Trp	Leu	Val
							85		90						95
Ile	Pro	Phe	Thr	Ser	Ile	Thr	Leu	Gln	Pro	Ser	Glu	Pro	Val	Lys	Asn
							100		105						110
Arg	Unk	Ser	Phe	Ile	Val	Gly	Ala	Phe	Unk	Unk	Asn	Unk	Pro	Asp	Unk
							115		120						125
Leu	Leu	Arg	Ala	Met	Ile	Gly	Ala	Cys	Phe						
							130		135						

## (2) INFORMATION FOR SEQ ID NO:842:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...138

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:842

Met	Ala	Leu	Asp	Lys	Arg	Ile	Trp	Met	His	Phe	Asp	Leu	Leu	Pro	Phe
1								5		10					15
Val	Phe	Ile	Ile	Pro	Leu	Leu	Val	Val	Ser	Phe	Leu	Leu	Ile	Phe	Glu

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Ser	Ser	Ala	Val	Leu	Ser	Leu	Lys	Gln	Gly	Val	Tyr	Tyr	Ala	Ile	Gly
20							25						30		
35							40						45		
Phe	Leu	Leu	Phe	Trp	Val	Val	Phe	Phe	Ile	Pro	Phe	Arg	Lys	Leu	Asp
50							55						60		
Arg	Trp	Leu	Phe	Ala	Leu	Tyr	Trp	Ala	Cys	Val	Ile	Leu	Leu	Ala	Leu
65						70			75				80		
Val	Asp	Phe	Met	Gly	Ser	Ser	Lys	Leu	Gly	Ala	Gln	Arg	Trp	Leu	Val
85							90						95		
Ile	Pro	Phe	Thr	Ser	Ile	Thr	Leu	Gln	Pro	Ser	Glu	Pro	Val	Lys	Asn
100							105						110		
Arg	Unk	Ser	Phe	Ile	Val	Gly	Ala	Phe	Unk	Unk	Asn	Unk	Pro	Asp	Unk
115							120						125		
Leu	Leu	Arg	Ala	Met	Ile	Gly	Ala	Cys	Phe						
130							135								

## (2) INFORMATION FOR SEQ ID NO:843:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...279

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:843

Met	Lys	Leu	Asn	Asp	Pro	Phe	Thr	Ser	Pro	Asn	Lys	Ala	Lys	Lys	Glu
1							5				10			15	
Leu	Ser	Pro	Lys	Gly	Phe	Arg	Gly	Gly	Leu	Glu	Ser	Glu	Ile	Leu	Leu
									20	25			30		
Gly	Phe	Val	Leu	Gln	Lys	Glu	Arg	Val	Phe	Leu	His	Thr	His	Glu	His
								35	40		45				
Leu	Glu	Leu	Ser	His	Glu	Glu	Glu	Thr	Arg	Phe	Phe	Glu	Leu	Val	Gly
								50	55		60				
Lys	Arg	Leu	Asn	Asp	Cys	Pro	Ile	Glu	Tyr	Leu	Leu	Gly	Ser	Cys	Asp
							65	70		75		80			
Phe	Tyr	Gly	Arg	Ser	Phe	Phe	Val	Asn	Glu	His	Val	Leu	Ile	Pro	Arg
							85	90		95					
Pro	Glu	Thr	Glu	Ile	Leu	Val	Gln	Ala	Leu	Asn	Ile	Ile	Ser	Gln	
							100	105		110					
Tyr	His	Leu	Lys	Glu	Ile	Gly	Glu	Ile	Gly	Ile	Gly	Ser	Gly	Cys	Val
							115	120		125					
Ser	Val	Ser	Leu	Ala	Leu	Glu	Asn	Pro	Asn	Leu	Ser	Ile	Tyr	Ala	Ser
							130	135		140					
Asp	Ile	Ser	Pro	Lys	Ala	Leu	Glu	Val	Ala	Leu	Lys	Asn	Ile	Glu	Arg
							145	150		155		160			
Phe	Cys	Leu	Lys	Glu	Arg	Val	Phe	Leu	Lys	Gln	Thr	Arg	Leu	Trp	Asp
							165	170		175					
His	Met	Pro	Thr	Ile	Glu	Met	Leu	Val	Ser	Asn	Pro	Pro	Tyr	Ile	Ala
							180	185		190					
Arg	Asn	Tyr	Pro	Leu	Glu	Lys	Ser	Val	Leu	Lys	Glu	Pro	His	Glu	Ala
							195	200		205					
Leu	Phe	Gly	Gly	Val	Lys	Gly	Asp	Glu	Ile	Leu	Lys	Glu	Ile	Val	Phe
							210	215		220					

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Leu Ala Ala Lys Leu Lys Ile Pro Phe Leu Val Cys Glu Met Gly Tyr  
 225               230               235               240  
 Asp Gln Leu Lys Ser Leu Lys Glu Cys Leu Glu Phe Cys Gly Tyr Asp  
 245               250               255  
 Ala Glu Phe Tyr Lys Asp Leu Ser Gly Phe Asp Arg Gly Phe Val Gly  
 260               265               270  
 Val Leu Lys Ser Phe Leu Arg  
 275

## (2) INFORMATION FOR SEQ ID NO:844:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...36

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:844

Met Ile Ser Phe Ile Gly Phe Glu Cys Ser Ala Leu Lys Val Phe Leu  
 1               5               10               15  
 Thr Phe Gly Tyr Ile Val Phe Lys Unk Trp His Tyr Ser Ala Ile Arg  
 20               25               30  
 Leu Ile Val Ile  
 35

## (2) INFORMATION FOR SEQ ID NO:845:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...129

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:845

Val Ile Gln Ser His Pro Lys Gln Thr Leu Ile Glu Asp Glu Asn Tyr  
 1               5               10               15  
 Phe Tyr Ala Asn Lys Gly Leu Tyr Lys Thr Asn Lys Glu Ala Phe Leu  
 20               25               30  
 Arg Val Tyr Lys Ile Pro Glu Ser Met Pro Ile Glu Lys Arg Glu Ser  
 35               40               45  
 Leu Ser Lys Val Ser Lys Ile Phe Leu Ala Leu Leu Phe Phe Ile Ser

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50	55	60
Ser Met Leu Phe Gly Ile Phe Trp Arg Leu Pro Lys Arg Leu Asp Thr		
65	70	75
Lys Met Ser Leu Glu Ser Ala His Lys Asn Glu Leu Glu Asn Ala Phe		80
85	90	95
Gln Arg Tyr Asp Ala Leu Gly Val Arg Phe Glu Asp Ile Ala Gly Val		
100	105	110
Asn Glu Val Lys Glu Glu Leu Leu Glu Val Ile Asp Tyr Leu Lys Lys		
115	120	125
Pro		

## (2) INFORMATION FOR SEQ ID NO:846:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...127

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:846

Met Phe Val Val Lys Met Val Leu Gly Phe Leu Ile Leu Leu Ser Pro		
1	5	10
Leu Cys Ala Thr Gly Leu Asp Ile Ser Gln Thr Asp Ile Ile Glu Arg		15
20	25	30
Ser Leu Asn Phe Leu Leu Phe Val Gly Ile Leu Trp Tyr Phe Leu Ala		
35	40	45
Lys Arg Leu Arg Ser Phe Leu His Ser Lys Ser Leu Glu Ile Ser Lys		
50	55	60
Arg Leu Glu Glu Ile Gln Ala Gln Leu Lys Val Ser Lys Glu His Lys		
65	70	75
Lys Lys Leu Leu Lys Glu Leu Glu Gln Ala Lys Glu Lys Ala Glu Leu		80
85	90	95
Ile Ile Ser Asp Ala Asn Lys Glu Ala Leu His Asp His Ala Lys Ile		
100	105	110
Arg Ile Thr Asn Gln Asn Gly Cys Gly Lys Phe Asp Gln Lys Phe		
115	120	125

## (2) INFORMATION FOR SEQ ID NO:847:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

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## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...276

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:847

Met	Arg	Val	Leu	Glu	Trp	Lys	Tyr	Trp	Leu	Asn	Thr	Asp	Lys	Trp	Asp
1				5					10				15		
Thr	Pro	Thr	Asn	Lys	Pro	Pro	Gln	Thr	Phe	Lys	Ile	Gln	Ile	Phe	Lys
							20		25				30		
Ile	Gln	Ile	Gly	Ile	Ile	Asn	Asn	Phe	Asn	His	Leu	Ile	Lys	Gly	Ser
						35			40			45			
Ser	Met	Lys	Asn	Ala	Phe	Lys	Ala	Phe	Ala	Leu	Leu	Ile	Val	Phe	Phe
	50				55					60					
Ser	Asn	Ala	Leu	Leu	Ala	Gln	Asp	Leu	Lys	Ile	Ala	Ala	Ala	Asn	
65					70				75				80		
Leu	Thr	Arg	Ala	Leu	Lys	Ala	Leu	Val	Lys	Glu	Phe	Gln	Lys	Glu	His
						85			90			95			
Pro	Lys	Asp	Ala	Ile	Asn	Ile	Ser	Phe	Asn	Ser	Ser	Gly	Lys	Leu	Tyr
						100		105			110				
Ala	Gln	Ile	Ala	Gln	Asn	Ala	Pro	Phe	Asp	Leu	Phe	Ile	Ser	Ala	Asp
						115		120			125				
Ile	Ala	Arg	Pro	Lys	Lys	Leu	Tyr	Asp	Glu	Lys	Ile	Thr	Pro	Phe	Lys
						130		135			140				
Glu	Glu	Val	Tyr	Ala	Lys	Gly	Val	Leu	Val	Leu	Trp	Ser	Glu	Asn	Leu
145					150			155			160				
Lys	Met	Asp	Ser	Leu	Glu	Ile	Leu	Lys	Asp	Pro	Lys	Ile	Lys	Arg	Ile
						165		170			175				
Ala	Met	Ala	Asn	Pro	Lys	Leu	Ala	Pro	Tyr	Gly	Lys	Ala	Ser	Met	Glu
						180		185			190				
Val	Leu	Asp	Arg	Leu	Lys	Leu	Thr	Pro	Ser	Leu	Lys	Ser	Lys	Ile	Ile
						195		200			205				
Tyr	Gly	Ala	Ser	Ile	Ser	Gln	Ala	His	Gln	Phe	Ile	Ala	Thr	Lys	Asn
						210		215			220				
Ala	Gln	Ile	Gly	Phe	Gly	Ala	Leu	Ser	Leu	Ile	Asp	Lys	Lys	Asp	Lys
225					230			235			240				
Asn	Leu	Ser	Tyr	Phe	Ile	Ile	Asp	Lys	Thr	Leu	Tyr	Asn	Pro	Ile	Glu
						245		250			255				
Gln	Ala	Leu	Ile	Ile	Thr	Lys	Asn	Gly	Ala	Asn	Asn	Pro	Leu	Ala	Lys
						260		265			270				
Val	Phe	Lys	Asp												
	275														

## (2) INFORMATION FOR SEQ ID NO:848:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...126

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:848

Val Ala Leu Leu Glu Pro Ser Val Met Tyr Leu Thr Glu Lys Tyr Gln

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1	5	10	15
Tyr Ser Arg Phe Lys Val Thr Trp Gly Leu Val Ala Leu Ile Phe Val			
20	25	30	
Val Gly Val Val Leu Ile Phe Ser Leu His Lys Asp Tyr Lys Asp Tyr			
35	40	45	
Leu Thr Phe Phe Glu Lys Ser Leu Phe Asp Trp Leu Asp Phe Ala Ser			
50	55	60	
Ser Thr Ile Ile Unk Pro Leu Gly Gly Met Unk Thr Phe Ile Phe Met			
65	70	75	80
Gly Trp Val Leu Lys Lys Glu Lys Leu Arg Leu Leu Ser Ala His Phe			
85	90	95	
Leu Gly Pro Lys Leu Phe Ala Thr Trp Tyr Phe Leu Leu Lys Tyr Ile			
100	105	110	
Thr Pro Leu Ile Val Phe Ser Ile Trp Leu Ser Lys Ile Tyr			
115	120	125	

## (2) INFORMATION FOR SEQ ID NO:849:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849

Val Gly Leu Met Lys Ile Arg Phe Met Gly Arg Ser Val Phe Val Gly			
1	5	10	15
Asp Leu Glu Arg Ile Glu Glu Val Ala Arg Phe Glu Glu Phe Trp Leu			
20	25	30	
Leu Gly Gly Gln Lys Ala Ile Lys Glu Pro Arg Arg Leu Val Leu Glu			
35	40	45	
Ile Ala Leu Lys His Gln Leu Asn Lys Leu Leu Lys Arg Val Gln Lys			
50	55	60	
His Phe Lys Glu Asp Glu Leu Gly Ile Phe Lys Gln Met His Asp Lys			
65	70	75	80
Lys Ile Gln Ser Val Ala Thr Asn Ser Ile Gly Arg Leu Phe Asp Ile			
85	90	95	
Val Ala Phe Ser Leu Gly Val Val Gly Thr Ile Ser Phe Glu Ala Glu			
100	105	110	
Ser Gly Gln Val Leu Glu Asn Leu Ala Leu Gln Ser Asp Glu Ile Ala			
115	120	125	
Phe Tyr Pro Phe Glu Ile Lys Asn Ser Val Val Arg Leu Lys Glu Phe			
130	135	140	
Tyr Gln Ala Phe Glu Lys Asp Leu Gly Val Leu Glu Pro Lys Arg Ile			
145	150	155	160
Ala Lys Lys Phe Phe Asn Ser Leu Val Glu Ile Ile Thr Ala Leu Ile			
165	170	175	
Ala Pro Phe Lys Gly His Val Val Val Cys Ser Gly Gly Val Phe Cys			
180	185	190	
Asn Gln Leu Leu Cys Glu Gln Leu Ala Lys Arg Leu Lys Lys Leu Gln			
195	200	205	
Arg Glu Tyr Phe Phe His Lys His Phe Pro Pro Asn Asp Arg Ser Ile			
210	215	220	

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Pro Val Gly Gln Ala Leu Met Ala Tyr Phe Asn Pro Thr Ile Ile Lys  
 225                           230                           235                           240  
 Lys Gly

## (2) INFORMATION FOR SEQ ID NO:850:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 151 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850

Val Ser Asp Ser Asn Ala Leu Lys Glu Val Phe Leu Asn Ile Ser Ala  
 1                           5                           10                           15  
 Lys Glu Asp His Cys Asp Val Leu Ile Asn Ser Ala Gly Tyr Gly Val  
 20                           25                           30  
 Phe Gly Ser Val Glu Asp Thr Pro Ile Glu Glu Val Lys Lys Gln Phe  
 35                           40                           45  
 Ser Val Asn Phe Phe Ala Leu Cys Glu Val Val Gln Leu Cys Leu Pro  
 50                           55                           60  
 Leu Leu Lys Asn Lys Pro Tyr Ser Lys Ile Phe Asn Leu Ser Ser Ile  
 65                           70                           75                           80  
 Ala Gly Arg Val Ser Met Leu Phe Leu Gly His Tyr Ser Ala Ser Lys  
 85                           90                           95  
 His Ala Leu Glu Ala Tyr Ser Asp Ala Leu Arg Leu Glu Leu Lys Pro  
 100                        105                           110  
 Phe Asn Val Gln Val Cys Leu Ile Glu Pro Gly Pro Val Lys Ser Asn  
 115                        120                           125  
 Trp Glu Lys Thr Ala Phe Glu Asn Asp Glu Arg Lys Asp Ser Val Tyr  
 130                        135                           140  
 Ala Leu Glu Val Asn Ala Ala  
 145                        150

## (2) INFORMATION FOR SEQ ID NO:851:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 154 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...154

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851

(2) INFORMATION FOR SEQ ID NO:852:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 326 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - ii) MOLECULE TYPE: protein
  - iii) HYPOTHETICAL: YES
  - vi) ORIGINAL SOURCE:
    - (A) ORGANISM: Helicobacter pylori
  - ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION 1...326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 852

Val	Leu	Met	Ala	Leu	Unk	Asp	Lys	Arg	Tyr	Gly	Leu	Glu	Ala	Gly	Ile
1				5				10						15	
Lys	Tyr	Phe	Thr	Met	Gly	Ala	Met	Ala	Ser	Ala	Phe	Phe	Ala	Met	Gly
				20				25					30		
Ala	Met	Ala	Phe	Tyr	Leu	Leu	Thr	Gly	Ser	Leu	Asn	Leu	Glu	Val	Ile
				35			40					45			
Thr	Leu	Tyr	Leu	His	Thr	Glu	Gly	Ile	Thr	Asn	Pro	Met	Leu	Phe	Ala
				50		55					60				
Met	Gly	Thr	Ile	Phe	Leu	Ile	Gly	Ala	Ile	Gly	Phe	Lys	Val	Ser	Leu
	65			70			75					80			
Val	Pro	Phe	His	Thr	Trp	Met	Pro	Asp	Val	Tyr	Glu	Gly	Asn	Asn	Pro
				85			90					95			
Val	Phe	Ala	Ser	Tyr	Ile	Ser	Ile	Val	Pro	Lys	Ile	Ala	Gly	Phe	Val
				100			105					110			
Val	Ala	Thr	Arg	Leu	Phe	Gly	Ala	Phe	Ile	Asp	Thr	His	Thr	Ala	Trp
				115			120					125			
Val	Glu	Asp	Ile	Phe	Tyr	Val	Leu	Ile	Leu	Met	Thr	Ile	Thr	Ile	Pro
	130			135						140					
Asn	Phe	Ile	Ala	Leu	Trp	Gln	Glu	Asp	Val	Lys	Arg	Met	Leu	Ala	Tyr
145				150					155			160			

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Ser Ser Ile Ser His Ser Gly Phe Ala Leu Ala Cys Val Phe Ile His  
 165 170 175  
 Thr Glu Asp Ser Gln Gln Ala Met Phe Val Tyr Trp Phe Met Phe Ala  
 180 185 190  
 Phe Thr Tyr Ile Gly Ala Phe Gly Leu Leu Trp Leu Leu Lys Ser Arg  
 195 200 205  
 Glu Lys Thr Trp Asp Glu Arg Tyr Asp His Pro Tyr Ser Lys Phe Asn  
 210 215 220  
 Gly Leu Ile Lys Thr His Pro Leu Val Ala Ile Leu Gly Ala Ile Phe  
 225 230 235 240  
 Val Phe Gly Leu Ala Gly Ile Pro Pro Phe Ser Val Phe Trp Gly Lys  
 245 250 255  
 Phe Leu Ala Val Glu Ser Ala Leu Glu Ser Asn His Ile Leu Leu Ala  
 260 265 270  
 Val Val Met Leu Val Asn Ser Ala Val Ala Ala Phe Tyr Tyr Phe Arg  
 275 280 285  
 Trp Leu Val Ala Met Phe Phe Asn Lys Pro Leu Gln Thr Gln Ser Tyr  
 290 295 300  
 Ala Lys Thr Ile Phe Thr Pro Lys Thr Pro Pro Cys Pro Phe Met Arg  
 305 310 315 320  
 Ser Leu Leu Pro Trp Arg  
 325

## (2) INFORMATION FOR SEQ ID NO:852:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...326

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:852

Val Leu Met Ala Leu Unk Asp Lys Arg Tyr Gly Leu Glu Ala Gly Ile  
 1 5 10 15  
 Lys Tyr Phe Thr Met Gly Ala Met Ala Ser Ala Phe Phe Ala Met Gly  
 20 25 30  
 Ala Met Ala Phe Tyr Leu Leu Thr Gly Ser Leu Asn Leu Glu Val Ile  
 35 40 45  
 Thr Leu Tyr Leu His Thr Glu Gly Ile Thr Asn Pro Met Leu Phe Ala  
 50 55 60  
 Met Gly Thr Ile Phe Leu Ile Gly Ala Ile Gly Phe Lys Val Ser Leu  
 65 70 75 80  
 Val Pro Phe His Thr Trp Met Pro Asp Val Tyr Glu Gly Asn Asn Pro  
 85 90 95  
 Val Phe Ala Ser Tyr Ile Ser Ile Val Pro Lys Ile Ala Gly Phe Val  
 100 105 110  
 Val Ala Thr Arg Leu Phe Gly Ala Phe Ile Asp Thr His Thr Ala Trp  
 115 120 125  
 Val Glu Asp Ile Phe Tyr Val Leu Ile Leu Met Thr Ile Thr Ile Pro  
 130 135 140  
 Asn Phe Ile Ala Leu Trp Gln Glu Asp Val Lys Arg Met Leu Ala Tyr  
 145 150 155 160  
 Ser Ser Ile Ser His Ser Gly Phe Ala Leu Ala Cys Val Phe Ile His

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165	170	175
Thr Glu Asp Ser Gln Gln Ala Met Phe Val Tyr Trp Phe Met Phe Ala		
180	185	190
Phe Thr Tyr Ile Gly Ala Phe Gly Leu Leu Trp Leu Leu Lys Ser Arg		
195	200	205
Glu Lys Thr Trp Asp Glu Arg Tyr Asp His Pro Tyr Ser Lys Phe Asn		
210	215	220
Gly Leu Ile Lys Thr His Pro Leu Val Ala Ile Leu Gly Ala Ile Phe		
225	230	235
Val Phe Gly Leu Ala Gly Ile Pro Pro Phe Ser Val Phe Trp Gly Lys		
245	250	255
Phe Leu Ala Val Glu Ser Ala Leu Glu Ser Asn His Ile Leu Leu Ala		
260	265	270
Val Val Met Leu Val Asn Ser Ala Val Ala Ala Phe Tyr Tyr Phe Arg		
275	280	285
Trp Leu Val Ala Met Phe Phe Asn Lys Pro Leu Gln Thr Gln Ser Tyr		
290	295	300
Ala Lys Thr Ile Phe Thr Pro Lys Thr Pro Pro Cys Pro Phe Met Arg		
305	310	315
Ser Leu Leu Pro Trp Arg		
325		320

## (2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 179 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853

Met Asn Tyr Pro Asn Leu Pro Asn Ser Ala Leu Unk Ile Ser Glu Gln		
1	5	10
Pro Glu Val Lys Glu Ile Thr Asn Glu Leu Leu Lys Gln Leu Gln Asn		15
20	25	30
Ala Leu Arg Ser Asn Ala His Phe Ser Glu Gln Val Glu Leu Ser Leu		
35	40	45
Lys Cys Ile Val Arg Ile Leu Glu Val Leu Leu Ser Leu Asp Phe Phe		
50	55	60
Lys Asn Ala Asn Glu Ile Asp Ser Ser Leu Arg Asn Ser Ile Glu Trp		
65	70	75
Leu Thr Asn Ala Gly Glu Ser Leu Lys Leu Lys Met Lys Glu Tyr Glu		80
85	90	95
Arg Phe Phe Ser Glu Phe Asn Thr Ser Met His Ala Asn Glu Gln Glu		
100	105	110
Val Thr Asn Thr Leu Asn Ala Asn Ala Glu Asn Ile Lys Ser Unk Ile		
115	120	125
Lys Unk Leu Glu Asn Gln Leu Ile Glu Thr Thr Arg Leu Leu Thr		
130	135	140
Ser Tyr Gln Ile Phe Leu Asn Gln Ala Arg Asp Asn Ala Asn Asn Gln		
145	150	155
Ile Thr Lys Asn Lys Thr Unk Ser Leu Glu Ala Ile Thr Gln Ala Lys		160
165	170	175

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Asn Asn Ser

## (2) INFORMATION FOR SEQ ID NO:854:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...240

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:854

Met	Ile	Asn	Ser	Lys	Ser	Leu	Lys	Gly	Leu	Arg	Gly	Phe	Phe
1							5	10			15		
Lys	Ile	Leu	Lys	Asp	Arg	Asn	Gly	Ala	His	Phe	Ser	Cys	Gly
							20	25			30		
Ser	Gly	Phe	Gly	Leu	Glu	Ile	Ala	Lys	Ala	Phe	Leu	Gln	Lys
	35					40					45		
Val	Val	Phe	Gly	Thr	Gly	Arg	Arg	Gln	Glu	Asn	Leu	Gln	Lys
	50					55					60		
Leu	Ala	Tyr	Pro	Lys	Arg	Phe	Ile	Pro	Leu	Cys	Phe	Asp	Leu
	65					70				75		80	
Lys	Pro	Glu	Thr	Lys	Arg	Ala	Ile	Glu	Thr	Ile	Phe	Ser	Met
	85					90				95			
Arg	Ile	Asp	Ala	Leu	Ile	Asn	Asn	Ala	Gly	Leu	Ala	Gly	Leu
	100					105				110			
Lys	Ala	Tyr	Glu	Cys	Glu	Leu	Asp	Asp	Trp	Glu	Val	Met	Ile
	115					120				125			
Asn	Ile	Lys	Gly	Leu	Leu	His	Leu	Thr	Arg	Leu	Ile	Leu	Pro
	130					135				140			
Ile	Glu	His	Asp	Gln	Gly	Thr	Ile	Ile	Asn	Leu	Gly	Ser	Ile
	145					150				155		160	
Thr	Tyr	Ala	Tyr	Pro	Gly	Gly	Unk	Val	Tyr	Gly	Ala	Ser	Lys
	165					170				175			
Val	Lys	Gln	Unk	Ser	Unk	Asn	Leu	Arg	Ala	Asp	Val	Ala	Gly
	180					185				190			
Thr	Arg	Gly	Arg	Arg	Trp	Asn	Pro	Gly	Cys	Val	Ala	Lys	Pro
	195					200				205			
Ser	Arg	Val	Arg	Gly	Lys	Gly	Asp	Lys	Pro	Lys	Pro	Lys	Tyr
	210					215				220			
Glu	Lys	His	Pro	Leu	Pro	Gln	Thr	Thr	Arg	Gln	Gly	Leu	Thr
	225					230				235		240	

## (2) INFORMATION FOR SEQ ID NO:854:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854

Met	Ile	Asn	Ser	Lys	Lys	Ser	Leu	Lys	Gly	Leu	Arg	Gly	Phe	Phe	
1				5				10			15				
Lys	Ile	Leu	Lys	Asp	Arg	Asn	Gly	Ala	His	Phe	Ser	Cys	Gly	Ala	Thr
				20				25			30				
Ser	Gly	Phe	Gly	Leu	Glu	Ile	Ala	Lys	Ala	Phe	Leu	Gln	Lys	Asn	His
				35				40			45				
Val	Val	Phe	Gly	Thr	Gly	Arg	Arg	Gln	Glu	Asn	Leu	Gln	Lys	Leu	Gln
				50				55			60				
Leu	Ala	Tyr	Pro	Lys	Arg	Phe	Ile	Pro	Leu	Cys	Phe	Asp	Leu	Gln	Asn
				65				70			75			80	
Lys	Pro	Glu	Thr	Lys	Arg	Ala	Ile	Glu	Thr	Ile	Phe	Ser	Met	Thr	Asp
				85				90			95				
Arg	Ile	Asp	Ala	Leu	Ile	Asn	Asn	Ala	Gly	Leu	Ala	Gly	Leu	Asn	
				100				105			110				
Lys	Ala	Tyr	Glu	Cys	Glu	Leu	Asp	Asp	Trp	Glu	Val	Met	Ile	Asp	Thr
				115				120			125				
Asn	Ile	Lys	Gly	Leu	Leu	His	Leu	Thr	Arg	Leu	Ile	Leu	Pro	Ser	Met
				130				135			140				
Ile	Glu	His	Asp	Gln	Gly	Thr	Ile	Ile	Asn	Leu	Gly	Ser	Ile	Ala	Gly
				145				150			155			160	
Thr	Tyr	Ala	Tyr	Pro	Gly	Gly	Unk	Val	Tyr	Gly	Ala	Ser	Lys	Ala	Unk
				165				170			175				
Val	Lys	Gln	Unk	Ser	Unk	Asn	Leu	Arg	Ala	Asp	Val	Ala	Gly	Thr	Asn
				180				185			190				
Thr	Arg	Gly	Arg	Arg	Trp	Asn	Pro	Gly	Cys	Val	Ala	Lys	Pro	Lys	Val
				195				200			205				
Ser	Arg	Val	Arg	Gly	Lys	Gly	Asp	Lys	Pro	Lys	Pro	Lys	Ser	Gly	Tyr
				210				215			220				
Glu	Lys	His	Pro	Leu	Pro	Gln	Thr	Thr	Arg	Gln	Gly	Leu	Thr	Ser	Gly
				225				230			235			240	

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855

Val	Phe	Ala	Thr	Asp	Ser	Ser	Ser	Phe	Ser	Met	Gly	Leu	Thr	Met	Ala
1					5				10			15			

712

Ser Ala Tyr Glu Pro Ile Ser Gly Ser Gln Lys Pro Ile Val Gly Gln  
 20 25 30  
 Ala Leu Leu Leu Ala Ile Leu Ile Leu Asp Leu Ser Phe His  
 35 40 45  
 His Gln Ile Ile Leu Phe Val Asp His Ser Leu Lys Ala Val Pro Leu  
 50 55 60  
 Gly Arg Phe Val Phe Glu Pro Glu Leu Ala Lys Asn Ile Val Lys Ala  
 65 70 75 80  
 Phe Ser His Leu Phe Val Ile Gly Phe Ser Met Ala Phe Pro Ile Leu  
 85 90 95  
 Cys Leu Val Leu Leu Ser Asp Ile Ile Phe Gly Met Ile Met Lys Thr  
 100 105 110  
 His Pro Gln Phe Asn Leu Leu Ala Ile Gly Phe Pro Val Lys Ile Ala  
 115 120 125  
 Ile Gly Phe Val Gly Ile Ile Leu Ile Ala Ser Ala Ile Met Gly Arg  
 130 135 140  
 Phe Lys Glu Glu Ile Ser Leu Ala Phe Ser Val Ile Ser Lys Ile Phe  
 145 150 155 160

## (2) INFORMATION FOR SEQ ID NO:856:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 94 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856

Met Tyr Gly Val Lys Glu Ile Lys Asp Lys Ile Asp Lys Gln Leu His  
 1 5 10 15  
 Asn Asn Asp His Leu Phe Glu Gly Leu Phe Gly Glu Lys Glu Asp Leu  
 20 25 30  
 Lys Lys Leu Val Ser Met Phe Gly Gln Leu Arg Phe Gln Lys Arg Trp  
 35 40 45  
 Ser Gln Thr Pro Arg Val Pro Gln Thr Ser Val Leu Gly His Thr Leu  
 50 55 60  
 Cys Val Ala Ile Met Gly Tyr Leu Leu Ser Phe Asp Leu Lys Ala Cys  
 65 70 75 80  
 Lys Ser Met Arg Ile Asn His Phe Leu Gly Gly Leu Phe Pro  
 85 90

## (2) INFORMATION FOR SEQ ID NO:857:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 146 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

713

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857

```

Met Thr Leu Asp Asp Leu Leu Gly Gly Ser Leu Asp Pro His Cys Phe
1           5          10          15
Cys Lys Pro Leu Ile Lys Thr Lys Lys Asp Gln Glu Arg Leu Leu Ser
20          25          30
Leu Ala Leu Lys Ala His Pro Lys Ile Ser Phe Gly Lys Asp Ser Ala
35          40          45
Pro His Phe Ile Ser Lys Lys His Ser Ala Asn Ile Pro Ala Gly Ile
50          55          60
Phe Ser Ala Pro Ile Leu Leu Pro Ala Leu Cys Glu Leu Phe Glu Lys
65          70          75          80
His Asn Ala Leu Glu Asn Leu Gln Ala Phe Ile Ser Asp Asn Ala Lys
85          90          95
Lys Ile Tyr Ala Leu Asp Asn Leu Pro Ser Lys Lys Ala His Leu Ser
100         105         110
Lys Lys Pro Phe Ile Val Pro Thr His Thr Leu Cys Leu Asn Glu Lys
115         120         125
Ile Ala Ile Leu Arg Gly Gly Glu Thr Leu Ser Trp Asn Leu Gln Glu
130         135         140
Ile Ala
145

```

(2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 204 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858

```

Val Ser Gly Val Val Leu Ser Lys Phe Asp Ser Asp Ser Lys Gly Gly
1           5          10          15
Ile Ala Leu Gly Ile Thr Tyr Gln Leu Gly Leu Pro Leu Arg Phe Ile
20          25          30
Gly Ser Gly Glu Lys Ile Pro Asp Leu Asp Val Phe Met Pro Glu Arg
35          40          45
Ile Val Gly Arg Leu Met Gly Ala Gly Asp Ile Ile Ser Leu Ala Glu
50          55          60
Lys Thr Ala Ser Val Leu Asn Pro Asn Glu Ala Lys Asp Leu Ser Lys
65          70          75          80
Lys Leu Lys Lys Gly Gln Phe Thr Phe Asn Asp Phe Leu Asn Gln Ile
85          90          95
Glu Lys Val Lys Lys Leu Gly Ser Met Ser Ser Leu Ile Ser Met Ile
100         105         110

```

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Pro Gly Leu Gly Asn Met Ala Ser Ala Leu Lys Asp Thr Asp Leu Glu  
 115 120 125  
 Ser Ser Leu Glu Val Lys Lys Ile Lys Ala Met Val Asn Ser Met Thr  
 130 135 140  
 Lys Lys Glu Arg Glu Asn Pro Glu Ile Leu Asn Gly Ser Arg Arg Lys  
 145 150 155 160  
 Arg Ile Ala Leu Gly Unk Gly Leu Glu Unk Unk Glu Ile Asn Arg Ile  
 165 170 175  
 Ile Lys Arg Phe Asp Gln Ala Ser Lys Met Ala Lys Arg Leu Thr Asn  
 180 185 190  
 Lys Lys Gly Ile Ser Asp Leu Met Asn Leu Unk Unk  
 195 200

## (2) INFORMATION FOR SEQ ID NO:858:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858

Val Ser Gly Val Val Leu Ser Lys Phe Asp Ser Asp Ser Lys Gly Gly  
 1 5 10 15  
 Ile Ala Leu Gly Ile Thr Tyr Gln Leu Gly Leu Pro Leu Arg Phe Ile  
 20 25 30  
 Gly Ser Gly Glu Lys Ile Pro Asp Leu Asp Val Phe Met Pro Glu Arg  
 35 40 45  
 Ile Val Gly Arg Leu Met Gly Ala Gly Asp Ile Ile Ser Leu Ala Glu  
 50 55 60  
 Lys Thr Ala Ser Val Leu Asn Pro Asn Glu Ala Lys Asp Leu Ser Lys  
 65 70 75 80  
 Lys Leu Lys Lys Gly Gln Phe Thr Phe Asn Asp Phe Leu Asn Gln Ile  
 85 90 95  
 Glu Lys Val Lys Lys Leu Gly Ser Met Ser Ser Leu Ile Ser Met Ile  
 100 105 110  
 Pro Gly Leu Gly Asn Met Ala Ser Ala Leu Lys Asp Thr Asp Leu Glu  
 115 120 125  
 Ser Ser Leu Glu Val Lys Ile Lys Ala Met Val Asn Ser Met Thr  
 130 135 140  
 Lys Lys Glu Arg Glu Asn Pro Glu Ile Leu Asn Gly Ser Arg Arg Lys  
 145 150 155 160  
 Arg Ile Ala Leu Gly Unk Gly Leu Glu Unk Unk Glu Ile Asn Arg Ile  
 165 170 175  
 Ile Lys Arg Phe Asp Gln Ala Ser Lys Met Ala Lys Arg Leu Thr Asn  
 180 185 190  
 Lys Lys Gly Ile Ser Asp Leu Met Asn Leu Unk Unk  
 195 200

## (2) INFORMATION FOR SEQ ID NO:859:

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859

Met	Gly	Val	Leu	Gly	Met	Phe	Ala	Phe	Phe	Ser	Trp	Val	Phe	Leu	Phe
1					5							10			15
Lys	His	Asn	Leu	Ser	His	Lys	Ile	Arg	Leu	Tyr	His	Glu	Lys	Lys	Asp
					20							25			30
Phe	Asp	Lys	Leu	Leu	Lys	Gln	Ile	Leu	Ser	Gln	Asp	Thr	Gln	Lys	Thr
					35							40			45
Phe	Leu	Lys	Thr	Lys	Phe	Lys	Ser	Asp	Leu	Ala	Lys	Asn	Leu	Ser	Gln
					50							55			60
Ile	Leu	Ala	Arg	Tyr	Asp	Leu	Lys	Ala	Asp	Leu	Asn	Thr	Pro	Asn	Ser
					65							70			75
Gly	Cys	Glu	Lys	Val	Asp	Asn	Leu	Phe	Lys	His	Tyr	His	Asn	Ile	Glu
					85							90			95
Asn	Asn	Thr	Leu	Glu	Pro	Lys	Asp	His	Ala	Lys	His	Ser	Leu	Ala	Tyr
					100							105			110
Glu	His	Ala	Tyr	Phe	Ser	Lys	Arg	Leu	Lys	Ala	Phe	Ile	His	Asn	Asp
					115							120			125
Leu	Lys	Asn	Ala	Phe	Glu	Val	Leu	Thr	Asn	Ala	Gln	Ile	Pro	Leu	Glu
					130							135			140
Leu	Arg	Arg	Tyr	Ala	Tyr	Arg	Asn	Arg	Pro	Lys	Arg	Gln	Gln	Lys	Arg
					145							150			155
Gly	Phe	Lys	Gly	Cys	Glu	Cys	Asp	Ala	Arg	Gly	Phe	Gly			160
					165							170			

(2) INFORMATION FOR SEQ ID NO:860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860

Val	Ser	Val	Pro	Ala	Thr	Ser	Ala	Asn	Leu	Gly	Pro	Gly	Phe	Asp	Cys
1					5							10			15
Leu	Gly	Leu	Ser	Leu	Asn	Leu	Arg	Asn	Arg	Phe	Phe	Ile	Glu	Pro	Ser
					20							25			30

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Asn Ile His Ala Val Lys Leu Val Gly Glu Gly Glu Ile Pro Lys  
 35 40 45  
 Phe Leu Thr Asn Asn Ile Phe Thr Lys Val Phe Tyr Glu Ile Leu Lys  
 50 55 60  
 Lys His Gly Asn Asp Gly Ser Phe Lys Phe Leu Leu His Asn Lys Val  
 65 70 75 80  
 Pro Ile Thr Arg Gly Met Gly Ser Ser Ala Met Ile Val Gly Ala  
 85 90 95  
 Val Ala Ser Ala Phe Ala Phe Leu Gly Phe Ala Phe Asp Arg Glu Asn  
 100 105 110  
 Ile Leu Asn Thr Ala Leu Ile Tyr Glu Asn His Pro Asp Asn Ile Thr  
 115 120 125  
 Pro Ala Val Phe Gly Gly Tyr Asn Ala Ala Phe Val Glu Lys Lys Lys  
 130 135 140  
 Val Ile Ser Leu Lys Thr Lys Ile Pro Ser Phe Leu Lys Ala Val Met  
 145 150 155 160  
 Val Ile Pro Asn Arg Val Ile Ser Thr Lys Gln Ser Arg His Leu Cys  
 165 170 175  
 Pro Ser Val Thr Ala Cys Lys Ala Cys Leu Thr Phe Arg Met Arg  
 180 185 190  
 Val

## (2) INFORMATION FOR SEQ ID NO:861:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861

Val Ala Lys Asn Leu Val Ala Ser Gly Val Cys Asp Lys Ala Thr Val  
 1 5 10 15  
 Gln Leu Ala Tyr Ala Ile Gly Val Ile Glu Pro Val Ser Ile Tyr Val  
 20 25 30  
 Asn Thr His Asn Thr Ser Lys His Ser Ser Ala Glu Leu Glu Lys Cys  
 35 40 45  
 Val Lys Ser Val Phe Lys Leu Thr Pro Lys Gly Ile Ile Glu Ser Leu  
 50 55 60  
 Asp Leu Leu Arg Pro Ile Tyr Ser Leu Thr Ser Ala Tyr Gly His Phe  
 65 70 75 80  
 Gly Arg Glu Leu Glu Phe Thr Trp Glu Lys Thr Asn Lys Val Glu  
 85 90 95  
 Glu Ile Lys Ala Phe Phe Lys Arg  
 100

## (2) INFORMATION FOR SEQ ID NO:862:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 355 amino acids  
 (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862

Val	Arg	Leu	Phe	Arg	Phe	Val	Gly	Trp	Tyr	Tyr	Phe	Lys	Tyr	Phe	Leu
1						5			10			15			
Ile	Val	Leu	Leu	Ala	Leu	Glu	Leu	Phe	Phe	Val	Gly	Ile	Asp	Ser	Leu
						20			25			30			
Lys	Tyr	Ala	Asp	Lys	Met	Pro	Asp	Ser	Ala	Asn	Met	Ile	Ile	Leu	Phe
					35			40			45				
Phe	Thr	Tyr	Asp	Ile	Leu	Phe	Ala	Leu	Asn	Tyr	Thr	Leu	Pro	Ile	Ser
				50		55				60					
Leu	Leu	Leu	Ala	Met	Val	Leu	Phe	Tyr	Ile	Thr	Phe	Ile	Lys	Ser	Asn
					65		70			75			80		
Gln	Tyr	Thr	Ala	Leu	Leu	Ser	Ile	Gly	Phe	Ser	Lys	Cys	Gln	Ile	Leu
					85			90				95			
Ser	Pro	Ile	Phe	Leu	Ile	Ser	Leu	Phe	Phe	Thr	Ala	Val	Tyr	Val	Gly
					100			105			110				
Leu	Asn	Ala	Thr	Pro	Phe	Val	Tyr	Met	Glu	Glu	Lys	Thr	Gln	Asn	Leu
					115			120			125				
Ile	Tyr	Lys	Asp	Asn	Ser	Leu	Ser	Val	Ser	Glu	His	Leu	Leu	Val	Lys
					130			135			140				
Tyr	Asn	Asp	Asp	Tyr	Val	Tyr	Phe	Asp	Lys	Ile	Asn	Pro	Leu	Leu	Gln
					145		150			155			160		
Lys	Ala	Gln	Asn	Ile	Lys	Val	Phe	Arg	Leu	Lys	Asp	Lys	Thr	Leu	Glu
					165			170			175				
Ser	Tyr	Ala	Glu	Ala	Lys	Glu	Ala	Phe	Phe	Glu	Asp	Lys	Tyr	Trp	Ile
					180			185			190				
Leu	His	Asp	Thr	Thr	Ile	Tyr	Glu	Met	Pro	Leu	Ser	Phe	Glu	Leu	Gly
					195			200			205				
Ala	Asn	Ala	Leu	Asn	Thr	Thr	His	Leu	Glu	Thr	Phe	Lys	Thr	Leu	Lys
					210			215			220				
Asn	Phe	Arg	Pro	Lys	Val	Leu	Asp	Thr	Ile	Tyr	Gln	Asn	Lys	Pro	Ala
					225		230			235			240		
Val	Ser	Ile	Thr	Asp	Ala	Leu	Leu	Ser	Leu	His	Ala	Leu	Val	Arg	Gln
					245			250			255				
Asn	Ala	Asp	Thr	Lys	Lys	Val	Arg	Ser	Phe	Leu	Tyr	Val	Phe	Ala	Ile
					260			265			270				
Leu	Pro	Phe	Phe	Val	Pro	Phe	Leu	Ser	Val	Leu	Ile	Ala	Tyr	Phe	Ser
					275			280			285				
Pro	Ser	Leu	Ala	Arg	Tyr	Glu	Asn	Leu	Ala	Leu	Gly	Leu	Lys	Phe	
					290			295			300				
Ile	Ile	Ile	Thr	Leu	Val	Val	Trp	Gly	Leu	Phe	Ala	Leu	Gly	Lys	
					305			310			315			320	
Phe	Ser	Ile	Ser	Gly	Ile	Leu	Ile	Pro	Glu	Ile	Gly	Val	Leu	Ser	Pro
					325			330			335				
Phe	Phe	Val	Phe	Leu	Ala	Leu	Ser	Leu	Trp	Tyr	Phe	Lys	Lys	Leu	Asn
					340			345			350				
Lys	Arg	Leu			355										

(2) INFORMATION FOR SEQ ID NO:863:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 92 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...92
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:863

Val Glu Lys Ala His Pro Asp Val Phe Asn Leu Leu Leu Gln Val Leu  
1 5 10 15  
Asp Glu Gly His Leu Thr Asp Ser Lys Gly Val Arg Val Asp Phe Lys  
20 25 30  
Asn Thr Ile Leu Ile Leu Thr Ser Asn Val Ala Ser Gly Ala Leu Leu  
35 40 45  
Glu Glu Asp Leu Ser Glu Ala Asp Lys Gln Lys Ala Ile Lys Glu Ser  
50 55 60  
Leu Arg Gln Phe Phe Lys Pro Glu Phe Leu Asn Arg Leu Asp Glu Ile  
65 70 75 80  
Ile Ser Phe Asn Ala Leu Asp Ser His Ala Ile Ile  
85 90

## (2) INFORMATION FOR SEQ ID NO:863:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 92 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...92
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:863

Val Glu Lys Ala His Pro Asp Val Phe Asn Leu Leu Leu Gln Val Leu  
1 5 10 15  
Asp Glu Gly His Leu Thr Asp Ser Lys Gly Val Arg Val Asp Phe Lys  
20 25 30  
Asn Thr Ile Leu Ile Leu Thr Ser Asn Val Ala Ser Gly Ala Leu Leu  
35 40 45  
Glu Glu Asp Leu Ser Glu Ala Asp Lys Gln Lys Ala Ile Lys Glu Ser  
50 55 60  
Leu Arg Gln Phe Phe Lys Pro Glu Phe Leu Asn Arg Leu Asp Glu Ile  
65 70 75 80  
Ile Ser Phe Asn Ala Leu Asp Ser His Ala Ile Ile  
85 90

## (2) INFORMATION FOR SEQ ID NO:864:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864

Leu	Val	Phe	Leu	Asp	Arg	Arg	Leu	Ile	Val	Met	Val	Thr	Asp	Ser	Lys
1															
															15
Gly	Ser	Arg	Tyr	Ile	Asn	Val	His	Ile	Leu	Phe	Arg	Gln	Ile	Ser	Leu
															30
Tyr	Ala	Leu	Leu	Ser	Val	Val	Gly	Ser	Leu	Leu	Phe	Leu	Gly	Val	Ser
															45
Leu	Leu	Val	Leu	Asn	Lys	Glu	Ile	Lys	Asn	Ile	Glu	Lys	Gln	His	Ala
															60
Leu	Unk	Thr	Lys	Glu	Phe	Glu	Lys	Lys	Arg	Glu	Thr	Asn	Glu	Unk	Leu
															80
Ser	Unk														

## (2) INFORMATION FOR SEQ ID NO:864:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864

Leu	Val	Phe	Leu	Asp	Arg	Arg	Leu	Ile	Val	Met	Val	Thr	Asp	Ser	Lys
1															
															15
Gly	Ser	Arg	Tyr	Ile	Asn	Val	His	Ile	Leu	Phe	Arg	Gln	Ile	Ser	Leu
															30
Tyr	Ala	Leu	Leu	Ser	Val	Val	Gly	Ser	Leu	Leu	Phe	Leu	Gly	Val	Ser
															45
Leu	Leu	Val	Leu	Asn	Lys	Glu	Ile	Lys	Asn	Ile	Glu	Lys	Gln	His	Ala
															60
Leu	Unk	Thr	Lys	Glu	Phe	Glu	Lys	Lys	Arg	Glu	Thr	Asn	Glu	Unk	Leu
															80

720

Ser Unk

## (2) INFORMATION FOR SEQ ID NO:865:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...233

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:865

Leu	Ser	Leu	Met	Unk	Val	Leu	Asn	Ala	Lys	Glu	Cys	Val	Unk	Pro	Ile
1				5					10				15		
Thr	Arg	Ser	Val	Lys	Tyr	His	Gln	Gln	Ser	Ala	Glu	Ile	Arg	Ala	Leu
				20					25			30			
Gln	Leu	Gln	Ser	Tyr	Lys	Met	Ala	Lys	Met	Ala	Leu	Asp	Asn	Asn	Leu
				35				40			45				
Lys	Leu	Val	Lys	Asp	Lys	Lys	Pro	Ala	Val	Ile	Leu	Asp	Leu	Asp	Glu
				50				55			60				
Thr	Val	Leu	Asn	Thr	Phe	Asp	Tyr	Ala	Gly	Tyr	Leu	Val	Lys	Asn	Cys
				65				70		75			80		
Ile	Lys	Tyr	Thr	Pro	Glu	Thr	Trp	Asp	Lys	Phe	Glu	Lys	Glu	Gly	Ser
				85				90			95				
Leu	Thr	Leu	Ile	Pro	Gly	Ala	Leu	Asp	Phe	Leu	Glu	Tyr	Ala	Asn	Ser
				100				105			110				
Lys	Gly	Val	Lys	Ile	Phe	Tyr	Ile	Ser	Asn	Arg	Thr	Gln	Lys	Asn	Lys
				115				120			125				
Ala	Phe	Thr	Leu	Lys	Thr	Leu	Lys	Ser	Phe	Lys	Leu	Pro	Gln	Val	Ser
				130				135			140				
Glu	Glu	Ser	Val	Leu	Leu	Lys	Glu	Lys	Gly	Lys	Pro	Lys	Ala	Val	Arg
				145				150		155			160		
Arg	Glu	Leu	Val	Ala	Lys	Asp	Tyr	Ala	Ile	Val	Leu	Gln	Val	Gly	Asp
				165				170			175				
Thr	Leu	His	Asp	Phe	Asp	Ala	Ile	Phe	Ala	Lys	Asp	Ala	Lys	Asn	Ser
				180				185			190				
Gln	Glu	Gln	Ala	Lys	Val	Leu	Gln	Asn	Ala	Gln	Lys	Phe	Gly	Thr	
				195				200			205				
Glu	Trp	Ile	Ile	Leu	Pro	Asn	Ser	Leu	Tyr	Gly	Thr	Trp	Glu	Asp	Gly
				210				215			220				
Pro	Ile	Lys	Ala	Trp	Gln	Asn	Lys	Lys							
				225				230							

## (2) INFORMATION FOR SEQ ID NO:865:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865

Leu Ser Leu Met Unk Val Leu Asn Ala Lys Glu Cys Val Unk Pro Ile  
 1               5                   10                   15  
 Thr Arg Ser Val Lys Tyr His Gln Gln Ser Ala Glu Ile Arg Ala Leu  
 20              25                   30  
 Gln Leu Gln Ser Tyr Lys Met Ala Lys Met Ala Leu Asp Asn Asn Leu  
 35              40                   45  
 Lys Leu Val Lys Asp Lys Lys Pro Ala Val Ile Leu Asp Leu Asp Glu  
 50              55                   60  
 Thr Val Leu Asn Thr Phe Asp Tyr Ala Gly Tyr Leu Val Lys Asn Cys  
 65              70                   75                   80  
 Ile Lys Tyr Thr Pro Glu Thr Trp Asp Lys Phe Glu Lys Glu Gly Ser  
 85              90                   95  
 Leu Thr Leu Ile Pro Gly Ala Leu Asp Phe Leu Glu Tyr Ala Asn Ser  
 100            105                   110  
 Lys Gly Val Lys Ile Phe Tyr Ile Ser Asn Arg Thr Gln Lys Asn Lys  
 115            120                   125  
 Ala Phe Thr Leu Lys Thr Leu Lys Ser Phe Lys Leu Pro Gln Val Ser  
 130            135                   140  
 Glu Glu Ser Val Leu Leu Lys Glu Lys Gly Lys Pro Lys Ala Val Arg  
 145            150                   155                   160  
 Arg Glu Leu Val Ala Lys Asp Tyr Ala Ile Val Leu Gln Val Gly Asp  
 165            170                   175  
 Thr Leu His Asp Phe Asp Ala Ile Phe Ala Lys Asp Ala Lys Asn Ser  
 180            185                   190  
 Gln Glu Gln Gln Ala Lys Val Leu Gln Asn Ala Gln Lys Phe Gly Thr  
 195            200                   205  
 Glu Trp Ile Ile Leu Pro Asn Ser Leu Tyr Gly Thr Trp Glu Asp Gly  
 210            215                   220  
 Pro Ile Lys Ala Trp Gln Asn Lys Lys  
 225            230

(2) INFORMATION FOR SEQ ID NO:866:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866

Met Ile Tyr Gly Val Leu Asp Gly Leu Phe Leu Ala Ile Leu Gln Ala  
 1               5                   10                   15

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Gln Asn Tyr Arg Phe His Ser Leu Tyr Leu Phe Glu Glu Asn Leu Asp  
 20 25 30  
 Leu Phe Lys Ile Ser Cys Tyr Phe Ala Arg Tyr Glu Asp Leu Ile Lys  
 35 40 45  
 Lys Gly Ala Lys Leu Phe Ile Gln Gly Phe Phe Asn Pro Asn Glu Leu  
 50 55 60  
 Lys Met Asp Phe Leu Lys Arg Pro Ile Thr His Ser Phe Leu Lys Leu  
 65 70 75 80  
 Glu Ile Met Pro Tyr Lys Ser Ala Phe Asn Leu Arg Met Arg Glu Asn  
 85 90 95  
 Ile Gln Ser Tyr Tyr Lys Gln Ala Leu Arg Gly Trp Gly Ser Phe Glu  
 100 105 110  
 Asp Glu Leu Leu Gly Leu Lys Asn Thr Leu Lys Asn Leu Pro Leu Tyr  
 115 120 125  
 Gln Thr Leu Lys Thr Lys Pro Lys Lys Ile Asn Ala Pro Ile Cys Val  
 130 135 140  
 Val Gly Asn Gly Pro Ser Leu Asp Leu Leu Leu Asp Phe Leu Lys Glu  
 145 150 155 160  
 Asn Glu Glu Lys Phe Ile Ile Phe Ser Cys Gly Thr Ala Leu Lys Pro  
 165 170 175  
 Leu Lys Ala His Gly Val Lys Val Asp Phe Gln Ile Glu Val Glu Arg  
 180 185 190  
 Ile Asp Tyr Leu Lys Glu Val Leu Glu Arg Ala Pro Leu Glu Asp Thr  
 195 200 205  
 Pro Leu Met Gly Ala Asn Met Leu Asn Pro Asn Ala Phe Asp Leu Ala  
 210 215 220  
 Lys Glu Ala Leu Met Phe Met Arg Gly Gly Ser Ala Cys Ala Val  
 225 230 235

## (2) INFORMATION FOR SEQ ID NO:867:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 85 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867

Met Leu Ala Ala Gly Leu Thr Leu Pro Glu Phe Gly Cys Tyr Leu Ser  
 1 5 10 15  
 His Tyr Leu Leu Trp Lys Glu Cys Val Lys Leu Asp Gln Pro Val Val  
 20 25 30  
 Ile Leu Glu Asp Asp Val Thr Leu Glu Ser His Phe Met Gln Ala Leu  
 35 40 45  
 Glu Asp Cys Leu Lys Ser Pro Phe Asp Phe Val Arg Leu Tyr Gly Cys  
 50 55 60  
 Tyr Trp Tyr Tyr Gln Arg Asp Lys Ile Pro Cys Phe Ala Gln Arg Ile  
 65 70 75 80  
 Cys Ile Ser Ser Leu  
 85

## (2) INFORMATION FOR SEQ ID NO:867:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 85 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...85
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:867

Met Leu Ala Ala Gly Leu Thr Leu Pro Glu Phe Gly Cys Tyr Leu Ser  
 1 5 10 15  
 His Tyr Leu Leu Trp Lys Glu Cys Val Lys Leu Asp Gln Pro Val Val  
 20 25 30  
 Ile Leu Glu Asp Asp Val Thr Leu Glu Ser His Phe Met Gln Ala Leu  
 35 40 45  
 Glu Asp Cys Leu Lys Ser Pro Phe Asp Phe Val Arg Leu Tyr Gly Cys  
 50 55 60  
 Tyr Trp Tyr Tyr Gln Arg Asp Lys Ile Pro Cys Phe Ala Gln Arg Ile  
 65 70 75 80  
 Cys Ile Ser Ser Leu  
 85

## (2) INFORMATION FOR SEQ ID NO:868:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 289 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...289
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:868

Met Leu Ala Phe Leu Lys Thr Pro Arg Asn Ser Ala Phe Ala Leu Gly  
 1 5 10 15  
 Ile Phe Val Gly Ala Leu Leu Phe Tyr Trp Cys Ala Leu Arg Leu Ser  
 20 25 30  
 His Ser Asp Phe Thr Tyr Leu Leu Pro Leu Ile Ile Val Leu Val Ala  
 35 40 45  
 Leu Val Tyr Gly Val Leu Phe Tyr Leu Leu Tyr Phe Glu Asn Pro  
 50 55 60  
 Tyr Phe Arg Leu Leu Ser Phe Leu Gly Ser Ser Phe Ile His Pro Phe  
 65 70 75 80  
 Gly Phe Asp Trp Leu Val Pro Asp Ser Phe Phe Ser Tyr Ser Val Phe  
 85 90 95

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Arg Val Asp Lys Leu Ser Leu Gly Leu Ile Phe Leu Ala Cys Ile Phe  
 100 105 110  
 Leu Ser Ala Gln Asn Leu Lys Lys Tyr Arg Met Ile Gly Val Leu Leu  
 115 120 125  
 Leu Leu Gly Ala Leu Asp Phe His Phe Phe Lys Ile Ser Asp Leu Lys  
 130 135 140  
 Glu Val Gly Asn Ile Glu Leu Val Ser Thr Arg Thr Pro Gln Asp Leu  
 145 150 155 160  
 Lys Phe Asp Ser Asn Tyr Leu Asn Asn Ile Glu Asn Asn Ile Leu Lys  
 165 170 175  
 Glu Ile Lys Leu Ala Gln Ser Lys Gln Lys Thr Leu Ile Val Phe Pro  
 180 185 190  
 Glu Thr Ala Tyr Pro Ile Ala Leu Glu Asn Ser Pro Phe Lys Thr Gln  
 195 200 205  
 Leu Glu Asp Leu Ser Asp Lys Ile Ala Ile Leu Ile Gly Thr Leu Arg  
 210 215 220  
 Ala Gln Gly Tyr Ser Leu Tyr Asn Ser Ser Phe Leu Phe Ser Lys Lys  
 225 230 235 240  
 Ser Val Gln Ile Ala Asp Lys Val Ile Leu Ala Pro Phe Gly Glu Ile  
 245 250 255  
 Met Pro Leu Pro Glu Phe Leu Gln Lys Pro Leu Glu Lys Leu Phe Phe  
 260 265 270  
 Ala Arg Ala Leu Ile Tyr Thr Ala Thr Leu Pro Ile Ser Ala Ile Leu  
 275 280 285  
 His

## (2) INFORMATION FOR SEQ ID NO:869:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...436

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:869

Met Asn Asp Pro Lys His Val Val Tyr Val Trp Leu Asp Ala Leu Leu  
 1 5 10 15  
 Asn Tyr Ala Ser Ala Leu Gly Tyr Leu Asn Gly Leu Asp Asn Lys Met  
 20 25 30  
 Ala His Phe Glu Arg Ala Arg His Ile Val Gly Lys Asp Ile Leu Arg  
 35 40 45  
 Phe His Ala Ile Tyr Trp Pro Ala Phe Leu Met Ser Leu Asn Leu Pro  
 50 55 60  
 Leu Phe Lys Gln Leu Cys Val His Gly Trp Trp Thr Ile Glu Gly Val  
 65 70 75 80  
 Lys Met Ser Lys Ser Leu Gly Asn Val Leu Asp Ala Gln Lys Leu Ala  
 85 90 95  
 Met Glu Tyr Gly Ile Glu Glu Leu Arg Tyr Phe Leu Leu Arg Glu Val  
 100 105 110  
 Pro Phe Gly Gln Asp Gly Asp Phe Ser Lys Lys Ala Leu Val Glu Arg  
 115 120 125  
 Ile Asn Ala Asn Leu Asn Asn Asp Leu Gly Asn Leu Leu Asn Arg Leu

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130	135	140
Leu	Gly Met Ala Lys Lys Tyr Phe Asn Tyr Ser Leu Lys Ser Thr Lys	
145	150	155
Ile	Thr Ala Tyr Tyr Pro Lys Glu Leu Glu Lys Ala His Gln Ile Leu	160
	165	170
Asp	Asn Ala Asn Ser Phe Val Pro Lys Met Gln Leu His Lys Ala Leu	
	180	185
Glu	Glu Leu Phe Asn Ile Tyr Asp Phe Leu Asn Lys Leu Ile Ala Lys	
	195	200
Glu	Glu Pro Trp Val Leu His Lys Asn Asn Glu Ser Glu Lys Leu Glu	
	210	215
Ala	Leu Leu Ser Leu Ile Ala Asn Thr Leu Leu Gln Ser Ser Phe Leu	
	225	230
Leu	Tyr Ala Phe Met Pro Lys Ser Ala Met Lys Leu Ala Ser Ala Phe	
	245	250
Arg	Val Glu Ile Thr Pro Asn Asn Tyr Glu Arg Phe Phe Lys Ala Lys	
	260	265
Lys	Leu Gln Asp Met Val Leu Gln Asp Thr Glu Pro Leu Phe Ser Lys	
	275	280
Ile	Glu Lys Ile	
	290	295
Glu	Lys Gly Glu Glu Ala Leu Ala Glu Lys Ala Glu Lys Lys Glu Lys	
	305	310
Glu	Lys Ala Pro Pro Thr Gln Glu Asn Tyr Ile Ser Ile Glu Asp Phe	
	325	330
Lys	Lys Val Glu Ile Lys Val Gly Leu Ile Lys Glu Ala Gln Arg Ile	
	340	345
Glu	Lys Ser Asn Lys Leu Leu Arg Leu Lys Val Asp Leu Gly Glu Asn	
	355	360
Arg	Leu Arg Gln Ile Ile Ser Gly Ile Ala Leu Asp Tyr Glu Pro Glu	
	370	375
Ser	Leu Val Gly Gln Met Val Cys Val Val Ala Asn Leu Lys Pro Ala	
	385	390
Lys	Leu Met Gly Glu Met Ser Glu Gly Met Ile Leu Ala Val Arg Asp	
	405	410
Asn	Asp Asn Leu Ala Leu Ile Ser Pro Thr Arg Glu Lys Ile Ala Gly	
	420	425
Ser	Leu Ile Ser	
	435	

## (2) INFORMATION FOR SEQ ID NO:870:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...114

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:870

Met	Lys Arg Pro Ile Ser Lys Leu Lys Gln Asn Phe Leu Gln Phe Lys	
1	5	10
His	Ser Phe Asn Lys His Leu Asp Lys Tyr Ser Leu Tyr Tyr Arg Leu	15
	20	25
		30

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Phe Asn Ile Ser Ser Ile Val Ile Gly Phe Leu Ile Ala Leu Phe Ser  
 35 40 45  
 Tyr Gly Ala Gly Val Ile Leu Val Tyr Pro Ile Leu Phe Leu Phe Ala  
 50 55 60  
 Leu Ile Ile Lys Pro Ser Phe Phe Tyr Tyr Thr Tyr Leu Leu Leu  
 65 70 75 80  
 Leu Val Ser Leu Ser Ile Ile Ser Lys Tyr Tyr Leu Leu Ser His Ala  
 85 90 95  
 Asn Phe Thr Met Lys Leu Ile Met Leu Met Thr Gln Trp Gln Asn Trp  
 100 105 110  
 Phe Leu

## (2) INFORMATION FOR SEQ ID NO:871:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...173

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:871

Met Gly Phe Glu Lys Ser Ile Leu Asp Asn Leu Asn Gly Ala Gln Lys  
 1 5 10 15  
 Ile Val Ala Cys His Ile Gln Gly Pro Leu Leu Ile Leu Ala Gly Ala  
 20 25 30  
 Gly Ser Gly Lys Thr Lys Thr Leu Thr Ser Arg Leu Ala Tyr Leu Ile  
 35 40 45  
 Gly Ala Cys Gly Val Pro Ser Glu Asn Thr Leu Thr Leu Thr Phe Thr  
 50 55 60  
 Asn Lys Ala Ser Lys Glu Met Gln Glu Arg Ala Leu Lys Leu Lys  
 65 70 75 80  
 Asn Gln Ala Leu Ile Pro Pro Leu Leu Cys Thr Phe His Arg Phe Gly  
 85 90 95  
 Leu Leu Phe Leu Arg Gln His Met Asn Leu Leu Lys Arg Ala Cys Asp  
 100 105 110  
 Phe Ser Val Leu Asp Ser Asp Glu Val Lys Thr Leu Cys Lys Gln Leu  
 115 120 125  
 Lys Ile Ser Asn Phe Arg Ala Ser Ile Ser Gln Ile Lys Asn Gly Met  
 130 135 140  
 Met Asp Leu Ser Val Gln Asp Ser Glu Cys Tyr Lys Ala Tyr Glu Leu  
 145 150 155 160  
 Tyr Gln Asn Ala Leu Lys Lys Asp Asn Leu Val Glu Phe  
 165 170

## (2) INFORMATION FOR SEQ ID NO:872:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872

Leu	Ile	Ala	Leu	Arg	Val	Thr	Ala	Trp	Lys	Val	Unk	Ala	Met	Lys	Arg
1			5					10					15		
Leu	His	Leu	Ser	Val	Lys	Asp	Ala	Glu	Asn	Phe	Asp	Ala	Ile	Leu	Arg
	20				25								30		
Glu	Arg	Pro	Phe	Phe	Lys	Asp	Leu	Ile	Glu	Phe	Met	Val	Ser	Gly	Pro
	35				40				45						
Val	Val	Val	Met	Val	Leu	Glu	Gly	Lys	Asp	Ala	Val	Ala	Lys	Asn	Arg
	50				55				60						
Glu	Leu	Met	Gly	Ala	Thr	Asp	Pro	Lys	Leu	Ala	Gln	Lys	Gly	Thr	Ile
	65				70				75				80		
Arg	Ala	Asp	Phe	Ala	Glu	Ser	Ile	Asp	Ala	Asn	Ala	Val	His	Gly	Ser
	85				90					95					
Asp	Ser	Leu	Glu	Asn	Ala	His	Asn	Glu	Ile	Ala	Phe	Phe	Ala	Ala	
	100				105			105					110		
Arg	Glu	Phe													
	115														

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872

Leu	Ile	Ala	Leu	Arg	Val	Thr	Ala	Trp	Lys	Val	Unk	Ala	Met	Lys	Arg
1			5					10					15		
Leu	His	Leu	Ser	Val	Lys	Asp	Ala	Glu	Asn	Phe	Asp	Ala	Ile	Leu	Arg
	20				25			25					30		
Glu	Arg	Pro	Phe	Phe	Lys	Asp	Leu	Ile	Glu	Phe	Met	Val	Ser	Gly	Pro
	35				40				45						
Val	Val	Val	Met	Val	Leu	Glu	Gly	Lys	Asp	Ala	Val	Ala	Lys	Asn	Arg
	50				55				60						
Glu	Leu	Met	Gly	Ala	Thr	Asp	Pro	Lys	Leu	Ala	Gln	Lys	Gly	Thr	Ile
	65				70				75				80		
Arg	Ala	Asp	Phe	Ala	Glu	Ser	Ile	Asp	Ala	Asn	Ala	Val	His	Gly	Ser
	85				90					95					
Asp	Ser	Leu	Glu	Asn	Ala	His	Asn	Glu	Ile	Ala	Phe	Phe	Ala	Ala	
	100				105			105					110		

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Arg Glu Phe  
115

## (2) INFORMATION FOR SEQ ID NO:873:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873

Val	Phe	Thr	Tyr	Ser	Leu	Gly	Gln	Val	Phe	Phe	Ser	Leu	Ser	Ile	Gly
1				5					10				15		
Leu	Gly	Ile	Asn	Ile	Thr	Tyr	Ala	Ala	Val	Thr	Asp	Lys	Thr	Gln	Asn
					20				25				30		
Leu	Leu	Lys	Ser	Thr	Ile	Trp	Val	Val	Leu	Ser	Gly	Ile	Leu	Ile	Ser
					35				40				45		
Leu	Val	Unk	Gly	Leu	Met	Ile	Phe	Thr	Phe	Val	Phe	Glu	Tyr	Gly	Ala
					50			55			60				
Asn	Val	Ser	Gln	Gly	Thr	Gly	Leu	Ile	Phe	Thr	Ser	Leu	Pro	Val	Val
					65			70			75			80	
Phe	Gly	Gln	Met	Gly	Ala	Ile	Gly	Val	Pro	Cys	Phe	Asn	Ser	Phe	Leu
					85			90			95				
Ala	Arg	Ala	Arg	Phe	Cys	Trp	His	His	Phe	Tyr	Gly	Gly	Phe	Ile	Arg
					100			105			110				
Ala	Lys	Arg	Asp	Val	Ser	Tyr	Arg	Lys	Val	Ser	Ile	Leu	Ser	Phe	
					115			120			125				

## (2) INFORMATION FOR SEQ ID NO:874:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874

Met	Lys	Pro	Leu	His	Phe	Ser	His	Leu	Asp	Arg	Glu	Gln	Ser	Gly	Asp
1					5				10			15			
Val	Gly	Phe	Ile	Ile	Lys	Asn	Leu	Ile	Phe	Leu	Gly	Val	Phe	Ser	Leu

729

20	25	30													
Leu	Gly	Trp	Leu	Asn	Thr	Glu	Tyr	Phe	Leu	Trp	Pro	Ser	Met	Leu	Glu
35						40							45		
Leu	Lys	Lys	Ile	Leu	Leu	Glu	Glu	Asn	Arg	Lys	Lys	Ser	Val	Leu	Glu
50						55						60			
Tyr	Ala	Gln	Arg	His	Phe	Glu	Thr	Ala	Leu	Ala	Asn	Tyr	Arg	Asn	Gln
65					70				75			80			
Lys	Glu	Thr	Ser	Glu	Ser	Leu	Leu	Lys	Ile	Phe	Asn	Asp	Glu	Glu	Ser
85						90						95			
Arg	Arg	Ile	Leu	Glu	Lys	Ile	Leu	Lys	Lys	Cys	Phe	Asp	Ala	Tyr	Lys
100						105						110			
Ile	Lys	Pro	Leu	Leu	Ser	Gln	Asn	Pro	Ser	Gln	Lys	Thr	Gln	Phe	Phe
115						120						125			
Ile	Met	Ala	Arg	Ala	Ser	Glu	Leu	Glu	Lys	Thr	Tyr	Leu	Phe	Phe	Thr
130						135						140			
Leu	Ile	Asn	Lys	Tyr	Leu										
145						150									

## (2) INFORMATION FOR SEQ ID NO:875:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...209

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:875

Met	Asn	Ala	Leu	Lys	Arg	Ala	Cys	Leu	Arg	Leu	Met	Gly	Glu	Thr	Asn
1								5			10			15	
Thr	Asp	Asp	Leu	Unk	Pro	Unk	Ser	Asp	Ala	Phe	Thr	Arg	Ser	Asp	Ile
								20			25			30	
Pro	Leu	His	Ala	Lys	Ala	Met	Leu	Lys	Asn	Arg	Ile	Glu	Asn	Tyr	Glu
								35			40			45	
Gln	Arg	Ile	Glu	Ala	Ile	Lys	Thr	Lys	Gly	Val	Pro	Val	Ala	Tyr	Val
								50			55			60	
Gly	Asp	Val	Val	Gly	Thr	Gly	Ser	Ser	Arg	Lys	Ser	Ala	Thr	Asn	Ser
								65			70			75	
Ile	Met	Trp	His	Phe	Gly	Lys	Asp	Ile	Pro	Phe	Val	Pro	Asn	Lys	Arg
								85			90			95	
Ser	Gly	Gly	Ile	Val	Ile	Gly	Gly	Val	Ile	Ala	Pro	Ile	Phe	Phe	Ala
								100			105			110	
Thr	Cys	Glu	Asp	Ser	Gly	Ala	Leu	Pro	Ile	Val	Ala	Asp	Val	Lys	Asp
								115			120			125	
Leu	Lys	Glu	Gly	Asp	Ile	Ile	Lys	Ile	Tyr	Pro	Tyr	Lys	Gly	Glu	Ile
								130			135			140	
Thr	Leu	Asn	Asp	Lys	Val	Val	Ser	Thr	Phe	Lys	Leu	Glu	Pro	Glu	Thr
								145			150			155	
Leu	Leu	Asp	Glu	Val	Arg	Ala	Ser	Gly	Arg	Ile	Pro	Leu	Ile	Ile	Gly
								165			170			175	
Arg	Gly	Leu	Thr	Asn	Lys	Ala	Arg	Lys	Phe	Leu	Gly	Arg	Arg	Ile	Gly
								180			185			190	
Ser	Val	Gln	Lys	Thr	Phe	Arg	Pro	Ser	Ser	Ala	Leu	Arg	Leu	His	Phe
								195			200			205	

730

Ala

## (2) INFORMATION FOR SEQ ID NO:876:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876

Met	Leu	Ser	Ala	His	Gln	Pro	Phe	Lys	Asn	Tyr	Pro	Asp	Leu	Ile	Lys
1					5			10					15		
Lys	Glu	Leu	Gln	Glu	His	Asn	Ala	Tyr	Ala	Ser	Val	Ala	Ser	Gly	Val
					20			25				30			
Pro	Ala	Met	Cys	Asp	Gly	Ile	Thr	Gln	Gly	Tyr	Glu	Gly	Met	Glu	Leu
		35				40					45				
Ser	Leu	Phe	Ser	Arg	Asp	Val	Ile	Ala	Leu	Ser	Thr	Unk	Val	Gly	Leu
	50					55				60					
Ser	His	Asn	Val	Phe	Asp	Gly	Ala	Phe	Phe	Leu	Gly	Val	Cys	Asp	Lys
	65				70				75			80			
Ile	Val	Pro	Gly	Leu	Leu	Ile	Gly	Ala	Leu	Ser	Phe	Gly	Asn	Leu	Ala
		85				90				95					
Ser	Val	Phe	Val	Pro	Ser	Gly	Pro	Met	Val	Ser	Gly	Ile	Glu	Asn	Tyr
	100					105			110						
Lys	Lys	Ala	Arg	Gln	Asp	Phe	Ala	Met	Gly	Lys	Ile	Asn	Arg		
	115					120			125						
Glu	Glu	Leu	Leu	Lys	Val	Glu	Met	Gln	Ser	Tyr	His	Asp	Val	Gly	Thr
	130					135			140						
Cys	Thr	Phe	Tyr	Gly	Thr	Ala	Asn	Ser	Asn	Gln	Met	Met	Met	Glu	Phe
	145					150				155			160		
Met	Gly	Leu	His	Val	Ala	Asn	Ser	Ser	Phe	Ile	Asn	Pro	Asn	Asn	Pro
		165					170				175				
Leu	Arg	Lys	Val	Leu	Val	Glu	Glu	Ser	Ala	Lys	Arg	Leu	Ala	Ser	Gly
		180				185				190					
Lys	Val	Leu	Pro	Leu	Ala	Lys	Leu	Ile	Asp	Glu	Lys	Ser	Ile	Leu	Asn
	195					200				205					
Ala	Leu	Ile	Gly	Leu	Met	Ala	Thr	Gly	Gly	Ser	Thr	Asn	His	Thr	Leu
	210				215					220					
His	Leu	Ile	Ala	Ile	Ala	Asp	Leu	Val	Gly						
	225					230									

## (2) INFORMATION FOR SEQ ID NO:877:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877

Leu Met Trp Leu Lys Thr Leu Thr Leu Gln Thr Leu Asn Thr Asp Lys  
 1               5               10               15  
 Ala Leu Gln Glu Phe Ser Lys Thr Met Glu Ala Phe Lys Thr Lys Leu  
 20              25              30  
 Ile Gln Ser Ala Asn Asp Val His Ser Glu Thr Ser Arg Ala Ala Ile  
 35              40              45  
 Ala Asn Asp Leu Glu Arg Leu Lys Glu His Met Ile Asn Val Ala Asn  
 50              55              60  
 Thr Ser Ile Gly Gly Glu Phe Leu Phe Gly Gly Ser Lys Val Asp Arg  
 65              70              75              80  
 Pro Pro Ile Asp Ser Asn Gly Lys Tyr His Gly Asn Gly Glu Asp Leu  
 85              90              95  
 Asn Ala Leu Ile Ser Ser Asp Asn Leu Val Pro Tyr Asn Ile Ser Gly  
 100             105             110  
 Gln Asp Leu Phe Leu Gly Thr Asp Lys Asp Lys His Lys Leu Ile Thr  
 115             120             125  
 Thr Asn Ile Lys Leu Leu Asn Gln Asn Lys Leu Unk Pro Asp Val Met  
 130             135             140  
 Asp Ala Leu Glu His Ser Ser Leu Pro Glu Glu Val Phe Ile Lys Pro  
 145             150             155             160  
 Ser Asp Thr Leu Arg Glu Leu Ile Gly Asp Asn Asp Lys Asn Pro Thr  
 165             170             175  
 Asn Asp Pro Lys Glu Phe Phe Tyr Leu Gln Gly Ile Arg Pro Asp Gly  
 180             185             190  
 Ser Ser Phe Lys Glu Lys Phe Ala Leu Asp Lys Ala Tyr Gln Asn Gln  
 195             200             205  
 Glu Ser Ala Thr Lys Val Ser Asp Leu Leu Asp Lys Ile Gly His Ala  
 210             215             220  
 Tyr Gly Asn Thr Ser Gln Asn Lys Val Val Asp Val Ser Leu Asn Asn  
 225             230             235             240  
 Trp Gly Gln Ile Glu Ile Lys Asn Leu Thr Pro Gly Ser Glu Asn Leu  
 245             250             255  
 Asp Phe His Leu Ile Ser Ser Asp Gly Asp Phe Asp Asp Leu Asp Ala  
 260             265             270  
 Leu Arg Ser Ser Gly Lys Arg Val Thr Glu Tyr Val Lys Ser Ala Phe  
 275             280             285  
 Val Thr Asp Arg Ser Leu Ser Gln Val Lys Ala Val Pro Asn Met Tyr  
 290             295             300  
 Asn Pro Lys Val Leu Glu Ile Pro Ser Val Phe Val Thr Lys Asp Asn  
 305             310             315             320  
 Val Leu Ala Asn Lys Asn Thr Lys Leu Ser Glu Ile Phe Gly Asp Lys  
 325             330             335  
 Val Glu Thr Leu Lys Ile Asn Ala Ser Arg Leu Gly Asp Glu Ser Ala  
 340             345             350  
 Ile Lys Ile Pro Asn Leu Pro Ile Asn Leu Asp Ile Pro Ile Leu Leu  
 355             360             365  
 Asp Val Lys Asn Ser Thr Ile Lys Asp Leu Lys Asp Ala Ile Lys Glu  
 370             375             380  
 Arg Phe Asn Asn Glu Gly Gly Cys Gly Asn  
 385             390

(2) INFORMATION FOR SEQ ID NO:877:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 394 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...394
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:877

Leu Met Trp Leu Lys Thr Leu Thr Leu Gln Thr Leu Asn Thr Asp Lys  
 1               5                           10                           15  
 Ala Leu Gln Glu Phe Ser Lys Thr Met Glu Ala Phe Lys Thr Lys Leu  
 20               25                           30  
 Ile Gln Ser Ala Asn Asp Val His Ser Glu Thr Ser Arg Ala Ala Ile  
 35               40                           45  
 Ala Asn Asp Leu Glu Arg Leu Lys Glu His Met Ile Asn Val Ala Asn  
 50               55                           60  
 Thr Ser Ile Gly Gly Glu Phe Leu Phe Gly Gly Ser Lys Val Asp Arg  
 65               70                           75                           80  
 Pro Pro Ile Asp Ser Asn Gly Lys Tyr His Gly Asn Gly Glu Asp Leu  
 85               90                           95  
 Asn Ala Leu Ile Ser Ser Asp Asn Leu Val Pro Tyr Asn Ile Ser Gly  
 100              105                           110  
 Gln Asp Leu Phe Leu Gly Thr Asp Lys Asp Lys His Lys Leu Ile Thr  
 115              120                           125  
 Thr Asn Ile Lys Leu Leu Asn Gln Asn Lys Leu Unk Pro Asp Val Met  
 130              135                           140  
 Asp Ala Leu Glu His Ser Ser Leu Pro Glu Glu Val Phe Ile Lys Pro  
 145              150                           155                           160  
 Ser Asp Thr Leu Arg Glu Leu Ile Gly Asp Asn Asp Lys Asn Pro Thr  
 165              170                           175  
 Asn Asp Pro Lys Glu Phe Phe Tyr Leu Gln Gly Ile Arg Pro Asp Gly  
 180              185                           190  
 Ser Ser Phe Lys Glu Lys Phe Ala Leu Asp Lys Ala Tyr Gln Asn Gln  
 195              200                           205  
 Glu Ser Ala Thr Lys Val Ser Asp Leu Leu Asp Lys Ile Gly His Ala  
 210              215                           220  
 Tyr Gly Asn Thr Ser Gln Asn Lys Val Val Asp Val Ser Leu Asn Asn  
 225              230                           235                           240  
 Trp Gly Gln Ile Glu Ile Lys Asn Leu Thr Pro Gly Ser Glu Asn Leu  
 245              250                           255  
 Asp Phe His Leu Ile Ser Ser Asp Gly Asp Phe Asp Asp Leu Asp Ala  
 260              265                           270  
 Leu Arg Ser Ser Gly Lys Arg Val Thr Glu Tyr Val Lys Ser Ala Phe  
 275              280                           285  
 Val Thr Asp Arg Ser Leu Ser Gln Val Lys Ala Val Pro Asn Met Tyr  
 290              295                           300  
 Asn Pro Lys Val Leu Glu Ile Pro Ser Val Phe Val Thr Lys Asp Asn  
 305              310                           315                           320  
 Val Leu Ala Asn Lys Asn Thr Lys Leu Ser Glu Ile Phe Gly Asp Lys  
 325              330                           335  
 Val Glu Thr Leu Lys Ile Asn Ala Ser Arg Leu Gly Asp Glu Ser Ala  
 340              345                           350  
 Ile Lys Ile Pro Asn Leu Pro Ile Asn Leu Asp Ile Pro Ile Leu Leu  
 355              360                           365  
 Asp Val Lys Asn Ser Thr Ile Lys Asp Leu Lys Asp Ala Ile Lys Glu

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370	375	380
Arg Phe Asn Asn Glu Gly	Gly Cys Gly Asn	
385	390	

## (2) INFORMATION FOR SEQ ID NO:878:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...102

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:878

Leu Lys Ala Leu Asn Asp Cys Met Val Phe Phe His Lys Lys Ile Ile			
1	5	10	15
Leu Asn Phe Ile Tyr Ser Leu Met Val Ala Phe Leu Phe His Leu Ser			
20	25	30	
Tyr Gly Val Leu Leu Lys Ala Asp Gly Met Ala Lys Lys Gln Thr Leu			
35	40	45	
Leu Val Gly Glu Arg Leu Val Trp Asp Lys Leu Thr Leu Leu Gly Phe			
50	55	60	
Leu Glu Lys Asn His Ile Pro Gln Lys Leu Tyr Tyr Asn Leu Ser Ser			
65	70	75	80
Gln Asp Lys Glu Leu Ser Ala Glu Ile Gln Ser Asn Val Thr Tyr Tyr			
85	90	95	
Unk Phe Lys Arg Cys Lys			
100			

## (2) INFORMATION FOR SEQ ID NO:878:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...102

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:878

Leu Lys Ala Leu Asn Asp Cys Met Val Phe Phe His Lys Lys Ile Ile			
1	5	10	15
Leu Asn Phe Ile Tyr Ser Leu Met Val Ala Phe Leu Phe His Leu Ser			
20	25	30	

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Tyr Gly Val Leu Leu Lys Ala Asp Gly Met Ala Lys Lys Gln Thr Leu  
 35                  40                  45  
 Leu Val Gly Glu Arg Leu Val Trp Asp Lys Leu Thr Leu Leu Gly Phe  
 50                  55                  60  
 Leu Glu Lys Asn His Ile Pro Gln Lys Leu Tyr Tyr Asn Leu Ser Ser  
 65                  70                  75                  80  
 Gln Asp Lys Glu Leu Ser Ala Glu Ile Gln Ser Asn Val Thr Tyr Tyr  
 85                  90                  95  
 Unk Phe Lys Arg Cys Lys  
 100

## (2) INFORMATION FOR SEQ ID NO:879:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...265

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:879

Met Lys Phe Leu Lys Phe Phe Ala Ser Ser Val Thr Leu Asp Glu Lys  
 1                  5                  10                  15  
 Phe Leu Met Phe Leu Leu Cys Asn Ala Leu Ser Asn Ala Tyr Lys Asn  
 20                  25                  30  
 Ser Asp Leu Phe Ser Phe Ser Lys Gly Phe Leu Gly Ala Phe Leu Ile  
 35                  40                  45  
 Gly Phe Val Val Tyr Tyr Gly Cys Ala Leu Ile Pro Lys Lys Arg Leu  
 50                  55                  60  
 Lys Tyr Ser Leu Glu Trp Leu Phe Ile Gly Ser Gly Ile Ile Phe Ser  
 65                  70                  75                  80  
 Val Ala Glu Ile Phe Thr Leu Phe Met Phe Lys Met Pro Phe Ser Lys  
 85                  90                  95  
 Gly Leu Ile Asp Thr Leu Leu Ala Thr Asn Ser Ser Glu Thr Met Ala  
 100                105                110  
 Phe Ile Lys Ser Tyr Lys Asn Tyr Leu Leu Tyr Tyr Ala Leu Ile Leu  
 115                120                125  
 Ile Ala Leu Leu Ile Ala Ile Lys Ile Ile Arg Phe Arg Ala Leu Val  
 130                135                140  
 Pro Gly Val Ile Ala Ser Val Leu Gly Leu Ser Ile Leu Thr Ile Gly  
 145                150                155                160  
 Ser Val Arg Asn Ile Lys His Leu Thr Lys Asn Asp Ala Ile Leu Lys  
 165                170                175  
 Arg Ser Leu Phe Ser Leu Ser Leu Ala Arg Gly Phe Tyr Ser Ala Tyr  
 180                185                190  
 Leu Ser Leu Phe Asp Arg Gln Gln Ala Ile Lys Phe Tyr Ser Phe Leu  
 195                200                205  
 Asn Asn Leu Tyr Leu Pro Ser Asp Tyr Leu Ser Ser Thr Gly Asp Ile  
 210                215                220  
 Ser Asn Val Val Leu Val Ile Ala Lys Ala Arg Ala Glu Ile Ser Cys  
 225                230                235                240  
 Asn Ser Met Ala Ile Ala Phe Leu Ile Ile Pro Tyr Thr Ser Glu Leu  
 245                250                255  
 Ala Asn Glu Arg Glu Arg Glu

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## (2) INFORMATION FOR SEQ ID NO:880:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...363

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:880

Met	Lys	Phe	Phe	Leu	Leu	Lys	Phe	Ser	Unk	Phe	Leu	Asn	Thr	Gln	
1				5					10				15		
Thr	His	Phe	Asn	Leu	Lys	Arg	Leu	Asn	Ala	Ser	Ser	Phe	Leu	Leu	Glu
				20				25					30		
Thr	Phe	Ser	Lys	Glu	Lys	His	Ala	Phe	Val	Val	Asp	Leu	Ser	Ala	Pro
				35			40				45				
Tyr	Ile	Gly	Leu	Ser	Lys	Lys	Pro	Pro	Glu	Ser	Val	Leu	Lys	Asn	Thr
				50			55			60					
Leu	Ala	Leu	Asp	Phe	Cys	Leu	Asn	Lys	Phe	Thr	Lys	Asn	Ala	Lys	Ile
65				70			75			80					
Leu	Gln	Ala	Asn	Val	Ile	Asp	Asn	Asp	Arg	Ile	Leu	Glu	Ile	Lys	Gly
				85			90			95					
Ala	Lys	Asp	Leu	Ala	Tyr	Lys	Ser	Glu	Thr	Phe	Ile	Leu	Arg	Leu	Glu
				100			105			110					
Met	Ile	Pro	Lys	Lys	Ala	Asn	Leu	Met	Ile	Leu	Asp	Gln	Glu	Lys	Cys
				115			120			125					
Val	Ile	Glu	Ala	Phe	Arg	Phe	Asn	Asp	Arg	Val	Ala	Lys	Asn	Asp	Ile
				130			135			140					
Leu	Gly	Ala	Leu	Pro	Pro	Asn	Ile	Tyr	Glu	His	Gln	Glu	Glu	Asp	Leu
145				150			155				160				
Asp	Phe	Lys	Gly	Leu	Leu	Asp	Ile	Leu	Glu	Lys	Asp	Phe	Leu	Ser	Tyr
				165			170			175					
Gln	His	Lys	Glu	Leu	Glu	His	Lys	Lys	Asn	Gln	Ile	Ile	Lys	Arg	Leu
				180			185			190					
Asn	Ala	Gln	Lys	Glu	Arg	Leu	Lys	Glu	Lys	Leu	Glu	Lys	Leu	Glu	Asp
				195			200			205					
Pro	Lys	Thr	Leu	Gln	Leu	Glu	Ala	Lys	Glu	Leu	Gln	Thr	Gln	Ala	Ser
				210			215			220					
Leu	Leu	Leu	Thr	Tyr	Gln	His	Leu	Ile	Asn	Arg	Arg	Glu	Asn	Arg	Val
225				230			235				240				
Ile	Leu	Lys	Asp	Phe	Glu	Asp	Lys	Glu	Cys	Met	Ile	Glu	Ile	Asp	Lys
				245			250			255					
Ser	Met	Pro	Leu	Asn	Ala	Phe	Ile	Asn	Lys	Phe	Thr	Leu	Ser	Lys	
				260			265			270					
Lys	Lys	Lys	Gln	Lys	Ser	Gln	Phe	Leu	Tyr	Leu	Glu	Glu	Asn	Leu	
				275			280			285					
Lys	Glu	Lys	Ile	Ala	Phe	Lys	Glu	Asn	Gln	Ile	Asn	Tyr	Val	Arg	Asp
				290			295			300					
Ala	Ala	Glu	Glu	Ser	Val	Leu	Glu	Met	Phe	Met	Pro	Val	Lys	Asn	Ser
305				310			315			320					
Lys	Ile	Lys	Arg	Pro	Met	Asn	Gly	Tyr	Glu	Val	Leu	Tyr	Tyr	Lys	Asp
				325			330			335					

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Unk	Lys	Unk	Gly	Leu	Gly	Lys	Thr	Lys	Lys	Arg	Ile	Ser	Ser	Phe	Tyr
				340		345				350					
Lys	Thr	Gln	Unk	Arg	Met	Ile	Unk	Gly	Cys	Unk					
				355		360									

## (2) INFORMATION FOR SEQ ID NO:880:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...363

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:880

Met Lys Phe Phe Leu Leu Lys Phe Ser Unk Phe Leu Asn Thr Gln  
 1               5                           10                       15  
 Thr His Phe Asn Leu Lys Arg Leu Asn Ala Ser Ser Phe Leu Leu Glu  
 20               25                           30  
 Thr Phe Ser Lys Glu Lys His Ala Phe Val Val Asp Leu Ser Ala Pro  
 35               40                           45  
 Tyr Ile Gly Leu Ser Lys Pro Pro Glu Ser Val Leu Lys Asn Thr  
 50               55                           60  
 Leu Ala Leu Asp Phe Cys Leu Asn Lys Phe Thr Lys Asn Ala Lys Ile  
 65               70                           75                       80  
 Leu Gln Ala Asn Val Ile Asp Asn Asp Arg Ile Leu Glu Ile Lys Gly  
 85               90                           95  
 Ala Lys Asp Leu Ala Tyr Lys Ser Glu Thr Phe Ile Leu Arg Leu Glu  
 100              105                           110  
 Met Ile Pro Lys Lys Ala Asn Leu Met Ile Leu Asp Gln Glu Lys Cys  
 115              120                           125  
 Val Ile Glu Ala Phe Arg Phe Asn Asp Arg Val Ala Lys Asn Asp Ile  
 130              135                           140  
 Leu Gly Ala Leu Pro Pro Asn Ile Tyr Glu His Gln Glu Glu Asp Leu  
 145              150                           155                   160  
 Asp Phe Lys Gly Leu Leu Asp Ile Leu Glu Lys Asp Phe Leu Ser Tyr  
 165              170                           175  
 Gln His Lys Glu Leu Glu His Lys Lys Asn Gln Ile Ile Lys Arg Leu  
 180              185                           190  
 Asn Ala Gln Lys Glu Arg Leu Lys Glu Lys Leu Glu Lys Leu Glu Asp  
 195              200                           205  
 Pro Lys Thr Leu Gln Leu Glu Ala Lys Glu Leu Gln Thr Gln Ala Ser  
 210              215                           220  
 Leu Leu Leu Thr Tyr Gln His Leu Ile Asn Arg Arg Glu Asn Arg Val  
 225              230                           235                   240  
 Ile Leu Lys Asp Phe Glu Asp Lys Glu Cys Met Ile Glu Ile Asp Lys  
 245              250                           255  
 Ser Met Pro Leu Asn Ala Phe Ile Asn Lys Lys Phe Thr Leu Ser Lys  
 260              265                           270  
 Lys Lys Lys Gln Lys Ser Gln Phe Leu Tyr Leu Glu Glu Asn Leu  
 275              280                           285  
 Lys Glu Lys Ile Ala Phe Lys Glu Asn Gln Ile Asn Tyr Val Arg Asp  
 290              295                           300  
 Ala Ala Glu Glu Ser Val Leu Glu Met Phe Met Pro Val Lys Asn Ser

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305	310	315	320
Lys Ile Lys Arg Pro Met Asn Gly Tyr Glu Val Leu Tyr Tyr Lys Asp			
325	330	335	
Unk Lys Unk Gly Leu Gly Lys Thr Lys Lys Arg Ile Ser Ser Phe Tyr			
340	345	350	
Lys Thr Gln Unk Arg Met Ile Unk Gly Cys Unk			
355	360		

## (2) INFORMATION FOR SEQ ID NO:995:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 822 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...822
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:995

GACGCCACGTA	GTTCCTTTT	AAGATTGGTA	GCTATGGCAT	TATGTTTGAT	CTTAATTAAAT	60
AGTAGAGGAG	TAGCGATGGG	ATACGCAAGC	AAATTAGCTT	AAAGATTTG	TTTGGTAGGT	120
TTATGTTTAT	TTAGCACCCCT	TGGTGACGAA	CACCTTGAGC	AAAAAGGGAA	TTATATTTAT	180
AAGGGAGGAG	AGGCTTATAA	TAATAAGGAA	TATGAGCGAG	CGGCTTCTTT	TTATAAGAGC	240
GCTATTTAAA	ATGGTGAGTC	GCTTGCTTAT	ATTCTTTAG	GGATCATGTA	TGAAAATGGT	300
AGGGGTGTAC	CTAAAGATTAA	CAAGAAAGCG	GTTGAATATT	TCCAAAAGC	TGTTGATAAC	360
GATATACCTA	GAGGGTATAA	CAATTGGGC	GTGATGTATA	AAGAGGGTAA	GGGAGTTCCCT	420
AAAGATGAAA	AGAAAGCGGT	GGAAATTTTT	AGAATAGCTA	CAGAGAAAGG	TTATACTAAC	480
GCTTATATCA	ACTTAGGCAT	CATGTATATC	GAGGGCAGGG	GAGTTCCAAG	TAACATATGCG	540
AAAGCGACAG	AATGTTTATG	AAAAGCGATG	CATAAGGGCA	ATGTGGAAGC	TTATATTCTC	600
CTAGGGGATA	TTTATTATAG	CGGGAAATGAT	CAATTGGGT	TTGAGCCGGA	CAAAGATAAG	660
GCTGTTGTCT	ATTATAAAAT	GGCGGGCCAT	GTGAGTTCTT	CTAGAGCTTA	TGAAGGGTTG	720
TCAGAGCCTT	ACCGGTATGG	GTTAGGCCGT	AAAAAAGATA	AAAAAAAGCC	TGAAGAATAC	780
ATGCAAAAG	CATGCGATT	TGACATTGAT	AAAAATTGTA	AG		822

## (2) INFORMATION FOR SEQ ID NO:996:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 447 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori

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## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...447

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:996

ACGATGAAAA ATACATCGTC ATCAACGACT TTAACAATGA ATGACACCAT TGCCGCTATC	60
GCTACCCCT TAGGCAAGGG AGCGATTAGC ATCAATTAAA TCAGCGGCCA TAACGCCCTA	120
AACATCCTCA ACAAACTCAC CCAAAACAA GACTCACC CCAGATAACGC TTACGTGTC	180
GACATTTTTT CTGATGGCGT TTTATTGGAC AAAGCGTTAG TGATTIATT CAAAGCCCCC	240
TATAGTTCA CCGGTGAAGA TGTGTGCGA ATCCAATGCC ATGGAAGGCC CCTTTAGCG	300
CAAAATATCC TTCAAGCTTG CTIGAATTAA GGGGCTAGGC TCGCTAAAGC GGGGGATT	360
AGCAAAAAAG CTTTTTAAAC CCATAAAATG GATTGAGCC AGATTGAAGC GAGCGTTAG	420
CTCATCCTTT GTGAAGATGA AACCGTT	447

## (2) INFORMATION FOR SEQ ID NO:997:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...804

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:997

AATCTAATTT ATCGGAGCTC ACAAAGGAGC GCAGCCGCTT GCGTGGTGC GTTGAATAAA	60
GAGCCGATGA TTGAATACCTT GAAATCCAT ATCAAGCTCA TTGATGAGAT GATTGCAAGC	120
GGTTATGAAG ACAAAAGAGAC TTTGAAAAAA CGCAGAGATG CGATGCAAGC TTGGGTGAT	180
AAGCCGTAT TGTTAGAGCC AGATAGTAAC GCCCAATACG CCGCTGTATC TGAAATTGAT	240
GTGGCAGAAA TCACGGAGCC TATTTTGGCA TGCCCTAAATG ACCCTGATGA CGTCGCTACT	300
TTGAGCGAAG TTTTAGCGGA TACGACCGGC AAAAGACCCC ACGCTATTGA TGAAGTGT	360
ATTGGCTCTT GCATGACGAA TATGGGCAT TTCAGAGCCT TTGGTGAAT CGTTAAAAAC	420
GCCCCCTCCA GTCAAGCAGC CCTTTGGTA GTGCCACCCA GTAAAATGGA CGAACAAAGAG	480
CTTATTAATG AGGGCTATTA TGGGATTTT GGGGCTGCGG GGGCAAGGAC TGAAGTACCA	540
GGCTGTAGCT TGTGCATGGG CAATCAAGCG AGGGTTAGGG ATAATGCGGT CGTTTTTCT	600
ACTTCCACAC GGAATTITGA TAATCGTATG GGTAGAGGGG CTAAAGTGT A TTGGGCAGT	660
GCGGAGCTTG GGGCGCGTG CGCTTTACTA GGGAGGATCC CCACTAAAGA AGAATACATG	720
AATTAGTGA GTGAAAGCT AGAGAGCCAA AAAGACAAGA TCTATCGCTA CATGAACCTT	780
AACTTAATGG AGAATTTCAG GCTC	804

## (2) INFORMATION FOR SEQ ID NO:998:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998

AAAATGCCAT	ACGCCTTAAG	AAAAAGATTT	TCAAACGCC	TTTATTGTT	TTTTTTAATT	60
GTTGTATGA	TAATTTGCA	TGCCAAAAGC	TATCTGTTT	CTCCTTGCC	CCCAGCGCAC	120
CAGCAAATCA	TTAACAGACA	GCCTTGCTCT	TTGGAGTGCT	TGAAAGACTT	GATGCTGCAA	180
AATCAAATCT	TTTCTTTGT	ATCCAATAC	GATGATAACA	ACCAAGATGA	GAGCCTTAAA	240
ACTTATTACA	AGGACATCTT	AAACAAACT	ACCCCGTAT	TCATCGCTTC	TCAAACCTCCA	300
GCTAAAGAAA	CCTATGAGCC	TAAGATTGAA	TTAGCGATT	TACTGCCTAA	AAAGGTGGTG	360
GGCGGTTATG	CGATTTTAGT	GATGAAACACC	CTTTTACCGT	ATTGAAACAC	CAGAAACAAAC	420
GATTCAATA	TCCAAGTCTT	TGACAGCGAT	GAAGAAAGCC	CTGAAAAATT	AGAAGAAACC	480
TATAAAGAAA	TTGAAAAAGA	AAAATTCCCT	TTTATCATCG	CTTATTGAC	TAAGAGGGC	540
GIGGAAAATT	TGCTCCAAAA	TACGACTATC	AATACCCCTA	CTTATGTGCC	TACGGTGAAT	600
AAAACGCAAT	TAGAAAATCA	TACCGAGCTT	TCCTTAAGCG	AGCGCTTGTA	TTTTGGGGG	660
ATTGAATTATA	AAGAGCAATT	AGGCATGCTC	GCAACTTCA	TTAGCCCTAA	TTCGCCCGTG	720
ATTGAATACG	ATGATGATGG	CCTGATAGGT	GAACGCTTGA	GGCAAATCAC	GGAGTCTTTA	780
AACGTGAAAG	TCAAACACCA	AGAAAACATT	TCTTACAAAC	AAGCGACCAAG	TTTTCTAAA	840
AATTITAGAA	AAACATGATGC	GTTTTTAA	AATTCTACCT	TAATTITGAA	CACCCCTACC	900
ACTAAAAGCG	GTCGTGATCCT	TTCTCAAATA	GGGCTTTAG	AGTATAAGCC	TCTTAAATC	960
CTTTCCACAC	AAATCAATT	CAACCCCTCT	TTACTCTTGC	TCACCCAGCC	TAAAGACAGG	1020
AAAATTTAT	TCATTGTCAA	TGCCCTTGAA	AACAGCGATG	AAACGCTGAT	AGAATACGCT	1080
TCCTTATTAG	AGAGCGATT	AAGGCATGAT	TGGGTGAATT	ATTCCAGCGC	GATAGGGCTA	1140
GAGATTTT	TAACACCGCT	AGATCCGAT	TTTAAAAAGT	CTTTCAAGA	GAGTTTGGAA	1200
GACAATCAAG	TCCGTTACCA	CAATCAAATT	TATCAGGCTT	TAGGGTATT	TTTGAGCCG	1260
ATAAAAAAACG	AAAGCGAAC	AAAAAAAGAA				1290

(2) INFORMATION FOR SEQ ID NO:999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999

TATTTAGATA	ATTATTTATT	TTTAATGGGT	TTTAAGAAA	GATAGACTAT	60
TATGCGAGTG	GGAAATTAAA	AAGGATTGGT	GCGGTGTTAA	AATTCAAAA	120
TTGTTTGT	CCATTCTTTA	TAATCAAAGC	CTTTTATGG	CTTTGATTA	180
GGGGTAGCGG	AATCTGTTTC	TAAAGTGGGG	TTAACCCATT	CCAAACTCAA	240
GGGATTTC	CTACAGCCAC	CTTGTAAACC	GCCACGATCA	GGATTCCAAT	300

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CTGCTCCCTA	AAAACATTGA	AAAACACAGC	TTAAAAATAG	GCGTTGGGGG	GATTTTAGGA	360
GCGCTCGCTT	ACGATTCAC	CAAACGCTC	ATAGACCAAG	CCACGCATCA	AATCTATGGC	420
TCAGAACTTT	TTTACCTCAT	AGGGCGTTGG	TGGGGGTTTT	TAGGCAACGC	TCCTTGAA	480
GAECTCCCTCA	TAGAATCTGA	CGCTCACACC	CGTAATTATG	TGCTGTATAA	TTCTATCTG	540
TTTATTCTT	ATGGCGATAA	ATTCCACCTA	AAATTAGGGC	GTATCTCTC	TAACATGGAT	600
TTTATGAGTT	CCTACACACA	GGGTTTGAA	CTGGATTATA	AAATCAATT	AAAATAGCG	660
TTAAAATGGT	TTAGCTCTTT	TGGGAGGGCG	TTGGCTTTG	GGCAATGGAT	ACGGGATTGG	720
TATGCCCTCA	TTGTAACTGA	AGATGGCAGA	AAAGAAGTTT	ATGATGGCAT	CCATGCCGCG	780
CAACTCTATT	TTTCTAGCAA	GCATGTCAA	GTCAIGCCCT	TTGCTTATT	TTGCCCTAAG	840
ATTACGGAG	CGCCCGGTG	AAAATCCAT	ATTGATAGCA	ACCCGAATT	CAAAGGCTTA	900
GGGTTAAGGG	CTCAACAC	TATTAATGTG	ATTTTCCCTG	TTTATGCTAA	AGATTTATAC	960
GATGTGTATT	GGCGTAACTC	TAAGATTGGC	GAGTGGGGCG	CATCGCTTT	GATCCACCAA	1020
CGCTTIGACT	ACAACGAATT	TAACTTGGC	TTGGTTATT	ACCAAAATT	TGGCAACGCT	1080
AACCGCAAGGA	TTGGCTGGTA	TGGTAACCCC	ATCCCTTTA	ATTATAGAA	TAACAGCGTT	1140
TATGGTGGGG	TCTTCAGTAA	CGCTATTACC	GCAGACGCGG	TTCTGGGTA	TGTCTTTGGT	1200
GGGGGGGTGT	ATAGAGGGTT	TTTATGGGT	ATTTTAGGCA	GATACACTTA	TGCCACTAGA	1260
GCGAGCAGAA	GATCCATCAA	CTTGAACCTG	GGCTATAAAT	GGGGTTCTTT	TGCTAGAGTT	1320
GATGTGAATT	TAGAATACTA	TGTGGTCAGC	ATGACAAACG	GCTATAGATT	AGACTATCTC	1380
ACCGGCCCTT	TCAACAAAGC	CTTTAAGGCT	GACGCCACAAG	ATAGGAGTAA	CCTTATGGTT	1440
AGCATGAAAT	TCTTTTTT					1458

## (2) INFORMATION FOR SEQ ID NO:1000:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...762

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000

GTITACCGGG	GGTGGCTAT	CGCTATAGC	ATGCTCATTG	ACTCATCTGT	GGTAGTGGTG	60
GAAAACGCTT	TTGAAAATT	GAGCGCTAAC	ACTAAAACCA	CTAAACTCCA	TGCAATCTAT	120
CGTTCATGCA	AAAGAAATCGC	CGTTTCAGTC	GTGAGCGGGG	TGGTGATCAT	TATTGTGTTT	180
TTTGTGGCGA	TTCTAACCTT	ACAGGGGTTA	GAGGGCAAGA	TGTTTAGGCC	TTTAGCCCAA	240
AGCATTGTGT	ATGCGCTTTT	AGGCACTTTA	GTTCATATCCA	TCACTATCAT	TCCTGTAGTG	300
ACCTCTCTTG	TCTTAAAAGC	CA CGCCCCAT	AGCGAACCT	TTTTAACGAG	GTTTTAAC	360
AGAATCTACG	CCCCTTTATT	GGAAATTTTT	GTGCATAACC	CTAAAAAAAGT	GATTTAGGA	420
GCGTTTGT	TTTTAATCGC	AAGCTTTCT	TTATTCCTT	TGTTGGGGAA	GAATTTCATG	480
CCTGCTTTAG	ATGAGGGCGA	TGTGGTTTG	AGCGTGGAAA	CCACCCCTC	TATTTCTTA	540
GATCAATCTA	AAGATCTCAT	GTAAACATT	GAAAGCGCGA	TTAAAAAGCA	TGTCAAAGAA	600
GTAAAAGCA	TGTGCGCGC	CACAGGGAGC	GATGAATTGG	GGCTGGATT	AGGGGTTTG	660
AATCAAACCG	ATACTTTTAT	TTCTTCTATC	CCTAAAAAAG	AATGGACGT	AAAAACCAAA	720
GATGAATTGG	TTAGAAAAAA	TCATGGATTC	TTTAAAAGAC	TT		762

## (2) INFORMATION FOR SEQ ID NO:1001:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid

741

(C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001

TGGTTGTTTC	TAACATGCTA	TGGTAGTGTG	ATAAAGAAAAG	GCTATATAAG	AGGAGATCTT	60
ATGCCATAG	TTAGAAATT	ATTTCTTGTA	TCGTTGTTG	CGTATAGTAG	TGCGTTGCA	120
GCGGATTAG	AAACCGGAAC	CAAAACCGAC	AAAAAGAGCG	GTAAAAAATT	TTACAAACTC	180
CATAAAAACC	ATGGCTCAGA	AACCGAGACT	AAAACGATA	AAAAGCTTTA	TGATTTCACT	240
AAAATAGCG	GATTAGAAGG	CGTGGATT	AAAAAAAGCC	CTAACCTTAA	AAGCCATAAA	300
AAAAGCGATA	AAAAGTTTTA	AAACAACTC	GCTAAAACA	ATATCGCTGA	AGGGGTGAGC	360
ATGCCGATTG	TGAATTTCAA	TAAAGCCCTA	TCTTTGGGC	CTTATTGGA	AAGGACTAAA	420
ACCAAAAAAA	CCCAATACAT	GGACGGCGGG	TTGATGATGC	ACATCCGTTT	T	471

(2) INFORMATION FOR SEQ ID NO:1002:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 675 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002

CCGAAAATTG	CACCGCTTGC	CATGGCATTA	AATCCCCAAA	CATTCCAGCC	CCTATGGATA	60
GCCTTAGTGC	GAGCAACTCT	TTTGGGGTGG	GGCCACCGGA	ATTAAGCCA	TGTGGCGGGG	120
GTITTGAAAC	CGAGTTCTT	AGCCCACITC	ATCAAAGACC	CGGTGAAAC	GGCGAAATTG	180
AGCCATAACT	TCAACCGATGA	AAGGCCCTAT	CCTATGCCGG	CGTTTTCTCA	ATTTAGCGAT	240
CAAGATTTGA	GCGATATTGT	GGCGTATCTC	ACTTCTATT	TGCTCTAAAAA	TTTGAGCGAT	300
AAGGAAGTGT	TCCCGCAAAAG	TTGTCAAAGG	TGCCATAGCC	TGGATTATGC	AAAAGATAAG	360
GCCTTTAGCG	ATCCTAAAGA	TTTAGCCAAAT	TATTTAGGCT	CTCATGCGCC	TGATTTGTCC	420
ATGATGATTA	GGGCTAAGGG	CGAACATGCC	TTGAATGTTT	TCATCAACGA	TCCGAAAAAG	480
CTTTTGCGCTG	GCACAGCCAT	GCCTAGAGTG	GGATTGAATG	AAAAAGCTCA	AAAACAAGTC	540
ATTTCTTATT	TGGAAAAGC	GGGCGATAGG	AAAAGCATG	AAAGGAATAC	TTTAGGGATT	600
AAGATCATGA	TTTCTTTGC	GGTGTGTGCG	TTCTTGGCTT	ACGACTGGAA	AAGAAAAGTT	660
TGGAGCGAAG	TGCAT					675

## (2) INFORMATION FOR SEQ ID NO:1003:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1143 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...1143
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003

ACTTGGCGGT	ATCAACTAGG	CTCATTAATA	GGCAAAATCC	AAATGATTAA	AAGCGTAGAG	60
ATTGAAAATT	ACAAAAAATT	TGAGCACCTT	AAAATGGAAA	ATTTTAAACT	CATCAACTTT	120
TTTACCGGTC	AAAACGATGC	GGGTAAAACC	AATCTTTAG	AAGCTTTTA	TACCAACACA	180
GGCCTTGTG	ATCCTACTGC	CAATCAAGTC	AGTCTTCCTC	CTGAACATGC	CGTGAAATT	240
AGTGAATTCA	GAAAATCAA	ACTCGATGCC	GACAACCTAA	AAACCTTTT	TTATCAAGGA	300
AACACCGCTA	ATCCCATTAG	TATCCGACT	GAATTGAAAC	ATGCTACTAT	CCCTCTTACT	360
ATCCAATACC	CCACACAAAC	CAGTTACAGC	AAAGACATCA	ATTTGAATAG	CGATGATGCT	420
CATATGACAA	ACCTTATAAA	CACAACAATA	ACGAAGCCAC	AGCTCCAATT	TTCCCTACAAT	480
CCATCCCTT	CCCCCATGAC	AATGACTTAT	GAATITGAAA	GGCAAAACCT	AGGTTAACATC	540
CATTCTAATT	TAGATAAAAAT	CGCTCAAACC	TATAAAGAAA	ATGCGATGTT	TATTCCCTATA	600
GAATTATCTA	TTGTTAACCT	TCTTAAAGCA	TTGGAAAATT	TACAATTAGC	AAGCAAGAA	660
AAAGAATTGA	TTGAAATCTC	ACAATGTTTC	AACCTTAATA	TTTTAAATGC	TAATACAATA	720
AGAAAGTCTG	TCTATATCCA	AATCAAAGAT	AAAAACACAC	CGCTAGAAGA	AAGTCCCAA	780
AGGCTTTAA	ATTTGTTTGG	TTGGGGTTTT	ATCAAATTCT	TTATTATGGT	GAGCATTCTT	840
ATAGACAATC	GTGTCAAGTA	TCTTTTTATT	GATGAAATAG	AAAGCGGTTT	GCACCATACA	900
AAAATGCAAG	AGTTTTTAAAG	AGCTCTGTTT	AACTTAGCTC	AAAAATTACA	GATTCAAATT	960
TTTGCACCA	CGCACAAATA	GGAATTTTTA	TTAACCGCCA	TCAACACGAT	ATCCGATAAT	1020
GAAACGGGAG	TTTTTAAAGA	CATAGCCTTG	TTTGAGCTTG	AAAAAGAAAG	CGCTTCTGGC	1080
TTTATCAGAC	ACAGCTATTTC	TATGCTAGAA	AAACCGCTTT	ATAGGGTAT	GGAGGTTAGA	1140
GGC						1143

## (2) INFORMATION FOR SEQ ID NO:1004:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 852 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...852

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004

ACCCATTGTT TATTCCTTGG TGGTAGTATC AAAATTTGT TAATCCTTAA AGAGGGCATT	60
GATTAAACC ATGGTTATTA CCAATTAGGA AAATACACCA TTAAAGACGA CTTTATCCCC	120
AGTAAAAGG CGTGTGGA AGACGTTTG ATCCAATCTA GCATGTGGG CATGATAAAA	180
ATCAGTAAAA GGCTCAACCC AGAGGATTT TATAACGGGC TTITAGGCTA TGGATTTCT	240
CAAAAACCG GCATTGATTT ATCCTTAGAA GCCACAGGA AGATCCCTCC TTIGTCCGCT	300
TTCAAGCGTG AAGTGTAAA GGGGAGCGTC TCCTATGGCT ATGGGTGAA TCGGACTTTT	360
TTGCAAGCTT TAAGGGCTTA TCGGGTGTTC TCTAATGAAG GCCTAATTGAC TACCCCTAT	420
TTAGTGCAAC GAGAAACCGC CCCTAATGGC GATATTTACA TCCCTAGGCC CAAACCCACC	480
TTTCAAGTCA TTAGCCCCAA AAGCGCTAGA AAAATGAAAG AAACCTTAAT TAAGGTGGTG	540
CGTTATGGCA CAGGCAAAAA CGCTCAATT GAAGGGCTAT ACATAGGGGG CAAACAGGC	600
ACGGCTAGGG TTGCTAAAAA CGGAAGCTAT AGCGCGGAGT CCTATAACAG CTCTTTTTT	660
GGGTTCGCTG AAAGTAAAG GCAGGTTTT ACTATCGCG TGTTATCTT AGGCTCGCAT	720
GGCAAGGAAG AGTATTACGC TAGCAAGATT GCAGCCCCCA TTTTAAAGA AATCACCGAA	780
ATTTAGTGC GTTACAATTA CCTATGCC TCTATTGCGA TTCAAAACGC TTGGAAAAA	840
AACCGCTTAA AA	852

## (2) INFORMATION FOR SEQ ID NO:1005:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...417

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005

GATAAAAAAA TACTTTAAT TATTCAGGA AAATTATGG AATTTCATCA AGTTTATGAC	60
CCATTAGGCC ATATTTGGCT GAGCGTTTA GTCGCACTTT CGCCTATTC GCTCTTTTT	120
ATCTCTCTTA TTGCTTTAA ACTTAAAGGG TATACCGCTG GGTTTTTAAG CTTAGCGCTT	180
TCAATCCTTA TTGCGTTATT TGTGTATAAA ATGCCTGTTA AAATGGTGGAG CGCGAGTTT	240
TTCTATGGCT TTCTTATGG CTTGCGCCCG ATCGCATGGA TTGTGATCGC TGCAGTTT	300
CTTTACAACC TTTCAGTGAA GTCCGGGTAT TTGAAATCT TAAAAGAAAG CGTCAGTCC	360
ATCACCTTAG ATCACCGCAT TTAGTGTATT TTGATTGGCT TTGTTGGC TCATTT	417

## (2) INFORMATION FOR SEQ ID NO:1006:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006

CCTAAACCTA AAGGGTTTG CCCTAAAAAT CTAATGAGTA AAAGAGCGAT CCGTTTCCCT	60
AACAAAGCTTT TTTCATACCC TAAACCCAAA ATAAAAGCGA CAAACACAAG CCACACCGTT	120
TTATTGCGAT ACCCGCTCAA ACCCCACGAA ATGGCCTTAT TAGCGCTCGC TACCTCACTG	180
CTCGCTCCAA TTTTAACGC TATACACAGC ACTAACGCGC TCAACGCTAT CAAACCTGAT	240
GGCACCGGCT CTAAAATTAA CCCTATAATC ATGCCCATGA AAATACAAAA A	291

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1596 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007

AGAAAACGATT TTAAAGGTGT TAGAAAAATG GCATTAAGGG TATTATTATT CTTTTGTTT	60
TTCCTTTTGC AAGCAGAAGA TAAGAGCAA GAATTATCAT CTATACAAAA ACAAAATGGCT	120
TTGGTGGATA AAAACTCGC CAAAGACGAT AACGTGTTGG TGAAAAAATT TGAAAACAT	180
AAAATTACA ACCAAATTAA TACTGAAAAA GAGAGCGTGA GGCAGGAATT AAGGCGCTTA	240
AAAACACAAA AAAGCAAGG TTATTAAG ATTAGCACCT TAGAGCATACT CTTAAAGGCT	300
TTAGAGTCCC AGCAGAAAGG GTTGGCTCA ATCCCTTTAA GGACTTGATA	360
GAGCGCCCCA ATATCCCCAA TATCCCTAAT ATCGCTAACCT ATTTGCGAT CATTGATGGC	420
ATTTCTTCA TCAAGAGCAT CGCTTAAAG CATGAAAATC TTAAAATAA CCAGACTTCT	480
TTAGGAGAAG TTTAAAGCT TTAGATCAA AAACACCAGC TTTAAATCA GTGGCACGCT	540
TTGGATAAAA GCGCAGAAATT AAGCGATGAG ATTATCAA CTCAAGCCAA ACGCTTAGAA	600
TTGCAAGGGG CTAAAACAT TCTAAAAACC ACGATGGGA TTTCCAAAAA AGACAGCGAT	660
GAAGCTATAA GCATTGCTAA ATCTCAAGTT AAAAACAGC TTTTAAATT GTTTTATGTG	720
TTTTTACGGG CCCTTTGAG CGTGGTGTG GCGTGGATT TAAAATCAT TTCCAGTAAA	780
TACATGAAA ATAATGAGCG CGTCTATACC GTGAATAAAG CCATTAACCT CGTGAATGTG	840
AGCGTGTGCTG TTAAATCTT TCTTTTCT TATTAGAAA ACGTTACTTA CTTGCTAACG	900
GTTTTAGGCT TTGCGAGCGC GGGCTTAGCG ATTGCGATGA AGGATTTATT CATGAGCTTG	960
CTCGGGTGGT TTATCATTTT GATTGGGGGG AGCGTGCATG TGGGCGATAG GGTGCGTATC	1020
GCTAAGGGGA CGGATATTCTT TATTGGCGAT GTGGTGGATA TTTCTATGTT GCACATTACG	1080
ATTTTAAAG ACGTAACCTT TACCACTTAC ACGAATAACA GGAGAGCGGG CCGAATTATC	1140
TTTGTGCTA ACAATTACAT TTTCACCAAC ATGGTGCCTA ATTACAGCCA TTTTGGATG	1200
AAAACCGTTT GGGATGGCGT GGATTTTGC GTTACATTG ATTCTGATT TAAAAAAGCG	1260
TCTAAAATTG CGCTCAATAT CGCTACGGAA TTGCTAAAG AATACACGGA TATTACCTAT	1320
AAACAGCTCA ATAAAATGCG CGACCGGTAT TCTTAAAGGA GTTGGAGCGT CAAGCCTCGA	1380
TGCTTTTGAA TGCGTGAAGGAA TAACGGATA AAAATCTCGG TGTGGTATCA AACCAATTGCG	1440
TATGCCACCA TGTCTTAAAG GAGCAAGATT GTGGCTGAAA TTGTTGAAGC CTTTTGAAA	1500

GAAGAAAATA TCCATATCGC TTATACGACC AGCAAGCTGC TTAAAGTGG A TGCTGATGCT  
 CTAGGCGATG GTTTTGGAA TAAAAGGAA CAAAAA 1560  
 1596

## (2) INFORMATION FOR SEQ ID NO:1008:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1041 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008

CGGAGTGAAA	GAATGCAAGA	AATCTTAATC	CCTTTAAAAG	AAAAAAGCTA	TAAAGTGT	60
TGCGGGAAAC	TGCTGAAAT	AAAAATTGAAA	CAAAAAGCGC	TCATCATTAG	CGATAGCATC	120
GTGGCCGGGT	TGCACTTGC	CTATTTGTTA	GAGCGCTTGA	ACGCCCTTAGA	AGTCAGAGTG	180
TGCGTGATAG	ACTCCGGGGA	AAAATACAAA	AATTTTCAATT	CATTAGAGCG	GATTTTAAAC	240
AACGCCCTTG	AAATGCAATT	AAACCGCCAT	TCTTTAATGA	TAGCCCTTGG	TGGGGAGTG	300
ATAAGCGATA	TGGTGGGGTT	TGCGAGCAGT	ATTTATTTC	GGGGGATTGA	TTTTTATTAAT	360
ATCCCCTACGA	CTTTACTCGC	TCAAGTGGAT	GCGAGCGTGG	GGGGGAAAAC	AGGGATCAAC	420
ACGCCCTATG	GCAAGAACCT	AATCGGATCG	TTCCACCCAGC	CTAAAGCGGT	TTATATGGAT	480
TTAGCTTTT	AAAAACCCCT	TGAAAAAAAGG	GAATTCAAG	CGGGGGTTGC	TGAAATCATT	540
AAAATGGCGG	TGTGTTTG	TAAAAACTTG	GTAGAAAAGAT	TAGAAAACAA	GGATTTAAAAA	600
GATTGTTAG	AAAGAGTAAT	CTTTCAAAGC	GTCAAATATCA	AAGCTCAAGT	CGTTGTTCAA	660
GATGAAAAAG	AGCGAAACAT	CAGGGCTGGG	TTGAACATAG	GGCATACCTT	TGGCATGCTG	720
ATAGAAAACG	AGACCAATT	CGAGCGATT	TTGCATGGCG	AAGCGATCGC	TATTGGCATG	780
CGCATGGCTA	ATGATTAGC	CCCTTCTTTA	GGCATGCTCA	CTTAAAAGA	ATACGAACGC	840
ATAGAAAAT	TATTGAAAAA	ATTTGATCTG	ATATTCAATT	ACCAAATCAC	TGATATTCAA	900
AAATTTTACG	AACGCTTGTT	TTTAGACAAA	AAAAGCGAGA	ACCAAACCC	AAAATTCAATT	960
TTGCTCTAAAG	GTGTTGGAGC	GTGAGATT	GCCTCTCAT	TCCCTAAAGA	AACGATTTA	1020
AAGGTGTTAG	AAAAATGGCA	T				1041

## (2) INFORMATION FOR SEQ ID NO:1009:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

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- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...588

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009

AAATCAAAGA GTATGAAATT AAGGGAGAGGG AAAATCATGC CGTTTCTAA ATTTTTAGAA	60
AACCTCACCG CTCCCTTAA ACAGCATCAA AACCGCTCGC TTGTTTGGC GTTAGGGTTT	120
TTGATCCTTA CTTTTGCTT GTTGCTTTT TTAATCTTAA GCGATGTTTC TAGGCTCATA	180
TCCAGTAAGG ATTTCTTAA TGTGATCCAG TCTCACCCCTA AACAAACTCT AATTGAAGAT	240
GAAAATTATT TTATGCTAA CAAGGGTCTT TATAAAACCA ACAAGAGAAC CTTTTAAGG	300
GTTCATAAAA TCCCAGAGAG CATGCCATA GAAAAACGAG AAAGTTTAAG CAAGGTTTCT	360
AAAATCTTCTT TAGCGTTGCT TTTTCATT TCTAGCATGC TTTTTGGAT CTTTTGGCGT	420
TTGCCCAAAC GATTGGACAC TAAAATGAGT TTAGAGAGCG CGCACAAAAA CGAATTAGAA	480
AATGCATTCC AACGATACGA TGCGCTAGGG GTGCCATTG AAGACATTGC AGGGGTGAAT	540
GAAGTCAGAAG AGAAATTACT AGAAAGTATA GATTATTTAA AAAAACCC	588

## (2) INFORMATION FOR SEQ ID NO:1010:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 537 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...537

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010

ATGAAACCAT TGCATTTTC ACACCTGGAC AGAGAGCAAT CAGCGATGT GGGTTTATC	60
ATTAAAAAAC TTATTTTTT AGGGGTTTTT TCCTTATTGG GTTGCTTGAA TACCGAGTAT	120
TTTCTATGGC CTAGCATGCT GGAATTTAAA AAAATCCTT TAGAAGAAAA TCGTAAAAAA	180
AGCGTTTAG AATACCGCAG AAGGCATTT GAAACAGCCC TAGCAAACCA CCGCAATCAA	240
AAAGAAACCA GCGAATCTT GTTAAAGATT TTTAATGATG AAGACTCCAG GCGGATTTTA	300
GAAAAGATCT TAAAAAAATG TTTTGACGCC TATAAAATCA AACCCCTGCT CTCTCAAAAC	360
CCCTCCAAA AAACCCAATT TTTTATCATG GCTAGAGCGA GCGAATTGGA AAAAACTTAT	420
CTTTTTTCA CCTTAATCAA CAAGTATTTA CCGAGCGCTC AAAGCCAATT GCCCTTAAAG	480
ATTCTAAAG ATAGCGACGG GTTGTGGTG CAATTGGCG TGAGTATTGA TCTCAA	537

## (2) INFORMATION FOR SEQ ID NO:1011:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1356 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011

TTTAAAAAGGT	ATTTTATAAC	GATGAAAATT	TTTGGGACTG	ATGGCGTGAG	GGGTAAAGCA	60
GGGGTGAAC	TCACCCCCAT	GTTTGTGATG	CGTTTAGGCA	TTGCTGCCGG	ATTGTATTTT	120
AAAAAACATT	CTCAAACGAA	TAAGGTTCTA	ATCGGTAAAG	ACACCAAGAAA	GAGCGGCTAT	180
ATGGTAGAAA	ACGCTTTAGT	GAGCGCTCTC	ACTTCATAG	GCTATAATGT	GATCCAAATA	240
GGGCCTATGC	CTACCCCTGC	GATCGCTTTT	TTAACCGAAG	ACATGCGCTG	TGATGCGGGC	300
ATTATGATAA	GCGCGAGCCA	CAACCCTTT	GAAGACAATG	GCATCAAGTT	TTTCAATTCC	360
TATGGTTATA	AACTCAAAGA	AGAAAGAAGA	AGAGCGATTG	AAGAAATCTT	TCATGATGAA	420
GAATTACTGC	ATTCCTAGCTA	TAAGTGGGC	GAGAGCGTCG	GTAGCGCTAA	AAGGATAGAC	480
GATGTGATAG	GGCGCTATAT	CGCGCATTG	AAGCACCTT	TCCCAAACAA	TTTGAATTTA	540
CAAAAATAA	GGATCGTGCT	AGATACGGG	AATGGCGCGG	CTTATAAGGT	GGCTCCGGTC	600
GTTTTGTAGCG	AGCTTGGGGC	TGATCTTTA	GTGATCAATG	ATGAGCCTAA	TGGGTGTAAC	660
ATTAATGAGC	AATGCGGGGC	TTTACACCT	AACCAATTGA	GCCAGGAAGT	GAAAAAATAC	720
CGTGGGATA	TAGGCTTTGC	TTTTGATGGC	GATGCCGATA	GGCTAGTGGT	GGCGGATAAT	780
TTAGGGAATA	TCGGTGCATGG	GGATAAGCCT	TTAGGGGTGT	TAGGGTTTA	TCAAAAATCT	840
AAAAACGCCC	TTTCTTCTCA	AGCGTTGTC	GCTACCGAGCA	TGACCAATT	AGCCCTTAAA	900
GAATAACCTGA	AATCCCAAGA	TTTAGAATTG	AAGCATIGCG	CGATTGGGG	TAAGTTTGTG	960
ACCGAATGCA	TGCGATTGAA	TAAGCCAAT	TTTGGGGCG	AGCAAAGCGG	GCATATCATT	1020
TTTACCGATT	ACGCTAAAAC	GGCCGATGGT	TTGGGTGCG	CTTTGCAAGT	GAGCGCGTTA	1080
GTGTTAGAAA	GCAAGCTTGT	AAGCTCTATT	GCGTTAAACC	CCTTTGAACT	ATACCCCCAA	1140
AGCCTAGTGA	ATTGAAATAT	CCAAAAAAAG	CCCCCTTTAG	AAAGCCTGAA	AGGTTATAGC	1200
GCTCTTTAA	AAAATTAGA	CCAACTAGAG	ATCCGCCATT	TGATCCGTTA	TAGCGGCACT	1260
GAAAACAAAT	TACGAATCCT	TTTAGAAGCT	AAAGACGAAA	AACTTTAGA	ATCCAAAATG	1320
CAAGAATTAA	AAAGAATTTTT	TGAAGGGCAG	TTGTGC			1356

(2) INFORMATION FOR SEQ ID NO:1012:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012

AATCATCAGC	GAATACGAAG	CCGCAACAA	TTTAGAAAGC	CGTTTGATCC	CTTTAGAAGA	60
GCAAGCGAGT	TAAAAGTGCG	ATCTGAAA	CAGATTTTG	ATAAGGGTTT	AAAGCCCTAT	120
TATAAACATT	CTGTTTGCTT	AAAGCCTTTT	TTTAGGTTTT	GTGTTCTCAA	AATTCTATGCT	180
TATCAACAGC	GTTATAGAGC	GTGCTCTTA	ACGCTCTTTT	CTTGTAAAGTT	TTTTAACGCT	240
TGTAAGATTT	TTAATCCCAT	AATTGATT	AAAATCGTTT	TTATCCCTAT	TCTAAAACAC	300
CAAGCCAAGC	AAAAAAGAGT	CTCTAATGCC	TAT			333

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## (2) INFORMATION FOR SEQ ID NO:1013:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 600 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...600
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013

AAGCGCATGA	AAGAATCTTT	TTACATAGAG	GGAATGACTT	GCACGGCGTG	TTCTAGCGGG	60
ATTGAACGCT	CTTTAGGAGC	TAAAAGTTT	GTGAAAAAAA	TAGAAGTGAG	CCTTTAAAT	120
AAGAGCGCTA	ACATTGAATT	TAACGAAAT	GAAACCAATT	TAGACGAAAT	TTTTAAACTC	180
ATTGAAAAAC	TGGGTTATAG	CCCTAAAAAA	ACTCTAGCAG	AAGAAAAAAA	AGAATTTTT	240
AGCCCTAATG	TTAAATTAGC	GTTGGCGGTT	ATTTCACGC	TTTTGTGGT	GTATCTTCT	300
ATGGGGCGA	TGCTTAGCCC	TAGCCTTTA	CCTGAAAGCT	TGCTTACGAT	TAACCATCAT	360
AGTAATTTTT	TAACGCTTG	CITACAGCCT	ATAGGCAGC	TCATTGTCAT	GCATTTGGGG	420
AGGGATTTTT	ACATTCAAGG	GTTTAACGCC	TTATGGCACA	GACAACCCAA	CATGAGCAGC	480
CTTATGCCA	TAGGCACAAAG	TGCTGCCCTA	ATTCAGCCT	GTGGCAATTG	TATTTGGTTT	540
ATACCAATCA	TTATACCGAT	CAGTGGCTT	ATGGGCATTA	TTATTTGAA	AGCGTGTGCG	600

## (2) INFORMATION FOR SEQ ID NO:1014:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 723 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...723
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014

AAAGAGTCTC	TAATGCCCTAT	TAACCCCTCTC	TATCTTTTCC	CCAATCTTTT	TACCGCTAGC	60
AGTATTTTTT	TAGGCATGAT	GAGTATTTTT	TACGCTTCCA	GTTCACCAATT	TGTCATGGCG	120
TGTTGGTTAG	TGGTGGCGAG	TCTTATTTA	GATGGGCTTG	ATGGGCGTGT	CGCAAGGCTT	180
ACCAACACCA	CTAGCAAGTT	TGGTATTGAA	TTTGAATCTT	TAGCTGATGT	GGTCGCTTTT	240
GGAGTCGCC	CAAGCCTTAT	TACTTACTTT	TATGTGGGGT	ATAACTTTGG	GCGTATAGGC	300
ATGGCGGTGA	GCCTGTTGTT	TGTGATTTT	GGAGCGATAC	GATTAGCGCG	ATTCAATATC	360
AGCACCAACA	CAAGCGATCC	CTATTCTTTC	ATCGGTATCC	CCATTCCCTGC	GGCGGGCGGTA	420

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TTGGTGGTGC	TTTGCCTGTT	ATTAGATAAT	AAATACCATT	TCTTAGAAGG	CAATACCGAA	480
AAGTTATTT	TAGGTTTAT	TGTCTTATTA	GGGGTGCTTA	TGGTGAGCAA	TATCCGCTAC	540
CCTAATTTA	AAAAAGTCAA	GTGGAATCTC	AAGCTTTCA	TCTTAGTGTT	GATCTTTTA	600
TCGTTAGTGT	TTGTGCGCCC	TTTAGAGGCT	TTGAGCGTGT	TTATGGGGTT	GTATTTGATC	660
TATGGCATCA	TTCGGTGGAT	CTTTTTAATG	CTAAAAATTA	CTTTTAATAA	AAATAAAAGC	720
GCA						723

## (2) INFORMATION FOR SEQ ID NO:1015:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015

TATTTGCCCG	CAAGCGAAAA	CGCCCCCTTG	CCCTCTAGTG	TTTTTAGTTTC	AATCGTGGCT	60
TTGACCTTGA	AAATAGACAG	CCTGTTTTCT	CTTTTTAGCG	TGGGTAAAAT	CCCTAGCGGA	120
TCTAAAGATC	CCTTTGCGTT	AAGGCGTTTG	AGTTTTGGGC	TATTGAAAAT	CATCGCGCAT	180
TACGGGTTAG	AAATTGATTTC	GAAAGCGGAT	TTAAAAAAACC	TCTTTGAAAA	AGTGGGGCGTT	240
TATCAAAGCT	TTGATTTAGA	GGTTTTAGAA	AAAGTTTTAC	TGGAGCGCTT	TCATAATTAA	300
ATAGATTGTA	ACCTCTCTAT	TATAAGAAGT	GTGTTAAACA	CCAACGAGCG	AGACATTGTT	360
AAAATCATTC	AAAAAGTCAA	AGCCTTAAAA	CGCTTTTTAG	ACAATCCTAA	GAACGCTCAA	420
AAAAAAAGAGT	TGCTTTTTAG	CGCTTTCAA	CGATTAGCTA	ATATCAATAA	AGACAGAAAC	480
CCTAACGAAT	CAAGCGGGTT	TTCTACGAGT	CTTTTCAAAG	AATTACAAGA	GCATGCCCTT	540
TTTGAAGCGT	TCAACGCGAT	CAAAACAAGC	ACTTTGAGA	GTGGATAG	CAAAATAGAG	600
GCTTATTTTG	GTTCGCATGC	GCCTTTAGAA	GAATATTTA	AAAGCGTGCT	AGTCATGGAT	660
AAAGATATAG	AAATCCAAAA	AAATCGTAA	AATTCTTGT	GGGGCGTGT	TCAAAGTTTC	720
TTAGAGATTG	GGGATATTAA	AGAAATTGCG	ATT			753

## (2) INFORMATION FOR SEQ ID NO:1016:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature

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## (B) LOCATION 1...1782

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016

GTGGCTTTA AAATTTAAG TTTATGGTTA GGGCTGTTT GTTCCCTTAG GGCTACGCAT	60
TTATACTTAG CGGAAGAAC CAAATATAAA GACAATTCTCA CGCATTGTA ATACGCTAAC	120
CCTAACGCTA AAAAGCCGG TGTTTGAGA AATGACGCTA TAGGGACTTT TGATAGCCTT	180
AACCCTTTG CGCTTAAAGG CACTAAAGCC GAAGGCTGG ATCTCATTTA TGACACTTA	240
ATGGTCAAA CCTTAGACGA ACCTTTGCA GAATACCCCT TAATCGCTAA AGACGCCGAA	300
GTGGCTAAGG ATAACAGCTA TGTGATTTT ACCCTAGATA AAAGAGCGAG ATTCAAGCAAT	360
AACGCTCCA TTTAGCGAG CGATGTGAAG TTTAGCTTG ATACGATAAT GAAATTAGGA	420
TGCCCTCTT ATAGGCAGTA TTACCAAGAT GTTAAAAGG CGGTTATCTT AGACAAGCAC	480
CATGTTAAAT TCATTTCAA AACCACTGAA AATAAAGAT TGCCCTCTAT TTTAGGGCAG	540
TTGAGATCT TTTCCAAAAA AGCGTTCTAA AAGGATTATT TTGAAAAAAA CCCTTTACTC	600
ATTCCTGTT CTAGTGGCCC TTATGTGATC GCTTCTTTG ATGTGGGCAA GAAAATCACC	660
TACCAAGAA ACCCTAACTA TTGGCGAAA AATTCCTCTA GCAGAAAGGG GCAATTCAAT	720
TTTGATCAA TCAATTTGAA GTATTACAAA GATGAAACCG TCGCTTACAA GGCTTTITA	780
AGGGGGCGT ATGATTGGCG CCTTGAAGC ACGGCTAAGG TTGGGCTAG GGGCTATGTG	840
GGGAAGCTA TGGATAATAA AAAATCACT AAATACCTCA TAGCCCACAA AATGCCAAC	900
GGCATGCAAG GTTTTTCTT CAACACGGCG CGAGAAATT TCAAGGATAA AAGGGTGCCT	960
GAAGCCTTAT TTATGCGTT TGATTTGAA TGGGGAATA AAAATTGTT TTTTCGCAA	1020
TACAACGGCA CCACTAGTTT TTTCAGTAACT TCTATCTAT CGTCCCCCTCC TCTCCCAAGC	1080
CCTGAAGAAA AAGCCCTGCT AGCCCCCTAT GAAAGAGTT TGATGAAAG GGTTTTTAAA	1140
GAGCCTTATA TCCTGCGCTAG AACCGATGGG CCTGATGTT TAGGCTATAA TTGAGGGAA	1200
AATTAAAT ACGCCAAAAA GCTTTAGAG AGCGGGCGT TTCTACAA AAACATGCGT	1260
TTGGTGGATA AGAATAACAA GCCTTTCAGT TTCACTTGTC TTTAAACAG CCCGCATT	1320
GAAAGACTGG CCCTAGCTTT TGCTAAAAAC TTAAGGGTGT TAGGGATTGA AATGAAAATC	1380
CAAAGACTGG ATTTAAGCCA GTATGCAAT CGGATCAAA GCTATGATT TGACATGATT	1440
GTAGGACTGA TTGGCCAATC GTCTTTCTCA GGATATGAGC AGCGCTTTA TTTGGCTCT	1500
TTGAGCCGA AAGCCAAAG CACAAGGAAT TATGCGCGAA TCTCTAGAA AGCGGTAGAT	1560
GATTGATTG AAGAATCAT TCACGCTAA GATTATAAGG AGCAATTGGC CGCCATTCAA	1620
GCGGATGATA GGGTGTGTTT CGGGGGTTT TACCGGATAC CGCATTTTTA TTGCTTAAT	1680
TACAGGATEG CAGCGTATAA TTACATTGGC ATGCTGAAA TCAGCCCTAG CTATGGATT	1740
TCGCCGTATT TATGGTGGAT AAAAAAGAA AGGGTCCTA AA	1782

## (2) INFORMATION FOR SEQ ID NO:1017:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 603 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017

TCTGTGATTG GTGTCTATAT CATTCTTTA AAAGAAAGTC AAAGGCCATT GGATACTGAA	60
AAACTCGTT TAGAATCAA TGAAAAATT AAAGGCCATT GCGTTCTCA AATCTTGAC	120
GCCATTAGCC CCAAACATCA AGATTTGAA AAATTACTTC AAGAGCTTTA TAACGCTAA	180
AGTTTATTGC AATCTGATTG GTATCATTCT TATGTTGGCG CTGGTTTGAC TTGCTGAA	240
TTGGGGTGTGTT ATTTAAGCCA TTATCTTTA TGGAAAGAT CGGTCAAATT AGATCAACCG	300
GTCGTTATT TAGAAGATGA TGTAACGCTA GAGTCTCATT TCATGCAAGC CTTAGAAGAT	360

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TGTTTGAAAA	GCCCTTTG	TTTGTGAGA	CTCTATGGGT	GTTATTGGTA	TTACCAAGGAG	420
ACAAAATTCC	ATGTTTGCC	CAAAGAATT	GTATTTCTC	CCTTGATCA	TTCTTTAAAG	480
AATAACCCTA	TTTTAGAAAA	ATTTAAAAAA	TTTTTGATG	TTCTAGATT	TTAAATCTT	540
TCTACCCATA	AAGTCATCCA	CCTATATTCT	CAAAAAATA	CAAAAAAGCT	ATTACCCAAC	600
GCA						603

## (2) INFORMATION FOR SEQ ID NO:1018:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018

TTTAGTGAGC	GGGACTTTG	GCTTTT	AGG CAAACAA	ACCCCTATGA	AAGATGTTCT	60
TGTGGATTG	GATTCTTG	TC AGACGCTTCA	AAAAGATCCC	TTAATCCAAC	CTTAATGATG	120
AATAATAATA	ATACCCCTACC	CAAACCCCTA	GAAGAAAGCC	TAGATTAAA	AGAGTTTATC	180
GCTCTTTTAA	AAACCTTTT	CGCAAAGAA	AGAGGTCTA	TTGCTT	AGAAGTCTC	240
AAACAGGCTT	TCACCTATT	AAATGAAGTG	GATGCGATCG	GTTGCCTGC	CCCCAAAAGC	300
GTGAAAGAAA	GCGATCTT	TGTTGTCAA	CTCACCAAT	TAGGGACGCT	CCATTTAGAT	360
GAAATCTATG	AGATIGTCAA	ACGATTGCGC	TACATIGTCG	TTTTACAAA	CGCTTTAAA	420
CCTTTCACGC	ATTAAAATT	TCATGAACGC	CTTAACGCCA	TTATTTTAC	CCCTTTTTT	480
AATGATTG	TCCTTTTATT	GGATGATGAA	GGGCAAATCA	AACAAGGGGC	GAACGCTACC	540
CTAGACGCTT	TGAATGAAAG	CTTGAACCGC	CTTAAAAAAG	AGAGCACTAA	AATCATTCA	600
CATTACGCC	ACTCTAAAGA	GCTTGCCTCT	TATTTAGTGG	ATACGCAAAG	CCACCTTAAG	660
CATGGTTATG	AATGCC	TTTAAAGC	GGCTTITCTA	GCGCGATCAA	AGGGCTTGTG	720
CTAGAAAGGA	GTGCTAATGG	TTATTTCTAT	CTTTGCTCTG	AAAGCGCGCA	AAAATCGCC	780
CAAAAATCG	CGCAAATTG	TAATGAAATA	GATTGCTGTA	TCGTTGAAAT	GTGCCAAACT	840
CTAAGCGTA	GCTTGCAAAA	ACACCTTTA	TTTTAAAAT	TCCCTTTAA	AGAATTGAT	900
TTTTAGACA	GCTTGCAAGC	ACGGCTTAAT	TTCGCTAAAG	CCTACAATTT	AGAATTGTC	960
ATGCCAAGCT	TTACGCAAAA	AAAAATGATT	TTAGAAAACT	TTTCGCACCC	CATTTTAAA	1020
GAGCCAAAGC	CTTAAATTT	GAAGTTTGA	AAATCCATGC	TCGCTGTTAC	CGGCGTGAAT	1080
GCGGGCGGGA	AAACCATGCT	CTTAAATCG	CTTTTAAGCG	CAGCTTTTT	GAGCAAGCAT	1140
CTCATTCTCA	TGAAAATCAA	CGCCCCATCAT	TCTACTATCC	CCTATTTAG	AGAAATCCAC	1200
GCCATTATTA	ATGACCCCCA	AAACAGCGG	AACATATCT	CTACTTTG	AGGCAAGATG	1260
AAGCAATT	CCCCTCTTT	ATCAAAGAA	AACATGCTCT	TAGGCCTTGA	TGAATTGAG	1320
CTAGGGACTG	ACGCTGATGA	AGCGAGCACT	TTGTATAAAA	CCCTGTTAGA	AAAATTGCTT	1380
AAGCAAACAC	ACCAAATCGT	TATCACCACG	CACCACAAAC	GCCTGAGCGT	GTTAATGGCA	1440
GAAAACAAGG	AGTGGAAATT	ACTGGCCGCT	CTTTATGACG	AGGAAAAGA	ACGGCCCAC	1500
TACACTTTT	AAAAGGGGT	TATGGCAA	AGCTATGCGT	TTGAAACCGC	TTTGCCTAT	1560
GGCGTGCCGC	CTTTTTGAT	TGAAAAGCGA	AACCTTCTA	TGGCGAAGAT	AAGGAAAAT	1620

## (2) INFORMATION FOR SEQ ID NO:1019:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1365 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

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(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019

AAGCTTACCG	AGAAAATTAT	GCTTGAAACC	CCAAAAGTTT	TACTCAAAAA	CCTGCAAGAT	60
TGCAAGATCC	ATTCATCGG	TATAAGGGGG	ATTGGCATT	CAGGCTTAGC	CAAATACCTT	120
AAAGCGCAAG	GGGCTAAGAT	CAGCGGATCT	GATATTGCCA	TAAGCCCTAG	CGTTAAGTAT	180
TTGAAAGCTT	TAGGCCTAGA	AATTAATATC	CCGCATGATC	CAAAGCGAT	CAACCATCAA	240
GATGTCATCA	TCCATTCAAGC	CATTATCAA	GAAGACAATA	CCGAAATACA	AAGGGCTAAG	300
GAATTAGAAA	TCCCTATTTT	GTCTCGTAA	GACGCTTGT	ATTCTATCCT	TAAGACAAG	360
CGCGTTTTTA	CGCTGTGTGG	GGCTCATGGA	AAGAGCAGTA	TCACGGCCAT	GTIGAGCGCG	420
ATTGGCCCCG	CTTTGGAGC	GATTATTGGG	GGCGATTCTA	AAAGAGTTGA	TTCCAATGTG	480
CGAGAGAGCG	CGGATATGAG	TTTGGTTTTT	GAAGCCGATG	AAAGCGATT	AAGTTTTTA	540
TTTCCAACC	CTTTTGCGC	GATTGCGCT	AACACGGAGC	CAGAACATT	GGAGCATTAT	600
GACCACGATT	TAGAACGCTT	TTTCTTCGCT	TATAAATATT	TTTTAGACCA	TGCTAAAAAA	660
AGAGTGTATCT	ATAAGAAGA	TCCCTTTTTA	AAAAACTATT	CTAAAGACGC	CATTGTTTA	720
GAAAAAAAAG	ACATTTATATA	TATCCAATAC	ATTTAAAAG	ACGGAGAGCC	TTACACTTCG	780
TTTGAATTGA	AAAATTGGG	GGCTTTTTG	GTGTGGGGGT	TAGCGAACAA	TAACGCCACG	840
AATGCGAGTT	TGGCGATTTT	AAGCGCTT	GATGAATTAA	ATTTAGAAGA	AATTAGAAAT	900
AATTATTATGA	ATTTAAAGG	CATTAaaaaaa	CGCTTGTATA	TTTGCAAAA	AAACGATCTC	960
ATTCCTATTG	ATGATTACGC	CCACCACCC	ACTGAAATTG	GCACCACTT	AAAAAGCCGT	1020
AGGATTATG	CCAATTATT	GAATACGCAA	AAAAAAATTA	TAGTGATCTG	GCAAGGCCAC	1080
AAATACTCTC	GCTTAATGGA	CAATTAGAA	GAATTAAAAA	AATGTTTTT	AGAGCATTGC	1140
GACAGGTGTA	TCATTATAC	CGTTTATAGC	CGCAGTGAAG	TTAAAAGAGA	CATTGATTG	1200
AAAGCCCATT	TTAACCATTA	TAACCCACC	TTTATAGACA	GGGTGCGTAA	AAAGGGGGAT	1260
TTTTAGAGC	TGTTAGTCAA	TGATAATGTG	CTAGAAACGA	TTGAAAAGG	CTTGTGATA	1320
GGCTTGGAG	CGGGGGATAT	TACCTATCAG	TTGAGAGGCG	AAATG		1365

(2) INFORMATION FOR SEQ ID NO:1020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020

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GCGGTAACCG CCATTTAGG GTGGGACGAA GAGGGCAAGC TCAAGTTGG GAAAAATL <sup>AGG</sup>	60
CACAAATATT TAGAACGAG CAACGTGAAT GCCGGGAACG CCCTAACCAA TCTCATTTA	120
ATGCAAAGAG GCTATTCTAT GAACGCTAGA GCCTTGGCG CGGGCGATGA CATGATCAA	180
GAAGCCATTA GCTTGAAAAA A	201

## (2) INFORMATION FOR SEQ ID NO:1021:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 558 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
  
- (ii) MOLECULE TYPE: DNA (genomic)
  
- (iii) HYPOTHETICAL: NO
  
- (iv) ANTI-SENSE: NO
  
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Helicobacter pylori*
  
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...558

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021

AAGCTACATC GTGGATCCC AAAACAAAAAC CCTATCAATG ATCCTACTTG GGAAATTGTC	60
GGCTTGATT CAGCCACGCA CAAAATGAAA TCCGCCCGCA TGACTTGGG TTTTAAGGGC	120
AATAAACTCA CCTATTCTTT GGATAAGAGC GAAAACATGA TTCTAACCAA ATTGTTCTAC	180
CAAGACTCTA AACTCTTAAA AACGAGTCAA GAACGCAAGC CTAGGGGCAT TTTTAGAGAC	240
ATGCGCATTG AAGAAAATGG CGTGATTCT CTAGCCTTTA GTAACGGGGT GGTAGAGCCG	300
GTCGCTCGCA TCGGTATTT AGCTTCACT AACGATCAAC GCTTAAGGAA AATCGCCGGT	360
AACCTCTATG AAATGCAAGA AGGCACCATT AATGGCGAAA ACAGACCCCT AAGCGGTAAAC	420
CGCCATTCTA GGGTGGGACG AAGAGGGCAA GCTCAAGTTT GGGAAAATCA GGCACAAATA	480
TTTAGAAACG AGCAACGTGA ATGCCGGAA CGCCCTAACC AATCTCATT TAATGCAAAG	540
AGGCTATTCT ATGAAACGC	558

## (2) INFORMATION FOR SEQ ID NO:1022:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 516 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
  
- (ii) MOLECULE TYPE: DNA (genomic)
  
- (iii) HYPOTHETICAL: NO
  
- (iv) ANTI-SENSE: NO
  
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Helicobacter pylori*
  
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...516

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022

TGGATTTG TAGTTAAAT GGTGTTAGGG TTTTGATCC TTTTAAGGCC TTTGTGGCT	60
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ACTGGATTGG ATATTCACA AACAGACATT ATAGAGCGTT CTTTAAATTG CCTCTTGTT	120
GTGGGGATTT TGTGGTATTG TTTGGCTAAA AGATTGCGTT CATTGGCA TTCCAAAAGC	180
CTTGAATCT CCAAACGCTT AGAAGAGATT CAAGCCCAAC TTAAAGTGAG TAAAGAACAT	240
AAGAAAAAAC TCCTTAAAGA ATTAGAGCA GCCAAAGAAA AAGCTGAATT GATTATTCT	300
GATGCCATAA AAGAAGCCTA CACGATCAGC CAAAATACG ATTACAAAC CAAAATGGAT	360
GTGAAAATT TGATCAAAA TTCTAAGGC TTGATGGATT TAGAAGTTAA AAAGATCAA	420
AGAGAGTTGG TTGAAAGCGT TTTTAAGAT CTAAGAGAGA GTAAAAAAAGT GTCTTCAAT	480
GGCAGAGATT CGGTGAATAT TTTGAAACAA AGGCTT	516

## (2) INFORMATION FOR SEQ ID NO:1023:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 744 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
  
- (ii) MOLECULE TYPE: DNA (genomic)
  
- (iii) HYPOTHETICAL: NO
  
- (iv) ANTI-SENSE: NO
  
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
  
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...744

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023

ATGCAAAAAA GTATATTCAA AATAACTCTG TTGTTGGTTT TCCTCTTTT AAGGAATGCT	60
GTTGGTTTAG ACGATAAAA AGCAGCTCCT AAAAGCGTTC AAAATACCCC TAAAAATTTA	120
CCCCCTATCC AGTTAAGGCT CGATCAAGCC TATGAAGACC TTATCAAAAT GTTAGACAAT	180
ATGGGAAAAA GCACGCAGTA TGAGTTCCCT AAAATTAAAG AAATCTAGA ACAAAGCGAA	240
GAGGAATGCC TAGGAGTCGC CCATGAAGAA TGTGTTGGCGT TAGTCATGTT AATAAGCCCT	300
AAGGCTTCTA TTGAAAACAG CCCGATTAT AAGAATTGCT ATGAAGCTTA TGTGAAACAA	360
AGAATCCATG ATTTATATGA TTTTATATA GAGGGCAAAA AAGTGAAAAG AAAAATCAAG	420
AAAGCCCATG AGCATGAAAT GGCCCTCAAC AAATCCCAAC CCTTAAAAAA GGAACCGCCT	480
AAAAGCGAGA ATAAAAAGGG CTIAACAAAA CCTAGCTIGA AAGACGCCAA GATCCCTAAA	540
GGGTATTACT TGCAAATTGG GGCTTTTTA AATTGCCCCA GTAAGGATT TTTGCAAACG	600
CTCAAAACTT TCCCTCACCA AATGGAGGAA AAAGACTCCC TCACGCATTA TTTGATTGGC	660
CCTTATAAAA CCAAGAAGA AGCCCTAAAA CAGCTTGAAA ATGCCGCTAA AAGCTTAAA	720
AATAAGCCTG CGTTGGTAGA GAAG	744

## (2) INFORMATION FOR SEQ ID NO:1024:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 681 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
  
- (ii) MOLECULE TYPE: DNA (genomic)
  
- (iii) HYPOTHETICAL: NO
  
- (iv) ANTI-SENSE: NO
  
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...681

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024

AGTGGATGCT	ATTTGAATC	CAACTCTGAT	GTGTATGTGG	TTATCATTGG	CTTGGCCGAT	60
CAAAAATTC	GGCGTATCGT	GGATTATTG	ATCGCTCAAG	AAGAAGTGTT	CATCAAGTCT	120
TTAGGTTATT	ATCTTAAAAA	CACTAGAGGC	ATTGCTGGCG	CTACGGTGAG	GGGCGATGGG	180
AAAATCACTC	TCATTGTAGA	TGTGGGGCG	ATGATGGAA	TGGCAAAGAG	CATTAAAGTC	240
AATATCACTA	CCTTGATGAA	CGAGTCAGAA	AACACGAAAA	GCAAAAATTC	TCCTAGCGAT	300
TATGTTGCT	TGGCGATTGA	TGACAGCAGC	ACGGACAGAG	CGATTATCCG	CAAATGTTA	360
AAACCAATTAG	GCATCACGCT	CTTAGAGGCC	ACTAACGGCT	TAGAGGGCTT	AGAAATGCTC	420
AAAAATGGCC	ATAAGATTCC	GGACGCTTT	TTAGTGGATA	TTGAGATGCC	TTAAATGGAT	480
GGCTACACTT	TGGCCTCTGA	AGTGCCTAA	TACAATAAT	TCAAAAAACCT	GCCCTTGATC	540
GCCGTTACCA	GTCGGGTAAC	AAAACGGAC	AGAATGCGCG	GGCTTGAATC	CGGCATGACT	600
GAATACATCA	CCAAACCTTA	TAGCGGTGAA	TATTAACCA	CCGTAGTGAA	GGCGACGATT	660
AAATTAGAAG	GAGACCAATC	G				681

## (2) INFORMATION FOR SEQ ID NO:1025:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...828

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025

ATGACCCCTT	CACAAGCCCT	AAATAAAAGCC	AAAAAAGAAAT	TATCGCCAAA	AGGCTTTAGG	60
GGGGGGTTAG	AGTCTGAAAT	TTTATTAGGC	TTTGTCTTGC	AAAAAGAAAG	GGTTTTTTTG	120
CACACGCATG	AGCATTTGGA	ATTAAGCCAC	GAAGAAGAAA	CAACGTTTTT	TGAATTGGTA	180
GGAAAGCGTT	TGAATGACTG	CCCCATAGAG	TATTTATTAG	GAAGCTGTGA	TTTTTATGGG	240
CGCTCTTTTT	TCGTGAATGA	GCATGTTTA	ATCCCACGGC	CTGAAACCGA	GATTTTAGTC	300
CAAAAAGCCC	TTAATATTAT	TTCTCAATAC	CATTTAAAG	AAATAGCGGA	AATCGGCATA	360
GGGAGCGGAT	GCGTGTCCGT	GAGTTTGGCT	TTAGAAAACC	CTAATCTCTC	TATTTATGCG	420
AGCGATATT	CACAAAAGC	TTTAGAATG	GGCTTAAAAA	ATATTGAACG	CTTTTGTCTA	480
AAAGACGTG	TTTTTTTAAA	ACAAACGCGC	CTTTGGGATC	ATATGCCAAC	GATAGAAATG	540
CTTGTCTCTA	ACCCGCCCTA	TATCGCTAGA	AATTATCCCT	TGGAAAATC	CGTTCTCAA	600
GAACCGCACG	AAGCCCTTTT	TGGGGGGTT	AAAGGGCATG	AAATCTTAAA	AGAAATCGTT	660
TTTTTAGCCG	CTAAATTAAA	AATCCCTTTT	TTGGTTTGTG	AAATGGGGTA	TGACCACTTA	720
AAGAGCTTGA	AAAATGCTT	GGAGTTTGC	GGTTATGATG	CAGAGTTTA	CAAGGATTG	780
AGCCGCTT	ATAGAGGGTT	TGTGGCGTT	TTAAAAAGTT	TTTTAAGA		828

## (2) INFORMATION FOR SEQ ID NO:1026:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

756

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026

AAAGCCGTGT	TGTTCAACCC	ACTACCAACA	AAAAGGTCCG	TCATGCCCA	TTCTTTAAAA	60
AACCGTTTT	TAATCGTTA	TACCCCTTCT	ACCTTGTTT	TAGTGGGGGT	TTTGTAGCG	120
TTGTTTTCT	TTTATGCGAA	AAATAACCTT	TTGAAAACA	CCCAAATACG	CATGCAATAC	180
ACCGCTGATG	CGATCGCTAA	AAGCCTTTA	GAATTAAATA	ATGCCTCTTC	TTTAGAGCCT	240
TTAAAAATCT	TAGAAGAACG	ATTCAAAAC	ACCCCTTIG	TTTGTGTTGGA	CCGAGACAAAC	300
AGAGTCAGT	TTCTAATAT	CGGGGTGTT	GTCGGCTCTT	TTAAAAATGA	CGCCCTTAATC	360
AAAACCCCTT	ATTTTGCGCT	AAAAAACAG	GGCTTTTACC	TCACAGACAG	CGCCCCAACT	420
AACCGCTTAG	GGGTTCCTAA	AATCATTATT	GCAGAAGAAG	AAATCAAAA	AATCTTATC	480
CCCTTTATA	AAATGATAGG	CTATGTGTTT	TTGGGCGCGA	TTTGTGTTGT	CGCGCTAATA	540
GGCATGTGGC	TTTATAAAAT	CCCA				564

(2) INFORMATION FOR SEQ ID NO:1027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027

AAATATGCTTG	ATATATGGAT	AGATATGATA	ATCTGTATTT	TTTATTTGCT	CTTTTTTACG	60
ACTCCTTACA	TTGTTAGGGA	TATTTGCAA	TTGAAATTAA	TCCGTCAAAA	ACTCTGCGAG	120
AAGGCTGTCT	TACTCCCACA	AAAGGATTAT	GAAGAAGCGG	GAAATTATGCA	TATTAGGAAA	180
ATGCAATTAT	CCATTATTC	TCAAATTTTA	GATGGGTGA	TCTTTGCTGG	TTGGGTCTTT	240
TTTGGTTTGA	CGCATTTAGA	AGATCTCACG	CATTATTTAA	ACCTTCCCTGA	AACGCTAGGT	300
TACTTGGGTGT	TTGCTTGTGTT	GTTTTTAGCG	ATTCAAAGCG	TTTTAGCTTT	ACCCATTAGC	360
TACTATACCA	CCATGCATTT	GGATAAGGAA	TTTGGCTTT	CTAAGGTGAG	TTTATCGTTG	420
TTTTTTAAGG	ATTTTTTCAA	AGGATATTAG	CTCACTTTAG	GGCTGGGGTT	TTTGTGATT	480
TACACTCTCA	TAATGATCAT	TGAACATGTG	GAGCATTGGG	AGATCAGCTC	TTTTTTGTC	540
GTGTTTGTCT	TCATGATTTC	GGCTTAATCTT	TTTTACCTTA	AAATGCCCA	GCTTTCAAC	600
CAATTCAACCC	CTTGAATAA	TAGGGATTAA	GAAAGTCAAA	TTGAGAGCAT	GATGGATAAG	660
GTGGGTCTTA	AATCTCAAGG	CATCTTGTG	ATGGACGCTA	GCAAGAGGGA	TGGCGTTTG	720
AACGCGTATT	TTGGAGGCTT	GGGTAAAAAC	AAGCGGGTGG	TGTTGTTGA	CACTTTGATC	780

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TCTAAAGTTG GGACAGAAGG GCTTTAGCC ATTTAGGGC ATGAGTTAGG GCATTTAAA	840
AATAAGGATT TGTTGAAAAA TTTAGGGATT ATGGGAGGCT TGCTCGCTCT TGTTTTTGCT	900
TTGATCGCTC ATTTGCCGCC GTGGTTTT GAAGGCTTTA ATGTCACGCA AACGCCAGCG	960
AGTTGATCA CGATTCCTACT CTGTTTTG CCGGTGTTT CCTTTACGC CATGCCCTTG	1020
ATTGGGTTT TAGCCCAA GAACGAATAC AATGCCGACA AGTTGGGC GAGTTTAAGC	1080
TCTAAAGAGA CTTTAGCCAA AGCGTTAGTG TCCATTGTGA ATGAAAATAA AGCGTTCCCC	1140
TATTCGCACC CTTTTATGT TTCTTGATC TTCACGCACC CGCCGCTATT AGAACGCCTA	1200
AAAGCTTGG ATTATGAAAT TGAA	1224

## (2) INFORMATION FOR SEQ ID NO:1028:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...432

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028

ATAGAAGGA GACCAATCGT GAGCAATCAA TTAAAAGATT TATTTGAAAG ACAAAAAGAA	60
GCTAATGCAA GCTCTAAACA AGAAGACAT GAAGAATTIT TGCAATTATG TGGCTTTATT	120
ATTGGCGATG AAGAATACGC CATTCCCATT TTGAATATTG TAGAGATCGT CAAACCCATT	180
GGCTACACGC GAGTCCCTGA AACCCAAAC TATGTGCTTG GCGTGTCAA TTAAAGGGC	240
AATGCTTCTC CTTTGATCAG TTTGCCTTA AAGTTGGCT TGAAAGCCGA AAAACAAAAC	300
AAAGACACTC GTTATTGGT GGTACCCAT AACGATCGAT CGCTGGTTT TTCATCGCTT	360
TCTGGACTGA TGCCATCCGA ATCAGCATCC ACTATTGACC CGTCGCAGAA ACTGTGCGCG	420
ATAACAATAA TT	432

## (2) INFORMATION FOR SEQ ID NO:1029:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...897

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029

TCGTTCTCTA TCAATAGTTT TAAAAAGGCA AAGGGAATGA AATCTACAAG AATTGGTTCT	60
AAAATTGTCA TGATGGTGTG TCGGGTTGTT ATTGTCATTA GCGCTGTTAT GGGCGTTATT	120
ATCAGCTACA AGGTTGAAAG CGTGGTGCCTA AGCCAAGGCCA CAGAATTGCT GCAGAAAAAA	180
GCTCAGTTAG TCAGTTTTAA AATTCAAGGC ATTATGAAAGC GCATTTTTAT GGGCGCTAAC	240
ACCCCTGAAA GTTTTTAAAG CGATGAAAT GGCGCTATTAT ATGACACCCCT AAAAAGACGC	300
ATGCTCTCTG AGTTTTGTT AGCAAACCCCT CATGTTATG TGGTAGCGC GATTATACG	360
AATAATAATG AACGAATGAT CACTGCAATG AACATGGATT CAAAATCGC CTACCCCTAAT	420
ACCCCACTCA ATGAAAACAT GACCAACCAA ATCCATTGCGC TCAAAAGTAT AACCGTTCA	480
GATCCTATT ATAAAGAGGT TAATGGCGAT AAAATCTATG GCATGGACAT TACCCCTCCC	540
CTAATGGGCA AGAATCAAA TGTTATAGGC GCGCTGAAIT TCTTTTTAAA CATTGACGCT	600
TTTTATACTG ATGTGGTAGG CAAGAAAAAG AGCAACACCT TTTTAATGGG GAAAGACGGC	660
AGGATTTAA TCAACCCCTAA TCGTGAGATT CAAGATAAGA TTTTAAGCGC TATCAATCCG	720
GATAAAAGAG TCGCTAAAGC TGTGGAGTAT TACAATCAAA ACGAAGCGGG CACTTTGAGC	780
TACCATTCAT TGAGCGGGAA TACAGAAACC TTTTAGCCA TACAGCCCTT TGATTTTTT	840
GAAGAAAAAG GGAATAACGG CCAATCATTG CGCTTGGGCA ATTGGGAAAT ATGTCAA	897

## (2) INFORMATION FOR SEQ ID NO:1030:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...303

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030

GGGGTATTTT ACAATAGCTC TCTCCACAG CCCCCAACTA AAAACCCCT AACCCGAGAA	60
TACCGTTTT TAAAGAGATT ATCACTTATT TATGCAAGCT CTTTTATTGT ATTTATTTTA	120
AAAATGCCCT TTAAGCTTTT TTAAATTGTT TTACTCATGC TTAAATAAGCC AAAGCCCTTA	180
TTTTGCTCT TGGTTAAGCC TTCTCTCTAT CTTTTGATT TGGGGCTCA TTGAGCACT	240
CGCATTTGATT TGATTGATAA GCATGTAAAG GTTTATCATC ATCAAAAGCA CCACCACAAAG	300
CCC	303

## (2) INFORMATION FOR SEQ ID NO:1031:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

759

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...333

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031

TTTATCACTG GGATAGAAAT CCACCCGGGC GCTAAGATTG GGAGAGGGCT TTTTATTGAT	60
CATGGCATGG GTGTGGTGTGAGGAC ACAGAGATTG GAGATGATGT TACCATTAT	120
CATGGCGTAA CTCTGGGGGG TACGGGCAAG TTTAAGGGCA AACGCCACCC TACTTTAGGC	180
AACCGAGTGG TAGTTGGGGC AGGGGCTAAG GTCTTGGCG CGATTTGCGT GGGCGATGAT	240
GTGAGGATTG GGGCTAATGC GGTGGTGCTT TCAGATTAC CCACGGGTTTC TACGGCTGTA	300
GGTGCTAAAG CAAACCAT CACAAAGGAT CGT	333

## (2) INFORMATION FOR SEQ ID NO:1032:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1131

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032

AAAGGTTTT TAGGTGTTAA AAAAGTTATT GTTTTATTAA AAAAAAAGGG TGAGATGGTC	60
GTCAACTCCA AAGTGAAAC GCTTAAAGTC TTTCAAAAT TTTCAGCAA TTTCAAAATC	120
ACTAAACTCA AAGACAACCA CGAAGAACCC CACAAACTTT TTGGAGAAA TAGCGTAAA	180
GCCCATGACA CTGAGATCAT TTACTCCACT TTGCAAGTGG TCCCCAGGTA TTCAATAGAA	240
ACCGTGGGCT TTAGTTGTT GATTITAGCG GTCCGTTACA TCTTATTCAA ATACGGCGAA	300
GCTAGAATGG TACTCCCTAC CATTCTATG TATGCCCTAG CGCTTATCG CATACTCCCT	360
TCTGTAACTG GAGTGATCG CTATTATAAT GAAATCGCTT ACAACCAGCT TGCAACCAAT	420
TTTGTGTTAA AAAGCCTTC TAAGACCATC GTTGAAGAGG ATTAGTCCC TTAGACTTT	480
AATGAAAAAA TCACTCTCCA AAACATTTC TTCGCTTATA AAAAAAAACCA CCCGGTTTTA	540
AAAAATTTCACCTCACCAT TCAAAAGGT CAAAAAATCG CTCTCATAGG CCATAGCGGG	600
TGCGGAAAAT CCACGCTGGC GGATATTATT ATGGGGCTTA CCTACCCCTAA AAGTGGGAA	660
ATTTTATTG ATAACACCCCT TTAAACCAGC GAAAACAGGC GCTCATGGCG TAAAAAAATA	720
GGCTATATCC CCCAAATAT TTACCTTTT GATGGCACTG TGGGGATAA TATCGCTTTT	780
GGGAGTGTCA TAGATGAAAA ACGCTTGATT AAGGTGTGCA AAATGGCTCA TATCTATGAT	840
TTTGTATGCG AGCATGAGGG CCTTAAACAC CAAGTGGCG AAGGGGGCGC TAAGCTTAGC	900
GGCGGTCAAA AACAGCGCAT AGGCATCGCA AGAGCTTAT AGCATAACCC TGAAATTTC	960
TTTTAGATG AAGCCACTTC AGCCCTAGAC AATGAAACCG AGAGTAAAAT CATGGATGAA	1020
ATCTATCAAA TCGCTAAAAA TAAAACCTA ATCGTTATCG CCCACCGCTT AAGCACGATT	1080
GAACGCTGTG AAGTCATCAT TGACATGAGC CAACACAAAG ACAATCTCGG C	1131

## (2) INFORMATION FOR SEQ ID NO:1033:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

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(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033

GCCTATAAAA	AAGGGGAAAT	CATGGCGCTT	GAAGTGGTT	TATGGGATT	TGATGGCGTG	60
ATTTTGACA	GCATGCATT	AAAATATGAA	GGGTAAAGG	CGTTGTTCA	AAACCATGGC	120
AACGATAGTA	AAGAGGTTT	GAAACAATT	GAAGTTTATC	ACTATCAAAG	TGGGGGGATT	180
TCAAGGAATG	AAAAGATCCA	ATATTTTAT	AACCGAGATT	TAAAAACCCC	TATCGCTCAA	240
GAAGAAATAG	ATGCATTAGC	CCTAGAGTTT	GGCGCTATCA	TAGAGCAAA	GCTTTTGAT	300
AGGGGGCATT	TGAATAGCGA	AGTGATGGCG	TTTATTGATA	AGCATTATCA	AAATTATATT	360
TTCCATATCG	CTTCAGCGGC	CTTGCATAGC	GAATTGCAAG	TGTTGTGCAG	GTTTTTAGGG	420
ATTACTAAGT	ATTTTAAGAG	CGTTGAAGGG	AGTCCGCCTG	ATAAACCCAA	GATTATCGCT	480
AATATCATTC	AAAATACCC	CTATGACCCA	AGCCGTATGC	TAATGATAGG	CGATAGCGTC	540
AATGATTATG	AAAGCGCTAA	GGCTAAATAAA	GTGGCTTTT	TGGGCTATAA	CAGCAAGGTT	600
TTGAAAAATT	TAGTGGGCA	AGATGGCTAT	CAAGGAACT	ATTTGGAGAG	CTTTAAGGGG	660
TTTGTATTAC	AAAACCTCCG	AAAAGAG				687

(2) INFORMATION FOR SEQ ID NO:1034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034

AATAAAAGCA	TGCAGCCATT	AGTCTTAATC	GGTTTTATGG	GGAGCGGTAA	AAGCTCTCTA	60
GCACAAGAAAT	TGGGCTGGC	TTTGAAATT	GAAGTCGCTGG	ATACGGATAT	GATCATTAGC	120
GAGAGGGTGG	GCTTGAGCGT	GAGAGGGATT	TTTGAAAGAGC	TTGGCGAAGA	CAATTTCAGG	180
ATGTTTGAAA	AAAATTTGAT	TGATGAATTA	AAAACGCTCA	AAACCCCCCA	TATCATTCT	240
ACCGGTGGGG	GCATTCTGAT	GCATGAAAAT	CTTAAGGGTT	TAGGCACAAC	TTTTTACCTC	300
AAAATGGATT	TTGAGACCTT	GATTAAGCGT	TTGAATCAA	AAGAAAGGG	AAAACGCC	360
CTTTGAATA	ACCTCACTCA	AGCCAAAGAG	CTTTTGAAA	AACGACAAGC	CCTCTATGAA	420
AAAAACGCTT	CCTTTATCAT	TGATGCAAGG	GGTGGTTAA	ATAATTCTTT	AAAACAAGTG	480
CTACAATTCA	TCGCA					495

## (2) INFORMATION FOR SEQ ID NO:1035:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 975 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...975
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035

ATTTTTTTTA AAGGCCTTGT GATGTTAAGT AGAGACATTG TCCAATATTG CAAGATCCGC	60
ACCGAGTTAT ACGCCTACCT CACTTATTG TTTTCGCACA ATATCCGCAA CCACCTTCCT	120
GAAATCACTT TGGATTATTAA AACAGGCAA ATCAAGTAAGA TGCAAGCTGA AATCAAATG	180
GCAAAAAGTT TTTTGTGTTT AGACGCTAAG GGCATGCTCA TGCTTAAGCC AAGCCAATT	240
AAAGAGCAGG GGCATAAGGA AGGGCTATTAG GAGCATGATT TAACAGAAGG GATTGAATT	300
GAATCGCATG TCAGTTTATAG CGATAAGTAT TATTTTTATC AAGCCGTGAA TGAAAAGCGT	360
TGCATTTTAA CGCACCCCTA TCCTCTAA AAAGGGAAACC ATTTCGGTAGT GAGCGCGTCT	420
TACCCGGTGT ATGATCAAAA TAACGATCTA GCGTTTGTGG TGTGCTTGCA AATCCCTTG	480
AGGGTGGCGA TTGAAATCAG CTCGCCTCTA AAGTATTAA AACTTTTAAAGGAGG 540	540
ATGGTCATGT ATTTTATGAT TTCTATCATG CTCACTTTAG TGTGCTGCT TTTATTGGT	600
AAATGCATTT CTAGCTTTG GACAGCGATC GTGCATTAA GCAGTTTGA CATTAAAGAA	660
GTGTTCCACC CCATTGTGCT TTTAACCTA GCTTTAGCCA CCTTTGATTT GGTCAAGGCG	720
ATTTTGAAAG AAGAAAGTGTGTT GGGTAAAAT AGCGGGGACA ACCACCATGC GATCCACCGC	780
ACCATGATCA GGTTTTAGG CTCTATCATT ATCGCATTAG CCATTGAAGC GTTAATGCTC	840
GTGTTAAAT TCAGCGTGAG CGAGCCGGAT AAAATCACTT ATGCCGTGTA TTTGGCTATC	900
GGCGTGGCGG TGCTTTGAT CAGTTGGCG ATTATGTTA AATTGCTTA TAGCGTGTG	960
CCCCAACGAG AACGC	975

## (2) INFORMATION FOR SEQ ID NO:1036:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 592 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...592
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036

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GAGAGTTATC AAACGGTATT TACACGCCAG AGGTATTATC AGCGGTTGTT TAGACGAGCT	60
GTTCGTAGGA ACCTGCGCGT CTGTGAGTTT ACAAAATCAAATAACAAGAG GGGTGATTGT	120
CAACGTCAGC AGTAGCTTTT CTATGGGCT TACCATGGCG AGTGCTTATG ATCCCATTTC	180
AGGATCGCAA AAACCCATTG TGGGGCAAGC CCTTTTATIG TTAGCGATTT TAATTTTATT	240
GGATTATCG TTCCACCATC AAATCATTAA ATTGTGGAT CACAGCTTAA AAGCCGTCCC	300
TTAGGGCGA TTGTGCTTTG AGCCAGAATT AGCTAAAAAC ATTGTCAAAG CCTTTTCACA	360
CTTGTGTC ATAGGGTTTT CTATGGCGTT CCCTTATTTA TGCTTGGTGT TATTGAGCGA	420
TATTATTTT GGCGATGATCA TGAAAACCCA CCCTCAATTIC AACCTGCTCG CTATCGGGTT	480
TCCGGTTAAA ATTGCGATCG GGTTTGTGGG CAATTATTTA ATCGCTTCGG CTATCATGGG	540
GCCTTTAAA GAAGAAATCA GCCTGGCCTT TAGCGTTATT AGTAAAATCT TT	592

## (2) INFORMATION FOR SEQ ID NO:1037:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1332

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037

GGGGTTTTGC GTTTCTCTAT CTTTTTAAA GTTGTGCGTT TGTTTATGAT AACGCTCTT	60
AGTTTTGGAG CGTTGCTTA CTATTCGTG TCTTCTAAA TCAGTCACGA AACTATCAA	120
AACGAAATGC GCCATTACCA GTTTGTTACC ACTATCAATG AAATTTAAA TAACTACTCT	180
GATTATAGAG CCATAGAAGA TTACCTCTAT AAAATTGGCT TTAGAGAAAC CACAATAGAA	240
AATTAGAAA AGGTTTATG CAAAGAGCG ACCAGTGTG ACCACAGAAA TATTGGTAT	300
GCTGAAGTGT TAAATTCAAG CGATATGGTT TTATCCTTT TAAAAAAAGGA TGAGCATT	360
GTGCTTATA AGATTTGCA TTCGGTTTCT TATAGGAATT ATTTCCTTAC CATTACGGTG	420
GGTTTATTAT TGATTTTATT CCTCTTTTTA TTGTTTGC AGAGTTTATT GCCTTTAAGA	480
GAGTTAACAT CTCAAGTGAAC CGCCTTCGCT CAAGGGATA AAAGCGTGAG TTGTAAAAGC	540
AAGAAAAAG ATGAAATAGG GGATTGGCT AACGAATTG ACAATTGCAT CCAAAAATC	600
AATGCGATGA ATGAATCTCG GGTTTTATTT TTGCGCTCTA TCATGCATGA ATTACGCACC	660
CCTATCACTA AGGCGAAGAT ACTAAGCTCT ATGTCAAAG AAGAGCTGTC TTGCAAACGC	720
TTTCATCTA TATTGATCA CTTGAACATG TTGATTGAGC ATTTCGCCCC CATTGAGCAG	780
CTCGCTTCCA AAAATTATGG GAGCAATAAA CAAATTATT TAATGAGCGA TTGATAGAT	840
AAGATTGAAA AAAATGCTTT AATTGATGAA GATAAAAAAA GCCCTATCCA TGTATCCTCT	900
TCAAATTACA TCATGAAAGC GGATTITGAA TTGTTGCTA TAGCGTTAAA AAACATGATA	960
GACAATGCGA TCAAATACAG CGATGACAAA CAGGTGTTT TGGATTTCAT AGGGATAAT	1020
TTAGTGGTGT CCAATAAAAG CAAACCTTTA AAAAGAATT TTGAAAAGTA TTGCAACCC	1080
TACTTTAAAT CTTCTAACCC CAGCCAAGCC CATGGTTTG GTTGGCAT GTATATCATT	1140
AAAAACGCTT TAGGGCTAT GGGATTGAAT TTGAGCTATC ATTATAGCAA TGAAGAATC	1200
TGTTTCACTA TCCATGATTG CGTTTTAAT AGTTTTACG ATTAGAAGC GGATAATGAA	1260
GAGCTACCCC CCCCGAAGAATTTGAGAGA GGTGAAGGGAA ATGAAGGGAA CAGAAAAGC	1320
CAATTGTGGG GT	1332

## (2) INFORMATION FOR SEQ ID NO:1038:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038

AGAAAAACAA AAAGAGAGAA CATGTTCAAA CGATTGAGAA GATTACGAAG CAGCGAAAAT	60
TTAACAGCGA TGGTGAGAGA AACACGTTTA AATATTAATG ATTTCATCGC TCCCTTATTT	120
GTCATAGAAA GCGATAGCGG TATTAAAAC GAAATCAGCT CCATGCCCTGG CGTGTATCAA	180
ATGAGTATAG AGCCTCTTTT AAAAGAATGC GAAGAATTAG TGGGTTTAGG CATAAAAGCC	240
GTTCATTGTTG TTGGCATTCG TAAACATTAAG GACGCTACAG GAAGCCATGC GTTAAATAAG	300
GATCACATTG TCGCAAAAGC TACGAGAGAA ATTAAAAAC GATTTAAGGA TTTGATCGTT	360
ATAGCGGATT TGTGTTTTTG CGAATACACC GACCATGGGC ATTGCGGGAT TTTAGAAAAC	420
GCTTCTGTGT CTAACGATAAA AACGCTAAAG ATTTAAATC TTCAGGGCT TATTTTGCGT	480
GAAAGCGGTG TGGTATTCT AGCTCCAAGC AACATGATGG ATGGCAATGT TTAAAGCTTG	540
AGAAAAGCAC TGGATAAGGC CGGGTATTTT CACACGCCA TCATGAGTTA TTCCACTAAA	600
TTTGCAGGCA GTTATTACGG GCCTTTAGA GATGTAGCCA ATTCTCCGCC GAGTTTTGGC	660
GATCGCAAA GCTATCAAAT GGATTACGCT AACCAAAAG AAGCGCTTTT AGAAAGCTTG	720
GAAGATGAAA AACAGGGTGC GGATTTTA ATGGTGAAGC CGGCTTACG GTATCTGGAT	780
ATTGTTAAAG AAATCAGAGA TCACACTTGT CTCCCTTGT CGCTCTATAA TGTGACTGGG	840
GAATACGCCA TGCTCAAACT CGCTAAAAAA CACAACCTGA TCAACTATGA AAGCGTTTA	900
TTAGAAACGA TGACTTGTGT TAAAAGAGCG GGAGCGGATA TGATTATTAG CTATCATGCT	960
AAAGAAGTGG CTAACCTTATT ACAAAAGGAAT	990

(2) INFORMATION FOR SEQ ID NO:1039:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1086 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039

AGCGCAGGGC GCATTTGGC AGAGGATATT ATTCGCTTC ACAGCTTGTCC TAAATTCAAT	60
CAAAGCGCTA TGGACGGCTA TGGGTTAAAT ATGCAAGACT TGGGCCAAA AACTCAAGTT	120
ATCCAACACA TCTTTGCCGG GGATGATGTG AGCGCTTTAG AAGTCAAAGA AAATGAATGC	180
GTTCATGCTAG TGACTGGAGC GATGGTGCCA AAGGAAATAG AACGATCGT TCCCCATAGAA	240
TGCATGCTAG AGAGTCATAA AGATTCGCC CTAGCTCTA AAGATTTAA AATTACACGCT	300

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AATATCCGTC	AAAAGGGCGA	GAACGCTTCT	TTAACACAGG	TTTTAGTCCC	AAAAAATACC	360
CGTTTGAATT	ATGGCCATAT	CGCGCTCATT	GCCTCTCAAG	GGTTCAAAGA	AATCAAAGCG	420
TTTAGAAAAT	TAAAATCGC	TCTCTTACT	AGCGCGATG	AATTAGTGCC	TTTAGGGCAA	480
AACCCCTAG	AGTGCCAGGT	TTATGATGTT	AATTCACTGG	GTGTTTTAA	CATGCTTAAA	540
AACTACAACA	CGCATTTCCT	AGGGGTTTA	AAAGATGATA	AAAATTACA	GCTTAAAATA	600
CTTGAATTGC	AAGGCTATGA	TGTCATCCTT	TCAAGTGCAG	GGGTGAGCGT	AGGGGATAAA	660
GACTTTTTA	AAGACGCTTT	GAAGAAAGA	AACGCCCTT	TTTATTACGA	AAAAGTCAAT	720
CTCAACCTG	AAAAGCCGGT	AACTTTAGCC	CAACTCAATC	AAAGCATTAT	TATAGGCTTA	780
CCGGTAATC	CTTTAAGTTC	CTTACTGGTT	TTACCGAGTT	TGATTCTACC	CTTATTGGAG	840
CGCTTATCCT	TAATAAAAGA	TTTTAAATTA	AAACCTTTA	AGGCTCAAAT	CAATGCCCT	900
TTAAAGCTTA	ATAACAAACG	GACGCATTA	ATCTTAGGCA	ACTATTCAA	CCACCAATT	960
ATTCCCTTACA	ACAACCGCTA	TGAATCAGGA	GGCATTCAAG	CCCTTGCAGCA	AGTGGATTCT	1020
ATCGCTTAA	TTGATGAAGG	AGTCGGATTG	GTTCAAGGGCG	AAATTGAAAT	TTTAAGGTTT	1080
GAAAAT						1086

## (2) INFORMATION FOR SEQ ID NO:1040:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040

GGGAATTACG	GCCTAGAGAT	TAGATTIAAG	GAAATGGCAG	TGTTAAAAAA	GATGATAGGT	60
TTGGTGGCGG	TTTTAAGCGT	TTTATTAGCC	AGAGACAAAC	CTTTTGAGCC	TGAAATCAA	120
TCCAAGAATT	TGCAAGGGGG	CTTTAGCGGG	ATCTATGATG	ACTACCTCAA	AGAAATCCAT	180
GTGGATTTCG	CCACGAGCGC	TAGGATCTTA	AAAAAAATCA	CCCTCACTTA	CCAAGATAATT	240
GATGGCTCTA	TCCATTCTAA	AGTCGTGGGT	ATTGATAAAA	GCATTGATTG	GCACTACCCC	300
TTAAAACCTT	CCCAACACAC	CCTTAATCAA	GACGCCCTTG	AAAAACGCTA	CCAGATCCAA	360
GATTTTGATT	TTTTAATGGC	AAAACACACG	ATGATTTCGC	GTTCCTTCA	TAAAATTTTG	420
CGCTCTTTTG	TGTTAGTCAA	TCTTATAGA	ATCGTGTGTTAG	ACACGCAAAA	AGGCCCTTTG	480
GATATTATC	AAAACATGGA	TTTAAACACG	AACTTTTTTT	CTCACATTAA	AGTCGGCAGC	540
CACAAAGGAT	ATTACCGCAT	CACGCTCATT	TTAGACGGGA	AATACCGCTA	TCTTTTGAA	600
GAAAAAAACG						633
GGCGTATGA	ATTAAAATG	AAA				

## (2) INFORMATION FOR SEQ ID NO:1041:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041

AAAGCAGTGG	CTACGCCTCA	CCACACCCCC	TTATGGCTCA	GCGTGTATGA	AAGCTTTAAA	60
GAAGCCCTAG	ACTTTAAGGA	AGTCATTCTA	GTGTTAGCG	AATTGGATT	TGTTTATATT	120
CAACGCCATT	ACCCCAAAT	CAAGCTTGTA	AAAGGCGGGG	CATCAAGGCA	AGAATCCGTG	180
CGTAAACGCTT	TGAAAGTAAT	TGATAGCACT	TACACGATCA	CCAGCGATGT	GGCTAGGGGT	240
TTAGCGAATA	TGGAAGCGCT	AAAAAGCTTG	TTTTTAACCC	TCCAACAAAC	GAGCCATTAT	300
TGCATCGCCC	CTTACTTGCC	TTGCTATGAC	ACAGCGATCT	ATTATAACGA	GGCTTTAGAT	360
AGAGAACGCA	TCAAACCAT	TCAAACCCCG	CAATTAAACCC	ACACCAAAAC	GCTCCAATCA	420
GCCCTAAACC	AAAGGGGTTT	AAAGATGAA	AGCAGCGCGA	TTTACAAGC	TTTCCCTAAC	480
TCTGTGAGCT	ATATTGAAGG	CACTAAGGAT	TTGCACAAAC	TACCCACAAG	CGGCGATTAA	540
AAGTTTTTA	CGCCTTTTT	TAACCCAGCA	AAGGACACTT	TTATAGGCAT	GGGTTTTGAT	600
ACGCATGCGT	TCATTTAAAGA	TAAGCCTATG	GTGTTAGGGG	GGGTTGTTT	GGATTGCGAG	660
TTTGGGTTAA	AGGCTCATAG	CGATGGCGAT	GCTTTATTGC	ATGCGGTTAT	TGATGCGATT	720
TTAGGAGCGA	TTAAAGGGGG	GGATATTGGC	GAATGGTCC	CTGATAATGA	CCCCAAATAC	780
AAAAACGCCT	CTTCTAAAGA	GCTTTTAAA	ATCGTGTGTTG	ATTTTCTCA	AAGCATTGGG	840
TTTGAATTGC	TTGAAATGGG	AGCGACCATC	TTGAGCGAAA	TCCCTAAAAT	CACTCCITAC	900
AAACCGGCGA	TTTTAGAGAA	TTTGAGCAA	CTTTGGTT	TAGAAAAATC	TCAAATCAGC	960
TTGAAAGTCA	CTACAACTGGA	AAAAATGGGG	TTCATGGCA	AAACAGAAGG	GCTGTTAGTC	1020
CAAGCGCATG	TGAGCATGCG	TTATAACAA	AAACCTT			1056

(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 615 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042

TGCTTGGGGA	TGTGTTTAT	TCTAAAGCCT	TTTTTGAGTT	GTCTAAAATG	GGCGAATCCA	60
TCGCTCAAGC	CCCTCTCTAA	TGCGGTTTTA	AGGCTCTCTA	GGGGCGAGAT	TGAAGACGTG	120
TTTGTTGGGG	AAATGTTTAA	TAGCGACAAA	CAAAAATACT	GGCGTATTTT	AGAAGACAAG	180
ACCGCCCAT	TCACTAGAACG	GAGCTTAAA	AGCATGGCGA	TTCTTTTAAA	AAAGACGCC	240
AAAATGTATC	CGGATTTGG	TTGCACTTTT	GGCATGGCGT	TTCAAATCAT	TGATGATTG	300
TTAGACATCA	CTCAAGACGC	CAACACTCTA	GGTAAGCCCA	ATTTTAGCGA	TTTTAAAGAG	360
GGCAAGACCA	CTCTACCCCTA	CTTGCTTTA	TATGAAAAT	TGAATCAGCA	TGAACAAGGG	420
CTTTAAATT	CCTATTTCAA	ACAAGATAGT	CATGAAATCA	TAGAATGGAC	TAAGGAAAAA	480
TTCAAGCAAC	ATGGTATCAT	AGAAGAAACC	CTTAAATCG	CTCAAGTTA	TTCTAAAAG	540
GCCCTTGAAG	CCATTAAGG	GGAAAACAAT	TTGATTAG	AAAAACTAGC	GCAAGATGTC	600
ATTTATAGGA	CTTTT					615

## (2) INFORMATION FOR SEQ ID NO:1043:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 393 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...393
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043

AAGAAGGTAA AGATGAATAT CAAAATTATA AAAATATTAG TTGGAGGGTT ATTTTTTTTG	60
AGCTTGAACG CCCATTTATG GGGAAACAA GACAATAGCT TTTTAGGGAT TGGTGAAGA	120
GCCTATAAAA GCGGGAATTAA TTCTAAAGCG GCGTCTTATT TTAAAAAAGC ATGCAACGAT	180
GGGTGAGTG AAGGCTGCAC GCAATTAGGA ATCATTTATG AAAACGGGCA AGGCACTAGA	240
ATAGATTATA AAAAAGCCCT AGAATATTAT AAAACCGCAT GCCAGGCTGA TGATAGGGAA	300
GGGTGTTTTG GCTTAGGGGG GCTTTATGAG GAGGTTTAG GCACGGCTCA AAATTATCAA	360
GAAGCCATTG ACGCTTACGC AAGGCATGCG TTT	393

## (2) INFORMATION FOR SEQ ID NO:1044:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 717 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...717
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044

TCCAGCAAAA CAGCATTTCAG GGCAAAGCAA ATCATCACCG CAACCGATAT TAGCGCTCAA	60
AAACGCCAAG AGCGGCTCGC TTCTATGGGG AAAATTTCAG CGCATTTAGC CCATGAAATC	120
AGAAACCCCC TAGGCTCTAT CTCTCTTTTA GCTTCGGTGT TATTAAGCA TGGAACCGAA	180
AAAACCTAAC CCATTGTTGT AGAATTGCAA AAAGCTTAT GGCAGCTAGA AAGGATCATT	240
AAAGCCACCT TGCTTTTTTC TAAAGGCATT CAAGCCAACC GCACCAAGCA AAGTTTGAAA	300
ACGCTAGAGA GCGATCTCAA AGAAGCCCTA AACTGCTACA CTTACTCTAA AGACATTGAT	360
TTTCTTTTTA ATTTCAGCGA TGAAGAAGGG TTTTTGACT TTGATTTAAT GGGGATTGTG	420
TTACAAAAATT TCTTGTATAA CGCCATTGAT GCGATTGAAG CCTTAGAAGA GAGCGAACAA	480
GGTCAGGTCA AAATTGAAGC GTTCATTCAA AATGAATTAA TTGTCCTTCAC CATTATTGAT	540

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AATGGCAAGG AAGTGGAAAA TAAAAGCGCT TTATTTGAGC CTTTGAAAC CACTAAATTA	600
AAGGGGAATG GCTTAGGGTT AGCCCTGTCT TTGCAAGTCG TTAAAGCCA TGAAGGGAGC	660
ATTGCGCTAT TAGAAAATCA AGAAAAAACC TTTGAAATTA AGATTCTTAA CGCTTCT	717

## (2) INFORMATION FOR SEQ ID NO:1045:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 465 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
  
- (ii) MOLECULE TYPE: DNA (genomic)
  
- (iii) HYPOTHETICAL: NO
  
- (iv) ANTI-SENSE: NO
  
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
  
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...465
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045

AAGCCTAAAA CAATTTAAA AAAAGGACTT TTGATGAAAA CATTGAAAT TTTAAACAT	60
TTGCAAGCGG ATGCCATCGT GTTATTTATG AAAGTCATA ACTTCCATTG GAATGTGAAA	120
GGCACCGATT TTTCATGTC GCATAAGCC ACTGAAGAAA TTATGAAGG CTTCGCGGAC	180
ATGTTTGATG ATTCGCTGA AAGGATCGT CAATTAGGAC ACCACCCCCCT AGTCACTTA	240
TCCGAAGCGA TCAAACTCAC TCCTGTTAAA GAAGAAACTA AAACGAGCTT CCACCTAAA	300
GACATCTTTA AGAAAATTCT AGAGGACTAC AAACACCTAG AAAAGAAATT TAAAGAGCTC	360
TCTAACACCG CCGAAAAAGA AGGCATAAA GTTACCGTAA CTTATGCGGA CGATCAATT	420
GCCAAGTTGC AAAAATCCAT TTGGATGCTA GAAGCCCATT TAGCT	465

## (2) INFORMATION FOR SEQ ID NO:1046:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 393 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
  
- (ii) MOLECULE TYPE: DNA (genomic)
  
- (iii) HYPOTHETICAL: NO
  
- (iv) ANTI-SENSE: NO
  
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
  
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...393
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046

GGAATTTGCA TCCAAGAAAA ACGACTTAAA GCCATTCAAA ACAAAATCGC TTCTTGGATC	60
AAGGAAATTG AAAGCGGCTT TATAGATGCA TTGTTTCTA AGATTGGCCC TTCAAAGATG	120
CTGCGCTCCA AACTCATGCT CGCTTTGTTA GACGAAAAAA CAGACGCTAT TTATTAGAT	180
AAAGCGCTCA ATTGTGTGCA GATGTGCAA ATGATACAGA CCGCTTCTT ATTGCATGAT	240

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GATGTGATTG ACAAGCGAC CATGCGCCGA AAGCTCCCTA GCATTAACGC TCTTTTGGG	300
AATTAAACG CCGTGATGCT TGGGGATGTG TTTTATTCTA AACCTTTT TGAGTTGTCT	360
AAAATGGCG AATCCATCGC TCAAGCCCC CTC	393

## (2) INFORMATION FOR SEQ ID NO:1047:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1731

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047

TGCATGCTAT TTTCAAAACT TTTTGCCTCA ACGCTCAAAG AACCCCCAAA AGACGCCGTG	60
TTAAAAAGCC CTAAGCACCC CGGGAACGGG GGACACCCCC TTCAAATAGG CAGTGGATT	120
TATAATTCC TACCCCTAGC TAAAAAAAGTG CTAGACAAAA TAGAAAACGT CACCCACAAA	180
CGCATGCAAG AGCATGGGC GCAAAATTATT TTAATGAGIT TCTGGTTTTT GGGAGTTTG	240
TGGGAAAAAT CAGGGCGTTT GGATAAAATAC GGCAAGGAAT TATGGTTTT TAAAGACCGA	300
AAAGACAATG ATTTTGTGTT AAGTCCCCT TTAGAAGAAA ATATCACCGA AATTGCCGCT	360
AATTTCATCA AAAGCTACAA GCAATTACCC GTGCATCTCT ATCAAATCCA CACGAAATTC	420
CGTATGAAA TCCGCCAAAG ATTGGGTG TGAGAGCGA GGGAAATTAT CATGAAAGAT	480
CGTTATAGCT TTCATGAAGA CGCTGAAAGC TTGGATAAGG AAATTTAAA CACGCAAAGC	540
GCTTATAAAG AGATTTTAAG CGATTTGGGT TTGGATTITC GCATTTGTTA AGCGGATAGC	600
GGGGCATTG GGGGGAGTAA AAGCAGGGAA TTGTCGTTT TAACAGAAATG CGGGGAAGAC	660
ACGATCGTGG TGTGTCAAAT TTGCGATTAT GCCGCCAATA TTGAATGCG TAAACGCTCT	720
AAAAGAACTG AGCCTTTAAT GTCCCCAAGC GCATTAGCGA AATTCCCCAC CCCTAATACC	780
ACCAAGCTC CAAGCGTGGC GGAGTTTTT AAAACAGAGC CTTATTTGT CTTAAAAGCG	840
CTTGTAAACA AAGTGTACCA TAAAGATAAA GAAACCTAG CGTGTCTTT TGTTAGGGC	900
GATGACAATT TAGAAGAGAC TAAAGCCCTA AACACTTGA ATCTTTTGGG GGCGAACGCT	960
TTAGAATTAA GAGAGGCCAA TGAAGAAGAT TAAATAAAG CAGGGTTAAT AGCGGGCTTT	1020
ATAGGGCCTT ATGGCTTGA AAAGCATGTT IGTATATAA TTTTGTGAGA AGATTTAAA	1080
GAGGGCATT GCTTGTATCGT TGGGGCTAAT GAAAAGGATT TTCAATGCGT GGGCGTGGAT	1140
TTAAAAGGT TTGAAACCT TGTGTATGCG GATATGTCG AGGTTAAAGA GAGCGATGTT	1200
TGCCCTAATT GTCAAGGAGC GTTGAATAC CATAAGAGTT TGGAAAGTGG GCATATTTC	1260
AAACTCGGGC AAAGCTATGC TAAAGCTTG AAGGCTAGTT TCTTGGATAA GAATGGCAA	1320
GAGCGGTTT TTGAAATGGG GTGCTATGGG ATAGGCATTA GCGGGTTGCT CAGCGTGT	1380
TTAGAGCAA AAAGCGATGA TCTAGGCTGT GTGTTGGCGA AAAATACCGC TCCTTTGAT	1440
GTGGTGATCG TGTTTCTAA CCTGAAAGAT GAAGCGAAA AAAAACTCGC TTTTGAAGTG	1500
TATGAAAGAC TGCTCCAAA GGGCGTTGAT GCGCTGTAG ATGACAGAGA CGCTCGTTT	1560
GGGGCGAAGA TGAGGGATT TGAATTGATT GGGGAACGAT TAGCCTTGAT TGTGAAAAG	1620
CAAACTTAG AGAGTAAGGA ATTTGAATGC ATCAAACCGC CTAATTAGA AAAGCAAACG	1680
ATCAAAGACA TAGAATTAGA AGAAAAATT TTAGAAATGT TAGCGAGCGA A	1731

## (2) INFORMATION FOR SEQ ID NO:1048:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

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(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048

ATTCGTGAGC CACAGGTTGC AATAATGACT GCAATGATGC GTTATTTCA CATCTATGCG	60
ACCACCTTTT CTCTCCCTTT GGCGCTCTT TTTGGGTTA GTGGGCTTTC ATTGCTCTTT	120
AAAGCGCGCC AAGACACTGG CGCTAACATC AAAGAATGGG TTTTAGAAAA ATCCCTTAAA	180
AAAGAAGAAC GATGGGACTT TTTAAAAGG TTTTAAAGG AAAACCATAT CGCTATGCC	240
AAAAGAGATAG ACCTAGAGA GTATAGGGGA GCGTTAGTCA TTGGCACGCC TTTGTATGAA	300
ATCAACCTTG AAACCAAAGG CACTCAAAGG AAAATCAAAGA CCATTGAAAG GGGCTTTTA	360
GGCGCGCTCA TCATGCTGCA TAAGGCTAAG GTGGGCATCG TGGTCAGGC GCTTTAGGG	420
ATTTTTGCG TGTTTTTATT GTTGTTCATC TTGAGCCGT TTTAATGGT GGCTTTAAA	480
GACACTAACAC GCATGTTAT AAGCGTTTA ATAGGGACCG TGGTGTCTT TGGAGCGATC	540
TATTGGTCTT TG	552

(2) INFORMATION FOR SEQ ID NO:1049:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049

CTAATAAAAA GCAAATCAA AAAAGTGGCTT TTGGTAGGGG AAGGGGGCGAA TAGTGAATC	60
TTTGAAAGCTT CCATGCAATC GCTTTTAAAAA ACGGATGGCG TTTATTCTAA CCACAAACCT	120
ATTTATCAAG AGTTTTACGA ACTCAATTG CATAACGGGT TGTTATTATCA GCCTAATGTG	180
TTTTTGCTT ATGAATCTTG CGCGTTAGGG TTTAGAAAAG GGGGGTTAAT TTTCGATAAT	240
TTTTCTAAAT TCGTGAGCCA CAGGTTGCAA	270

(2) INFORMATION FOR SEQ ID NO:1050:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 849 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

770

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050

ATCGTAGAGA	GCGTGAACGT	TAAAATTCT	GCAGACGATA	TTAAATCTAA	AAATGTCGCT	60
GGCGTGATGA	TTACAGCCTC	CTTCCCCCCC	TTTCAAGAC	AGGGCGATAA	AATTGATATT	120
CACATTCTT	CTATTGGCGA	TGCGAAATCC	ATTCAAGGAG	GGACTTTAGT	GATGACCCCT	180
TTAAATGCGG	TAGATGGAA	TATTTACGCC	CTCGCTCAAG	GGGCTATCAT	TTCGGGTAAT	240
TCTAGTAACT	TGCTCTCAGC	CAATATCATC	AACGGGGCGA	CTATTGAAAG	GGAAGTTTCG	300
TATGATTGTC	TCCATAAAAA	CGCCATGACT	TTAACGCTGA	AAAACCCCAA	TTTTAAAAAC	360
GCTATCCAAG	TGCAAAACAC	TTTAAATAAG	GTATTGGA	ATAAAGTAGC	CATAGCGCTA	420
GATCCCCAAA	CCATTCAAA	CACCCGCCA	GAGCGCTTT	CTATGGTGGA	GTTTTTAGCT	480
TTAGTCAAG	AAATCCCCAT	TTACTACCAC	GCGAAAAATA	AGATCATTGT	AGATGAAAAA	540
TCAGCCACGA	TCGTTTCAGG	AGTGGATATA	ATCGTCATC	CTATAGTGGT	TACAAGCCAA	600
GACATCACGC	TTAAAATCAC	AAAGAGCCT	TTAAATGATT	CTAAAAACAT	GCAGGATTAA	660
GACAATAACA	TGTCCTTAGA	CACCGCTCAC	AACACGCTGA	GTTCCTAACGG	AAAAAACATC	720
ACCATTGCCG	GGGTGGTAA	AGCCTTACAA	AAAATTGGCG	TGAGCGCTAA	GGGGATGGTT	780
TCAATCTTGC	AAGCCCTAA	AAAAGCGGC	GCGATTAGCG	CGAAATGGAG	ATACTATGAT	840
AAACAAACAA						849

(2) INFORMATION FOR SEQ ID NO:1051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051

ACGGGACATG	GCAGGTTAGG	GTGGATATTA	AATCCAAAGA	AGGCCAAGTT	TATCGCACTA	60
AAACAAGCCT	GGATTTATGA	GCGCATGCTA	TCTTTTATAA	GGCGGTTGA	AAAAAGGGGC	120
GTTCATAAC	GCCTCTAAC	AGCCTGTTA	CTGCTTTTA	TTTGGGTTT	GGCTAAAGAT	180
TTAGAAATCC	AAACTTTGT	GGCTAAATAC	CTTTCTAAA	ATCAAAAAAT	ACAAGCCCTA	240
CAGGAGCAAA	TGAGCCTTT	AGATTCTCAA	AAAAAGTCG	TTAGCAAATG	GGATAACCCCT	300
ATTTGTATT	TAGGCTATAA	CAACGCTAAC	GTGAGCGATT	TTTCAGGCT	GGATAGCACC	360
TTAATGCAAA	ACATGAGCTT	GGGTITGTCT	CAAAAAGTGG	ATTTAAATGG	AAAAAAACTC	420
ACCGAGTCTA	AAATGATCAA	TTTAGAAAAA	CAAAAAAAA	TATTAGAGCT	AAAAAAACC	480

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AAGCAGCAAT TGGTGTGTTAA TTTAATGATA AACGGCATTG AAAACTATAA AAACCAACAA	540
GAAATAGAGC TTTTAAACAC AGCGATTAAA AATTTAGAAA ACACCCCTCTA TCAAGCCAAC	600
CATTCCAGTT CGCCCGATTT AATAGCGATC GCCAAGTTAG AAATTTTAAA ATCGCAATTAA	660
GAAATC	666

## (2) INFORMATION FOR SEQ ID NO:1052:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1041 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052

ATTTGTTTTTC ATCAAGGGAG TTTGAGCGTG AGCGGGTTGT TTAAAATGCG TATTCTGAGT	60
TTTAAAAAGA ATAAGCGGGC GGTGTTTCA CTCTATCTTT TTATCGCTTT GTTAGCGCTT	120
TCTCTTTAG CCCCTTGTG GGTCAATGAT CGGCCCTTAT TCATCTATAA AGACAATAAA	180
GCGTATTTCC CTATTTAA AACATATGCG GAAGTGGAGT TTGGAGGCAGA TTTTTTCACC	240
CCTACGGACT ATAACGATCC TTATGTGCAA AACACCCCTT AAAAGACGCG TTTCATCATC	300
CATGCGCTCA TCCCTTATAG CTACGATACG ATCATTATGG ATTAGACTC GCCTGCCCCC	360
ACCCCCCCAA GCTTCAAACA CCTTTAGGC ACAGACGATC AAGCCAGAGA CGTGTAGGCC	420
AGGCTGGTTT ATGGCTATCG GGTTTCGTTA GTGTTGGGA TTTTACTCAC CCTTTTTAGC	480
GTTCCTATTG CGGTGAGTTT GGGGGCGTTT CAGGGCTATT ATGGAGGGCT AGTGGATTTA	540
GTGGGGCAAA GGTGAGCGA AATTGGAGC GCGATCCCCA TGCTTTTTT ACTCATTTGT	600
ATTTCTAGCG CGTCAATTCT TAATTTTGG ATCATTTGT TTTAGTCTT GCTCTTTAGC	660
TGGATGGGCC TTCTCAAGT CGTGCACG GAGTTTTAA AAGCAAGGAA TATGGACTAC	720
ACCAAAGCCG CTAGAGCGCT TGGGGTGAAT GATTTAAAAA TCATTTCTA CCATGTTTA	780
CCCAACGCTT TAGTGGCAAC GATCACTTAC ATTCCCTTTT TAATGGCGGC TAGTATTTC	840
ACTTTAGTGT CTTGGATTCT TTTAGGTTT GGCATGCCCTA TAGGGAGCGC GAGCTTGGGC	900
GAATTGGCTA ATCAAGGCAA GGATAACCTC ACCACGCCCTC ATTAGCGGT TGTAGCCTT	960
GTAGCCATTA GCTTGTGCT TTCTGTTTIG GTGTTCATG GCGAAGGGGT GCGCGATGCT	1020
TTCAACGCTA ACATGCTAA A	1041

## (2) INFORMATION FOR SEQ ID NO:1053:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

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## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1557

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053

AGGGGTTACA	TGCTAGAAAT	CAAGAATTAA	AACTGCCTTT	TAAAACCTCTCA	TTTTTCGCTC	60
CAAAACATCA	ATATTTCTT	AAGTTATAGT	GAAGGGTGG	CGATCGTGGG	CGAAAGCGGG	120
AGCGGGAAAA	GCTCTATCGC	TAATCTCGTC	ATGCGATTAA	ACCCCTAGATT	CAAGCCCCAT	180
AATGGCGAAA	TCCTGTTTGA	AACAACCAAT	CTTTTAAAGG	AAAGCGAACG	GTTCATGCAG	240
CATTAAAGGG	GGAATATTAT	CGCTTACATC	GCCCAAGACC	CCCTATCCAG	CCTAAACCCC	300
TTCATATAAA	TCGGCAAGCA	AATGAGTGAA	GCCTATTIT	TACACCATAA	AAACGCTTCT	360
CAAGTGCTCC	TTAAAGAACCA	ACTTTTAAAC	GCCATGAAAC	AAGTCCAATT	GGATGAAAAAA	420
TTTTGGATC	GTTACCCCTTA	TGAGCTCAGC	GGTGGGCAAC	GCCAAAGGGT	GTTGATCGCT	480
ATGGGCATTA	TTAACGCGCC	AAAACGTCTC	ATTGCGATG	AGCCTACAC	CGCGCTAGAT	540
GCGCAAATCC	AAAACCAGAT	TTTACAGTTG	CTCAAGCAAT	TGAGCGTGG	AAAAAACATC	600
GCCCTTTTAT	TCATTAGCCA	TGATTAAAG	GCGGTTAAC	GATGGCTGA	TAGGGTTTAT	660
GTGTTAAAAA	AAGGCAGAT	AGTAGAACACC	AATTGACTA	AAGAGCTTTT	TAATGACCCC	720
AAGCACGAAT	ATTCAAAACT	CTTGATTTCAG	GCTTCAAAC	TGCCCCCTAA	AAATTAAAAA	780
GCGCTAGATG	AGACGCTTTT	AGAGGTGAAA	GATTTAGCG	TTTATTACTT	GCAAAACAGC	840
TTCTTTAGGC	CTTCTTTAAA	AAAACCCCTT	ATGCCATCGG	TGGATTTTC	CCTCAAAGCT	900
AAAGAAAACA	TCGGCATCAT	TGGCGAACG	GGGAGCGGGA	AAAGCTCTCT	AGCGTTAGGG	960
CTTTAAAAC	TCGCTTTAAA	CAGCGGGGAA	GAAAAGATTT	TAGGCCAAAG	CGTGGGGCTT	1020
TTAAATTCTA	AGGCGTTCAA	ACCCCTACCGC	AAAGTTTGC	AAATGGTGT	TCAAGACCCC	1080
TACGCATCAT	TAAACCCCTCG	CTTAAGCATT	CAAAGCATTT	TAATAGAACG	TTTGCCTTT	1140
GCTTACCCCTA	AAGCTTCACA	ACAAGAATGG	CACCATTTAG	CTGAACTTTG	CTTAGAAGAA	1200
GTGTGTTTAA	ACCCCTGAATT	GCTTAACCTT	TACCGCTTATC	AGCTCAGCGG	AGGGGAGCGC	1260
CAAAGAGCTG	CGATCGCTAG	AGCGATTGCG	TTAAAACCTA	GAATCATTCT	TTTAGATGAG	1320
CCAACCTCTG	CTTTAGACAA	AAGCATCAA	AAAAGCGTGT	TGGAATTATT	GTTGAATTAA	1380
CAAGAAAAGC	AGGAGTTGAG	CTATTGTTT	ATCAGCCATG	ATTTAGATGT	GATCAAAGCT	1440
TTTGCATA	GGGTGTTAGT	GGTAGTGAG	GGGAAATCG	TGGAAACAGG	CGCTATTGAA	1500
GAGGTGTTTG	ACAACCCCAA	ACACGCTTAT	ACCAAGCGTT	TGTTGGAATC	CAGGCTT	1557

## (2) INFORMATION FOR SEQ ID NO:1054:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...549

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054

GGGGGACTTA	TGAATACTAT	TATAAGATAT	GCGAGTTTAT	GGGGCTTGTG	TATTACTCTA	60
ACTCTAGCGC	AAACCCCCCTC	AAAAACCCCT	GATGAAATCA	AGCAAATCCT	TAACAATTAT	120
AGCCATAAGA	ATTTAAAGCT	CATTGATCCG	CCGACAAGTT	CTTTAGAAGC	GACACCGGGT	180
TTTTACCCCT	CGCCTAAAGA	AACAGCGACC	ACGATCAATC	AAGAGATCGC	TAAATACCAT	240
GAAAAAAGCG	ATAAAGCCGC	TTTGGGGCTT	TATGAATTGC	TAAGGGGGC	TACCACCAAT	300
CTCAGTTTGC	AAGCGCAAGA	ACTCAGTGTC	AAGCAAGCGA	TGAGGAACCA	CACCATCGCC	360
AAAGCGATGT	TTTGCCCTAC	TTTGAACGCG	AGTTATAATT	TTAAAAATGA	AGCTAGGGAT	420

ACTCCAGAAT ATAAGCATTA TAACACCAA CAACTCCAAG CTCAAGTCAC ATTGAATGTG TTTAATGGCT TTAGCAATGT GAATAATGTC AAAGAAAAGT CTGCGACTAC CGATCCACTG TGGCTAATT	480 540 549
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## (2) INFORMATION FOR SEQ ID NO:1055:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055

GTGAAATTCA GCGTTTTAAC	CCTTTTCCCG CAACTCATCT	TGCCCTTATTT TGAAGATTCT	60
ATTTTAAAAA GAGCGTTAGA	AAAAAACCTT TTTGAATTGG	AAAGTGTAAA CCTTAGAGAT	120
TTTAGCGCTA ACAAAATATCA	AAAAGCGGAT CACACGCTCA	TTGGTGCGGG TGCGGGGCAA	180
ATTTTAGACC CTGAGATGAT	AGAAAACGCA CTCCACTCTG	TTAAAAACCC TAAACACACG	240
ATTTTTTAA GCGCGGTGGG	CAAGCCTTTC AAGCAAATAG	ACCGCATGCG TTTGGCTCAA	300
AAAAGACATG TCGTTTTGGT	GTGCGGGCGT TATGAGGGCT	TTGATGAACG CTCTATTGAA	360
TTGGGTGCTG ATGAGGGTTT	TTGTATAGGC GATTTATTT	TAACAGGGGG CGAGCTTGGG	420
GCGTTGTGCT TGATAGATAG	TATCGCTCGC CACATCAAG	GGGTTTTGGG TAACGCCCAA	480
TCTTITAGAAA ATGAGAGTTT	TGAAAATAAT TATTTGGAGA	CCCCTAAATT CGCTAACGCT	540
GTTTTTAAAT CCAAAGAAAT	CAATAAAATC CCTGCACCTT	TTAGAATATTIC TAAAGGAAAT	600
CATGCTAAAA TCAAGCAACT	AAAGCTTGAT TTGTCAAAAT	TAAGGACAAA ATTTACCGC	660
CTTGATTTAT TCAAACAGCA	CAAATCA		687

## (2) INFORMATION FOR SEQ ID NO:1056:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056

AGGGAGCAGT	CGTTTCACCT	TCGCTCAACG	CCCCCCACCG	TGGTTTTAAT	GGCAGGTTG	60
CAAGGGAGCG	GGAAGACAAC	CACCACCGCT	AAACTCGCCC	ACTATCTCAA	AACCAAAAAT	120
AAAAAAAGTGC	TTTATGCGC	ATGCGATTG	CAACGCTTAG	CAGCGGTGGA	GCAATTAAAG	180
GTTTTGGGCG	ACACGGTGGG	CGTGGAAAGT	TTTCATGAAG	AAAATAAAAG	CGTGAAGAA	240
ATCGCCAACA	ACGCCTTAAA	AAGGGCTAA	GAAGCGCAAT	TTGACGTGTT	AATCGTGGAT	300
AGCGCGGGGC	GTTTAGCGAT	TGATAAAAGAG	CTTATGCAAG	AATTAAAGGA	AGTTAAAGAA	360
GTCTTAATC	CCCATGAGT	GCTGTATGTC	GCAGACGCGT	TGAGCGGGCA	AGATGGGGTC	420
AAAAGTGCAGA	ACACCTTTAA	TGAAGAAATA	GGCGTGAGCG	GGGTGGGTGTT	AAGCAAATT	480
GATAGCGATT	CTAAAGGGGG	TATCGCCTTA	GGCATCACTT	ATCAATTGGG	CTTACCCCTG	540
CGTTTTATTG	GGAGTGGGGA	AAAAATCCCT	GATTTAGACG	TGTTTATGCC	TGAAAGGATT	600
GTGGGGCGTT	TGATGGGGGC	TGGAGATAATT	ATCTCGCTCG	CTGAAAAAAC	CGCCAGCGTT	660
TTAACCCCTA	ATGAAGCCAA	AGATTTAAGC	AAAAAGCTCA	AAAAGGGCA	ATTCACTTTC	720
AACGATTTTT	TAACCCAAT	TGAAAAAAGTG	AAAAAAATTAG	GCTCTATGAG	TTCTCTGATC	780
TCTATGATTC	CAGGTTTACGG	GAATATGCCA	AGCGCGCTAA	AAAGACACGGA	TTTAGAAAAGT	840
TCTTCTAGAAG	TGAAAAAAAT	CAAGGCCATC	GTAAATTCCA	TGACGAAAAAA	AGAGCGAGAA	900
AACCCCGAGA	TTTAAACCGG	CAGCGGAAGA	AAAAGGATCG	CTTTAGGGAG	CGGCTTAGAA	960
GTGCTCTGAAA	TCAATCGCAT	CATCAAACGC	TTTGATCAGG	CGAGCAAAT	GGCGAAACGA	1020
CTCACGAATA	AAAAGGGTAT	TAGCGATTG	ATGAATCTAA	TGAGTCAGGC	AAAAATCAA	1080
ACGCCCCCTA	AAATGCGC					1098

## (2) INFORMATION FOR SEQ ID NO:1057:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 810 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...810

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057

AGGAAAGCGA	TGAACACCCA	CCTAAACAA	TTGATTGAAA	TTTCGCACTT	GGATAAAAGAA	60
ATTGACTCTT	TAGAGCCGTT	GATCAGAGAA	AAACGGAAAG	ACTTGGATAA	AGCCTTGAAT	120
GATAAAGAAG	CTAAAAATAA	AGCGATTITG	AATTGGAAG	AAAGAAAAATT	AGCCCTAAA	180
TTACAGGTTT	CTAAAAAACGA	GCAAACCTTA	CAAGACACCGA	ACGCTAAAT	CGCCAGTATC	240
CAAAGAAAA	TGAGCGAGAT	CAAATCCGAA	AGGGAGTTGC	GCTCTTTAAA	CATTGAAGAA	300
GATATTGCTA	AAGAGCGATC	CAATCAAGCC	AACAGAGAAA	TTGAAAACCT	GCAAAATGAA	360
ATCAAGCACA	AAAGCGAAAA	ACAAGAAAGT	TTGAAAAGG	AAATGCTAGA	GCTTGAAGAA	420
TTAGCGTTG	AATTGGAAAA	TTTACTGCGA	AAAGAAGTCA	AAAACATCAA	AGAAACCCAA	480
CAGATCATCT	TTAAAAAGAA	AGAAGAAACTC	GTGGAAAAAA	CCGAGCCTAA	AATCTATAGC	540
TTTTATGAAA	GGATTAGGAG	GTGGCGAAA	AAACAGAGCA	TCGTAACGAT	CAAAAGACAG	600
GCTTGTGGGG	GTGTGTTAT	TGGTTGAAC	CATAAGATT	ATGCCGAAGT	GCTAACGAGT	660
GGGGACATGA	TCACTTGTCC	GTATTGCGGG	CGTATTGTTAT	ACGCTGAGAG	TACGCATGAA	720
AGTAACGCTC	ACACTCCAAA	AGAAAGCCAA	CCAAAGAAA	GCCAAGAAGA	AAGCCAAGAA	780
GAAAGCCAAG	AAGAAAGCCA	AGAATCCGTT				810

## (2) INFORMATION FOR SEQ ID NO:1058:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1701 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058

ATGAACGAAA	TTGACAATTC	CGTTGATATC	GGATTCTTAC	GGATTCTCGGA	TGTTATTAAA	60	
AAAGTTAAAA	CCCCAAAGGG	TGGTATTGAG	GTTTTAAGGA	CTTTAATTGA	TTTCACGCC	120	
AAAATGAAA	ACGCCTAAA	TTTACCGACC	AAAAGCCATA	AGGGGCAATA	CAGAAAAGAC	180	
GGTGAGCCTT	ATATTGTCCA	TCCTATTGTC	GTGGCGAGCG	TGGTGGCGTT	TTGTGGGGC	240	
GATGAGGCGA	TGGTGTGCGC	CGCGCTTITG	CATGATGTGG	TAGAAGACAC	GCCTTGTGAG	300	
ATTGAAACGA	TTGAGCGAGA	ATTTGGGCAA	GATGTGGCTA	ATTAGTGGGA	TGCGCTCAC	360	
AAAATCACTG	AAATCAGGAA	AGAAGAGTTA	GGCGTAGGT	CTCAAGATCC	CAGAATGGTG	420	
GTTTCAGCCC	TCACTTTTAG	AAAGATCCTT	ATTAGCGCGA	TACAAGATCC	AAGAGCCTTA	480	
GTGGTAAAGA	TTAGCGACAG	GTTCACAAAC	ATGCTCACCT	TAGACGCC	GCCTCATGAC	540	
AAGCAGGTGC	GTATTTCTAA	AGAAACTCTA	GCGGTGTATG	CCCCCATAGC	GAGTCGATG	600	
GGCATGCTT	CAATCAAAAA	CGAATTAGAA	GACAAGAGCT	TTTATTATAT	TTATCCAGAA	660	
GAGTATAAAA	ATATTAAGGA	GTATTTGCAC	AAAACAAAC	AGTCTTTACT	CTTAAAAC	720	
AACGCTTTG	CGAGCAAGTT	AGAAAAAAAG	CTTTTGACCA	GGGGGTTTTAG	CCATTGCGAT	780	
TTTAAACTCG	TTACAAGGGT	GAAACGCC	TATTCTATT	ATCTTAAGAT	GCAACGAAA	840	
GGGGCGGTTA	ATATTGATGA	AATTGAGC	TGTTAGCCA	TTAGGATTT	ATTGAAAAAAC	900	
CCGATTGATT	GCTACAAGGT	TTTAGGGATT	ATTCATTGTA	ATTTCAAACC	CATTGTTCT	960	
CGTTTTAAAG	ATTACATCGC	TTTGCCCCAA	GAAAATGGCT	ATAAGACAAT	ACACACGACG	1020	
ATTTTGATG	AACTCTCTGT	TTATGAGTG	CAGATCGCA	CTTTTGATAT	GCACATGGGG	1080	
CGGGAGTATG	GTAAATTCAAGC	CCATTGGAAG	TATAAAGCCG	GGGGCGTGG	TCATGAAGAA	1140	
CATCATGAGG	GCATGCGGTG	GTTGCAAAT	TTTAAATACC	ATGACAGCGA	TTTGAAAAAC	1200	
GACCTTAAGG	AAATTACGAA	ACTCGCTAAG	AACGATTGT	ATCGTGAAGA	TATTGTCGTT	1260	
TTTTCGCCCC	ATGGGGACAC	TTACACTTTA	CCGGTGGCG	CGATCGCTT	AGATTTCGCT	1320	
TACATGGTGC	ATAGTGATT	GGGCATAAA	GCCACGGACG	CTTATATCAA	TAGTAAAAAA	1380	
GCCTTACTCA	ATCAAGAATT	AAGGAGTGGG	GATGTGGTTA	AAATCATTA	AGGCATAAA	1440	
GTAATACCTC	GTTCATTTG	GATGGATCG	CTTAAACATT	CTAAGGCTAA	AAACCATTTG	1500	
CGCATCCAAA	GAAGAAACCG	CTTGAAAGAA	ATTGACACTA	AGAGCATGAT	CAATATCTTA	1560	
TCGACTTTT	TTGGGCGCTC	TGTTTTGAA	GATGCGGATT	TGAAGAGTTA	AAAAAACTTT	1620	
GAAGAAAAT	TAACAGATTG	TGGGTGGAG	ACCACCTAA	CAGAAGCGAT	GAAAAGCTTT	1680	
GAAAATTGG						GCCAAACTCA C	1701

(2) INFORMATION FOR SEQ ID NO:1059:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 594 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...594

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059

GT	TACAAATCA	AAAGCTTTAT	TAATGGATTA	AGAAGGGATC	ATGCAGGCAA	AGATAAAAAA	60
CA	AGCGGGTT	TIGGTGAAAT	TTTCTGGGGA	ACGCCTAGCT	GGGGACAACC	AGTTTGGATT	120
GAC	ATTCTCATG	TGTTAGATCA	CATCGCTAAA	GAGATCAGAA	TTTAGTGGA	AAACGATATT	180
GA	AAGTGGGTA	TGTTGATTGG	TGGAGGCAAT	ATCATTAGGG	GGGTTAGCGC	GGCTCAAGGG	240
GGG	ATCATTA	GGCGCACCA	TGGGGATTAT	ATGGGCATGT	TAGCCACCGT	GATTAATGCG	300
GT	AGCCATGC	AAGAAGCTTT	AGAGCATATC	GGTTTAGACCA	CAAGAGTGCA	GAGTCCATT	360
GAA	ATCAAAG	AGATTTGTGA	AAGTTTATATT	TATAGGAAAG	CGATCAGGCA	TTTAGAAAAG	420
GGT	AGGGTGG	TGATTTTGG	CGCTGGCACA	GGAAACCCGT	TTTCACCCAC	CGATACGCC	480
GCT	ACTTTAA	GAGCGATTGA	AATTGGATCG	GATCTAATCA	TTAAAGCGAC	AAAAGTGGAT	540
GGC	CATCTATG	ACAAAGACCC	TAACAAATT	AAAGACGCTA	AAAATTGGAC	ACTT	594

## (2) INFORMATION FOR SEQ ID NO:1060:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1017

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060

AT	GAATGCAT	TGAAGCGTG	GTGTTAACAG	TTGATGGCG	AAACCAATAC	CGATGATT	60
AG	CCCAGCGA	CCGACGCTT	CACACGGAGC	GATATTCTT	TACACGCCA	AGCCATGCTA	120
AA	AAAACCGG	TTGAAATT	CGAACAAACG	ATTGAAGCCA	TTAAACTAA	AGGCGTTCT	180
GT	AGCGTATG	TGGCGATGT	GGTTGGCACA	GGAAAGCTCTA	AAAAAAAGCGC	GACTAACTCT	240
AT	CATGTGGC	ATTTGGTAA	GGACATTCT	TTTGTGCCTA	ATAAAAGGAG	TGGAGGCATT	300
GT	GATGGGG	GGGTGATCG	TCCGATTTC	TTTGGCAGTT	GTGAAGATAG	GGGGCGTTA	360
CC	CATTGTTG	CTGATGTTA	GGATTTGAA	GAGGGCGATA	TCATTAAAAT	CTACCCATT	420
AA	AGGC	AA	TCACGCTAA	CGATAAGGTG	TTAACGCTACCT	TTAACGCTAGA	480
TT	ATTAGATG	AGTCAGGGC	TTCTGGCGT	ATCCCCTTAA	TCATTGGTAG	GGGTTTGACC	540
A	ATAAAGCGC	GTAAATTTT	AGGGCTAGGC	GAATCGGAAG	CGTTCAAAA	ACCATCCGCT	600
C	CCTAAAAGCG	ACGCTAAAGG	CTACACTTTA	GCCCCAAAAAA	TTGTAGGCCA	TGCTTGTGG	660
G	TAAAAGGG	TCTTACCTGG	TGCTTATTGT	GAGCCAAAGG	TTACCACCGT	GGGCAGTCAA	720
GAC	ACCCACAG	GGGGCATGAC	CAGAGATGAG	GTAAAGAAT	TAGCGAGTTT	GAAATTTGAT	780
GCG	CCTTTG	TGTTGCAGAG	TTTTGCGCAT	ACCGCTGCTT	ACCCAAAACC	TAGTGTG	840
A	GTTTGCGAT	CAACCTTGCC	TGGCTTATC	ACTCAAAGAG	GGGGCGTGGC	GTGCGATCCG	900
GGC	GATGGCG	TGATGATAC	ATGGCTTAAT	CGCATGGGAT	TGCGCTGACAC	TTTACGCCACA	960
GGG	GGGGGATA	GGCACACCCG	TTTCCCTTAA	GGCATCAGTT	TCCGGCAGGG	AGCGGGC	1017

## (2) INFORMATION FOR SEQ ID NO:1061:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061

ACATTTACTA	TAAAGAGATT	TGTTTGATG	AAAATAAAAA	TCCAAAAAAT	CCACCCAAAC	60
GCCCTTATCC	CTAAATACCA	AACCGAAGGC	TCTTCAGGCT	TTGATTTGCA	CGCTGTAGAA	120
GAAGTAGTGA	TCAAACCTCA	TAGCGTGGGA	TTGGTAAGGA	TTGGGATTTG	TTTGTCTTTA	180
GAAGTGGGT	ATGAACGTCA	GGTACGCACC	CGTACGGCCT	TGGCTTGAA	TCATCAGGTG	240
ATGGTGTAA	ATCCCCCTGG	CACGGTGGAT	AATGATTATA	GGGGCGAAAT	TAAGGTCAIT	300
TTAGCGAATT	TGAGCGATAA	AGATTTTAA	GTTCAAGTAG	GGGATAGGAT	CGCTCAAGGG	360
GTGGTCAAA	AAACTTATAA	AGCCGAATT	ATAGAATGCG	AACAATTAGA	TGAAACTTCA	420
AGGGTAGCG	GGGGTTTGG	CAGCACAGGA	GTGAGTAAGG	CA		462

(2) INFORMATION FOR SEQ ID NO:1062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062

AGAAAGAAAC	CATTCAAGGA	ACGCATTGAT	TTGATGAATA	AACCATTTTT	AATCTTACTC	60
ATAGCCTAA	TTGCCTTAG	CGGCTGTAAC	ATGAGAAAAT	ACTTCAAACC	CGCTAAACAC	120
CAAATTAAG	CGCAAGCGTA	TTTCCCTAAC	CATTGCAAG	AAAGCATCGT	TTCGTCTAAT	180
CGTTATGGAG	CCATTTGAA	AAATGGAGCG	TTATAGCGG	ATAAAGGTTT	AACGCAGCTA	240
AGAATTGGTA	AGAATTTCAA	TTATGAAAGC	AGTTTTTAA	ATGAGAGTCA	AGGGTTTTC	300
ATCCTTGCAC	AAGATTGTTT	GAACAAGATT	GATAAAAAAA	CAAGCAAAAG	CAGGGCGGCT	360
AAGACTGAAG	AAACCGAATT	GAAATTAAAG	GGCGTTGAAG	CGGAAGTCCA	AGATAAAGTC	420
TGTCACTAAC	TGGAATTGAT	TAGCAATAAC	CCTAACGCCA	GCCAACAATC	TATCGTTATT	480
CCTTTGGAGA	CTTTTGCCTT	GGCGCGAGCG	TTAAAGGAA	TCTT		525

(2) INFORMATION FOR SEQ ID NO:1063:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 657 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...657
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063

GGCATGAGCA TTAAGGAAAA TTTAGAGCAA GTTAGAAACG AATTAAAAG CGATGAAAAG	60
CTTTTAAAG GAGCGTTTAG ATTAGAAAAG TTTTCACAAAC GCTACAAGTG GGTGTTGTTG	120
TTTATCGGG TGCTTCTTAT CGCTTATTAA GGGGATAACAA ATTACAAGA TTATAACCAT	180
GAGCAAACGA GAGAGCGGAT CACTCAAATT TATAATGAAG TGCTAGAGAG TCCTAATAAT	240
ATAGCCTTGC AAAAACGATT GAAAGAAGTC GCCCCAGAGT TGATGACTT GTATCAGTTC	300
GCCAGAGCGA GTGAGAGGAA CGATGCAAC GAGTTAAAA GGCTTTCGCA ATCTTCAAT	360
GAAATCGTTA AAGCGTTCGC CAAATATTCT TACGCATCGC TCTCTAGAGA TAAAAACCTG	420
CTTGAAAAAA GCCCCATTCT TAAAGAAATG AGCGCTTAC AAGAAGTGAA CTTGTTGTAT	480
GAAGAAAATT CTAAAGACGC AATCAAAAAA GCGCATCAA GTTATCAAC TATCCCTCTA	540
AGTTCTTCAC TCTATGCTAT AATCTCTGTT TTAAACATT ATGGAATGTT AGAAGATATT	600
CAGCAAAACC CTTCCAAACC AACCAATCTA AAGAAAGAAA CCATICAAGG AACGCAT	657

## (2) INFORMATION FOR SEQ ID NO:1064:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 594 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...594
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064

AAGCGCTATA AAAGGCTAGA GCAAGAAAATA AAAAAAAGGG ATAAAATGAT AGTGGGTTTG	60
ATAGGGGTTG TGGAAAAAAAT CTCTGCTTTA GAAGCGCATA TAGAAAGTGCA AGGGGTTGTT	120
TATGGGGTGC AAGTTTCTAT GCGAACGGCT GCTTGCTCC AAACGGGCCA AAAAGCGCGT	180
TTGAAAATCT TACAAGTGAT TAAAGAAGAT GCGCATCTT TATACGGTT TTTAGAAAGAG	240
AGCGAAAAAA TTCTCTTIGA AAGGCTTTC AAAATCAATG GGGTAGGGGG GCGTATCGCT	300
TTAGCCATTG TTTCAAGCTT CCCAGCGAAT GAATTGAAA ACATTATCGC TACTAAAGAA	360
GTCAAAAGAC TCCAGCAAGT CCCAGGCATA GGGAAAAAGC TCGCCGATAA GATCATGGTG	420
GATTGATTG GCTTTTCAT TCAAGATGAA AACAGACCCG CGCGCAATGA AGTCTTTTA	480

GCCCTAGAGA GTTGGGCTT TAAAAGCGCT GAAATCAATC CAGTTTAAA AACCTAAAA CCCCATCTCA GCATAGAGGC AGCGATTAAA GAAGCCTTAC AGCAACTGCG CTCT	540 594
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## (2) INFORMATION FOR SEQ ID NO:1065:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065

AGTCGCACCC TTGTGCAAA AATCGTTTA CAAAAAGAAA GGAAGAAAAAT GGAAATACAA	60
CAAACACACC GCAAATCAA TCGCCCTTTA GTTCTCTCG TTTAGCAGG AGCGTTGATT	120
AGCGCCATAC CGCAAGAGAG TCATGCCGCC TTTTCACGGA CCGTGATCAT TCCAGCCATT	180
GTTGGGGTCA TCGCCACAGG CACTGCTGTA GGAACGGTCT CAGGGCTTCT TAGTTGGGA	240
CTCAAACAAG CGGAAGAACG GAATAAAACC CCAGATAAAC CCGATAAAAGT TTGGCGCATT	300
CAAGCAGGAA AAGGCTTTAA TGAATTTCCT ACAAGGAAT ACAGACTTATA CAAATCCCTT	360
TTATCCAGTA AGATTGATGG AGGTTGGAC TGGGGAAACG CCGCTAGGCA TTATTCGGTC	420
AAAGGCGGGC AATGGAACAA GCTTGAAGTC GATATGAAAG ACCTGTAGG GACTTATAAA	480
CTATCAGGGC TTAGAAACTT TACTGGTGGG GATTTAGACG TGAATATGCA AAAAGCCACT	540
TTGCGTTTGG GCCAATTCAA TGGCAATTCT TTCACAAAGCT ATAAGGATAG CGCTGATCGC	600
ACCACGAGAG TGAATTCAA CGCTAAAAAT ATTTCAATTG ATAATTTCGT AGAAATCAAT	660
AATCGTGTGG TTCTCTGGAGC CGGGAGAAAA GCCAGCTCTA CGGTTTGAC TTGCAAGCT	720
TCAGAAGGGA TCACTAGCAG TAAAAATGCG GAAATTCTC TTTATGATGG CGCCACGCTC	780
AATTGGCTT CAAACAGCGT TAAATTAAAT GGTAATGTGT GGATGGGCCG TTGCAATAC	840
GTGGGAGCGT ATTAGCCCCC TTCATACAGC ACGATCAACA CTTCAAAAGT TCAAGGGGAA	900
GTGGGATTTA ACCATCTCAC TGTGGGGAT CAAACAGCCG CTCAAGCGGG CATTATCGCT	960
ACCAATAAGA CTCATATTGG CACACTGGAT TTGTGGCAA GCGCCGGGTT AAATATCATT	1020
GCCCCCTCCAG AAGGTGGCTA CAAGGATAAA CCTAATAGTA CCACCTCTCA AAGTGGCACT	1080
AAAAACGACA AGAAAGAGAT CAGTCAAAAT AACAAATAGCA ACACAGAGGT CATTAACCCA	1140
CCCAATAACA CGAAAAAAC AGAAACTGAA CCCACCAAGT CATTGATGGG CCTTTTGCTG	1200
AAGGCAAAGA CTCGGTTGTC A	1221

## (2) INFORMATION FOR SEQ ID NO:1066:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1278

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066

GTAATAAAATA	CAACTAGTAT	GCTAAAAAAA	ATATTTTAA	CCAACAGCTT	AGGGATTITA	60
TGCTCTAGGA	TTTTTGGCTT	TTTACGGGAT	TTAATGATGG	CCAATATCCT	AGGGGCTGGG	120
GTGTATAGCG	ATATTTTCTT	TGTGGCTTTC	AAATTGCCTA	ATCTATTCA	GCGTATTTTT	180
CGGGAGGGCT	CTTTTCTCA	AAGCTTCTTA	CCGAGCTTCA	TACGGAGTTC	CATTAAGGGG	240
GGTTTGGCA	TTTGGTGGG	GCTTATTTTT	TCTGGCGTTT	TATTCAATGTG	GTGCTTATTA	300
GTAGCGCTCA	ATCCCTTATG	GCTAACAAA	CTCCTAGCTT	ACGGCTTGA	TGAAGAAACG	360
CTCAAACATAT	GCACCCCTAT	TGTAGCGATC	AATTTTGTT	ATCTTTTATT	GGTGTGTTATC	420
ACCACTTTT	TAGGCGCGCT	TTTACAATAC	AAACACAGCT	TTTTTGCCAG	CGCTTATAGC	480
GCAAGCTTAC	TCAATTTATG	CATGATTITA	GCCCTTTGA	TTTCTAAAGA	AAAAACGCAT	540
TTAGAAGCGT	TGTATTATTT	GAGCTATGGC	GTGCTTTAG	GGGGCGTGGC	TCAAATCTTA	600
TTACACTTTT	ATCCTTTAGT	AAAATTAGGC	TTATGGGGT	TATTATTTAA	AGGGTTGTTG	660
GGTTTTAAGA	CTAAAAAATAC	AAACAAAAAA	GAATATCGTT	TGAATAGGCC	TAAAAGGAT	720
CTAAAGCGT	TTTCAAGCA	ATTCTTCCCC	AGCGCTTCTAG	GCAATTCTAG	CGCTCAGATC	780
GCTTCTTTTT	TAGACACCCAC	AATCGCTCT	TTTCIGGCGA	GGGGGAGCGT	GTCTTATTG	840
TATTACGCCA	ATAGAGTCTT	CCAGCTCCCT	TTAGCCTTAT	TCGCTATCGC	TATCTCCACA	900
GCTCTTTTCC	CTAGCATTCG	GATCGCGCTT	AAAAACAACC	AGCAGGATT	AATCTTACAA	960
CGCTTGCAAA	AGGGCGTGGTT	TTTTTTGGTG	GGGCTTTGTC	TTCTTTGCGAG	CATTGGGGGG	1020
ATAATGTTAA	GCAAAGAAAT	CACCGAACTT	TTATTGAAA	GGGGGCAATT	TAGCCCTAAA	1080
GACACCCCTAA	TCACTTCGCA	AGTCTTTTCG	CTCTATCTTT	TAGGCTTGCT	CCCTTTGGG	1140
CTAACCAAAC	TCTTTTCTTT	ATGGCTTAT	CGAAGAAATTAG	AGCAAAAAAA	AGCGGCTAAA	1200
ATCTCTTTAA	TTTCGCTTTT	TTTAGGTTTA	GGGGCTTCTT	TGAGTTTAAT	GCCTTTGTTA	1260
GGGGTTTGG	TTTGGCGT					1278

## (2) INFORMATION FOR SEQ ID NO:1067:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 738 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...738

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067

TTTCGCTTAC	CAAGTCCCCT	TACCTCAATT	TTAATGCGCC	TAGATTACGC	CCTATTCAAC	60
CAGCATTAG	CAAATAGCAG	AGAAAAAGCT	AAAGCGTGG	TTTAAAAAAA	ACAGGTTTA	120
GTCAATAAAA	TGGTGGTTTC	AAACCCCTCT	TTTATCGTTA	AAAGGGCGA	TCAAATTGAA	180
CTCATCGCTC	CCAATCTATT	CGTTAGCAGG	GCTGGGGAAA	AAATTAGGGC	TTTTTAGAA	240
GATCATTITA	TAGATTTAA	AGAAAAGGTT	TTTTAGATG	TGGGAGCGAG	TAAGGGAGGC	300
TTTAGTCAAG	TGGCTTTTT	AAAAGGGGCT	AAAAGGTGC	TTTGCCTGGA	TGTGGGGAAA	360
ATGCAATTAG	ATGAAAGTTT	AAAAACGAC	CAACCGATAG	AATGTTACGA	AGAATGCGAT	420
ATTAGAGGGT	TTAAAACCCC	AGAAAAAATT	GATTTACAC	TTTGTGATGT	GACCTTTATT	480
CTTATATAIT	GTATTTTAA	AGCGATTITG	CCTTTAAGCG	GTGAATTITTT	AACGCTTTTC	540
CCGCAAT	TTGAAGTGGG	CAGAACAAATA	AAACGCAATA	AAAAGGGGGT	GGTGATGGAT	600

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AAAGAAGCCA TTTGAAACGC TTTAGAAAAC TTTAAAAACC ATTTAAAAC AAAGGATTT	660
CAAATCTTAA CGATCCAAGA AAGCTTAGTG AAAGGGAAAA ACGGGAATGT TGAATTTTT	720
ATCCATTCA AGCGAGCC	738

## (2) INFORMATION FOR SEQ ID NO:1068:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (v) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...2547

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068

AGACATGTGC AACCGATGAA ATCTAAAAAA CTTTATTTAG CTTTAATCAT AGGGGTTTTA	60
TTAGCGTTT TAACCTATC TTCACTGGCTA GGTAATAGCG GTTTAGTGGG GCGTTTTGGG	120
GTGTGGTTTG CGCGAACCAA TAAAAAAATAT TTTGGGTATC TTTCATTGAT TAATTTACCC	180
TATTTGGCGT GGTTTTATT CCTTTTATAC AGCGCTAAAA ACCCTTTTAC AGAAATCGTT	240
TTAGAAAAAA CCTTAGGGCA TCTATTAGGC ATTTTATCTT TACTCTTTTT GCAATCTAGC	300
CTGTTGAATC AAGGGAAAT CGCGAACACCG GCGCGTTTGT TTTCACACCC TTTTATAGGG	360
GACTTTGGGC TTTATGTGCT GATAATGCTT ATGCTAGTTA TCTCTTATT AATTTTATTC	420
AAACTGCCCT CTAAAAGCGT TTTTACCCCT TATATGAAACA AAAACACAAAG CCTTTTAA	480
GAGATTTACA AACAAATGCTT GCAGGCCTTT AGCCCTAATT TTAGCCTGAA AAAAGAGGGT	540
TTTGAAAACA CCCCATCAGA TTCTCAAAAA AAAGAAACCA ACAACGACAA AGAAAAAGAA	600
AACCTCAAAG AAAACCCATAT TGATGAAAC CACAACACCC CTAACGAAGA ATCGTTTTA	660
GCGATCCCTA CCCCCTATAA CACGACCTTA ATAATTCAG AGCCGCAAGA AGCCTTAGTC	720
CAAAATTCCTT CACACCCCCC TACCCATTAC ACCATTACCTT CTTAAAGAAA CCGATTGTAT	780
GATTGACTA ACCCCACTTT AAAAGAACCT AAGCAAGAAA CCAAAGAAAAG AGAACCCACG	840
CTAAAAAAAC AAACGCCAAC CACACTCAA CCTATCATGC CCATATCCGC ATCCAACACA	900
GAAAATCATG ACAAAACAGA AAACCACAAA ACCCTTAACC ACCCCATAAA AGAAGATGAT	960
TTACAAGAAA GCCCACAAGA AAACCCACAA AAAGAAAATA TAGAAGAAA TATAGAAGAA	1020
AAAGAAACGC AAAACGCTCC AAGCTTTAGC CCACTAACCC TCACCAAGCGC TAAAAAACCC	1080
GTTATGGTTA AAGAATTGAG CGAAAATAAA GAGATATTAG ACGGGTTGGG TTATGGCGAA	1140
GTGCAAAAC CCAAAGATTAA TGAGCTTCCC ACAACGCAAT TATTGAATGC GGTTTGCTTG	1200
AAAGAAACTT CTTTAGACGA AAACGAGATT GACCAAAAAA TCCAGGATT ATTGAGCAAG	1260
CTGCGCACCT TPAAAATTGA TGGCGATATT ATACGCACTT ATTCAAGGCC TATTGTAACC	1320
ACCTTTGAAT TCCGCCAACG CCCTAGCGTT AAGGTGAGCC GTATTTTAGG CTIGAGCGAT	1380
GATTTAGCGA TGACTTTATG CGCTGAATCC ATCCGCATTC AAGCCCTAT CAAAGGTAAA	1440
GATGTCGTTG GTATTGAAAT CCCTAACAGC CAAAGCCAAA TTATTTATT AAGAGAAATT	1500
TTAGAAAGCC AATGTTCTA AAAATCCAGC TCCCTCTAA CCCTAGCTTT AGGCACAGAC	1560
ATTGTTGGGTA ACCCTTTCAT CACGGATTAA AAAAGCTCC CCCACTTGCT CATGCCGGC	1620
ACGACAGGGG GCGGTAAAGAG CGTGGGCGTT AATGCGATGA TTATATCCTT ACTTTATAAA	1680
AACCCCCCTG ATCAACTCAA ATTAGTGATG ATCGATCCCA AAATGGTGGG ATTTAGCATT	1740
TATGCGGACA TCCCTCATTT ACTCACGCC ATTATCACTG ACCCTAAAAA AGCTATCGGG	1800
GCTTTGCAAAC CGCGGGCTAA AGAAATGGAG CGCCGATACT CTTTAATGAG CGAATACAAG	1860
GTTAAAACCA TTGATTCTTA TAATGAACAA GCCCAAAGTA ACAGCGTTGA AGCGTTCCCC	1920
TATTTGATTG TGGTGATTGA TGAATTAGCG GATTGATGA TGACAGGGGG CAAAGAAGCG	1980
GAGTTTCCTA TCGCTAGAAT CGCTCAAATG GGGCGAGCGA GCGGCTTGCA CCTCATTGTG	2040
GCGACCCAAAC GCGCGAGCGT GGATGTCGTA ACCGGCTTGA TAAAAACCAA CTTGCCTTCA	2100
AGGGTGAGTT TTAGGGTAGG CACTAAGATT GATTCTAAAG TGATTTTGAAC CACCGATGGG	2160
GCGCAAAGCT TACTAGGAAG GGGCGATATG CTCTTACCC CCCCCAGGAAC AAACGGGTTA	2220

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GTGCGCTTGC ATGCCCTT TGCCACTGAA GATGAAATCA	AAAAAATCGT GGATTITATT	2280
AAAGCCAAA AAGAGGTGGA ATACGATAAA GATTCTTGC TAGAAGAAC	GCGCATGCCT	2340
TTAGACACCC CTAACATCA AGGCGATGAC ATTCTAGAAA GGGCTAAAGC	GGTGATTITA	2400
GAAAAAAAGA TCACTTCTAC GAGCTTTTA CAACGCCAAT TAAAAATCGG	CTACAACCAA	2460
GCGGCCACCA TTACTGACGA ATTAGAAGCT CAAGGCTTTC TATCCCCAAG	AAACGCCAAA	2520
GGCACACAGAG AGATTTGCA AAATTT		2547

## (2) INFORMATION FOR SEQ ID NO:1069:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069

AATTACCTAA AAATTCATG TTCAAGGATA GCCATGAACC CCCAGATTCA	ACCCGCCACT	60
AAAAAACCTT TAAATCCCT TTAGCCCT AGTTCAAGGCA ATTTAGTGG	ATGGTATGAT	120
TTTACGCTT ATGCGTTCCT TGCTCCTTAT TTGCTTAAGG ATTTACCCA	CACCAATGAC	180
CCTACTCTAG CGCTCATCTC AGCTTTTTA GTTTTATGC TAGGGTTTT	CATGCGCCCT	240
TTGGGGAGTT TGTTTTTGG TAAATGGGG GATAAAAAGG GGGCTAAAAC	TTCCATGGTG	300
TATTCCATTA TCCTTATGGC GCTAGGCTCT TTCATGCTCG CATTGCTCCC	CACTAAAGAA	360
ATCGTAGGGG AATGGCGTT CTTGTTTTA TTGTTAGCCA GGCTTTTACA	GGGCTTTAGC	420
GTGGGAGGAG AATATGGCGT GGTCGCCACT TATCTCTCTG AATTAGGCAA	GAATGGTAAA	480
AAAGGTTTT ATGGCTCTT CCAATATGA ACTTGTAGTGG GAGGGCAACT	CTTAGCTATT	540
TTTCGCTCT TTATCGTTGA AAACGTTTAC ACGCATGAGC AAATCAGGCC	GTTGCTTGG	600
CGTTATTTAT CGCTTTAGA GGGTATTTA GCCCTACTCT CGCTCTTTT	GAGAAATATC	660
ATGGAAGAAA CTATGGATAA TGAAGGGACT CCTCAAAAAA AGACTAATGT	AAATAATACA	720
AAAGAAACCC ATATCAAAGA AACCCAAAGA GGCAGTTAA AGGAATTGCT	CAACCATAAA	780
AAAGCCTTAA TGATAGTCTT TGGGCTAACT ATGGGAGGGGA TTGTGCTT	TTACACTTTT	840
ACGGTGTATT TAAAATCTT TTAAACCAAC AGCTCATCGT TTAGCCTAA	AGAAAGCAGT	900
TTTATCATGC TTTCAGCGCT CTCTTATTC ATCTCTTAC AACCTTATG	CGGGATGCTT	960
GCGGATAAAA TCAAACGCA CCAAATGCTG ATGGTTTTTG CGATCACAGG	GCTTATTGTA	1020
ACGGCTATTG TATCAAGCAT GCCACTAGCG TGTATGAAGC	CCTATTITAT	1080
GAAATACTCG CATTGAGCAG CATGAGTTT TACATTTGCA TTGCTGGGT	TATTAAGGCG	1140
GAATTATTCC CTGAACATGT GCGAGGCCCTT GGCGTGGGTT TAGCCTATGC	GATCGCAAT	1200
GCGCTTTTG GAGGGAGGCC GAGTTATATA GCGTTAGAGT TCAAACAGCA	TGGTTTTGAA	1260
GAGGGGTTTG TGGGCTATGT CATGTTGAGT ATTGTTATCT TTATGGTTAT	GGTTATCATA	1320
TTCCCTAAAA AACCTATTG GGAG		1344

## (2) INFORMATION FOR SEQ ID NO:1070:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1938 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

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- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...1938
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070

AAATGGAAAA ATTGATGCA ATTGAGTAAC GCTGATTAG AACGATTAAA AAGCATGGCG	60
AACACGCTTC GCTTTTTGTG TCGGGACATG ATAGATAAGG CTAATAGCGG GCATCCAGGC	120
GTGTGTTTAG GGCTAGCTGA TGTGATGGTG GTTAAAGCT TGACACCAA CCTAAACCCC	180
ACCAACCTA ATGGCTCAA TAGGGACAGG TTGGTTTTA CGCGAGGGCA TCGGAGCCCG	240
TTAGTGTATA GTTGTGGCA TTTGTGGGC TTTGATTIGA GTTGTAGACGA TTAAAGCGT	300
TTCAGGCAAT TACACTCTAA AACCCCCAGGA CACCTGAAT TACACCACAC CGAAGGCATT	360
GAAATCACCA CAGGCCCTT AGGGCAAGGT TTTGCTAACG CTGTAGGCTT TAGCATGGCG	420
AGCCAATACG CTCAAACCCCT TTAGATAAA GAGGCATTCTCATAAAAGT CTATTGCTTG	480
TGTGGGGATG GGAGTTTGCA AGAAGGCATT AGTTATGAGA GCACTCTT AGCCGGGCAC	540
CTTCGCTTGT ATAATCTCAT TGTGATTAT GACAGCAACC AGATCAGCAT TGAAGGCCT	600
ATTAATATTA GTTTAGCGA ACAGGTTAAA ACACGCTTT TAGCGCAAA TTGCGAAGTG	660
CTAGAAATGCC ATGGGCATGA CTATCAAGCG ATTCAAAACG CTTAGAAGA AGCCAAAAAA	720
TCCCATAAAC CCACGCTTT AATCGCTCAT ACGATCATTG GTAAGGGGGC TATTGGCTTA	780
GAGGGGAGTG AAAAACGCA TGGCTCGCCT TTAAGTAAAG AAGTGTGAA ACAATCCAAA	840
GAAAACGCTC AAATCAATCC TAACGAAAGC TTTATAATTAA GCCCAAAAAA CAAAATGCAT	900
TTTGAAGAAG TGAAGGTTAG GGGTATTAGT TTAGAAGCCT TATGGGAAA GTCTTAAGC	960
CCTAAACAA AAGAAAAGAT CCATGCGTTA AAGAATTITG ATTAAACGC CATTAAATTAC	1020
CCCGCCCTTA AAAAAGGCGA ATCTCTAGCC ACGAGAGTGA GTAACGGCAT GATTITAAAC	1080
GCTATCGCTA AAAAATGCGA GGGCTTTTA GGAGGGAGTG CGGATTTAGC CCCATCCAAT	1140
AACACGCATT TGAAACACTC TGGCGATTTC CCTTTAGGGC AAAACCTGCA TTTGGGATC	1200
AGGGAGCATG CCATGGGGGC TATCACTAAC GCTTTAGCGG CGTATGGCTT TTTGTGCT	1260
TTTTGCGCGA CCTTTTTGTG GTTGTAGCGAT TATTAATGC CTAGCATTG TTTGAGCGCT	1320
TTAATGAAAT TAAAAGCCCT TTTTATCTTC ACGCATGACA GCATTGGGT GGGCGAAGAC	1380
GGGGCGACGC ACCAGCCCCAT AGAGCAATTG AGCCATTTC GAGCCTTGCC GCATTCTAT	1440
GCTTTAGGCC CTAGCGATGC TTTTGAAAT AAGGCTTGCA TGCAACTGGC ATTAAGTTG	1500
AACGCCCTTA GCGCTCTTAT TTTATCGCGC CAGAATTG TGAGGTTCT CATTATCACG	1560
AAAGAGCAGG TTCTAAAAGG GGGCTATGTT AAACACCACT CTAAGATCC 1620	
CTTGTGCGA GCGGGAGCGA AGTCTCTTA GCTTGTAGAGA GCGCTAAGAT TTTAGAGCGA	1680
GAAAATATTCC CCACTCAAGT AGTGAGCGG CCATGCTTG ACTTGTGTTG AGAGCAAGAT	1740
GAAAGCTATT TAAAGAAACT CTTTAAGGGT AAAGTCTTAG TGATTGAAGC GAGCCGCGCG	1800
ATAGAGTGGT ATCGTTTGCG GATAAAAATC ATTGGCATGG ATTCTTTGG GAGCTCAGCA	1860
AAGGGCGATA AACTCTTGA AAAATTGGC TTAGCGTTG AAAACATTAC CGCTCAAGCG	1920
AAAAGGTTAC TCAACGCA	1938

## (2) INFORMATION FOR SEQ ID NO:1071:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 819 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Helicobacter pylori*

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## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...819

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071

AAGGATTATT	GCATGCAAAA	TGGGTATTAT	GCGGCCACAG	GGGCAATGGC	TACACAATT	60
AACCGCTTGG	ATTAAACCTC	TAACAAITTA	GCCAACTAA	ACACCAAACGG	CTTTAAAAGA	120
GACGATGCGA	TTACAGGCAGA	TTTTTAAGG	CTTTTACCAAG	AATACCGAGA	GCAACTGCC	180
TTAGAAGATC	AAACCAAAGC	GAGCGCGAAG	TATCTAACCC	GCAACCTCAA	TCGTGTGCT	240
ATTCTATCAG	AAATCTATAC	GGATAGGAGT	CTTGGCGCGT	TTGAAGGGAC	GAATAACCCC	300
CTAGATTITG	CCCTAACAAAG	CCCTAACCTC	TATTTTGCGA	TACAGACTAA	TGAGGGCGTC	360
GCTTATACCA	AAGACGGGCA	TTTCAGCGTT	GATAAAAGACG	GCTTTTTGGT	AACCCCTTAAT	420
GGTTTAAGG	TGCTTTACG	CTCCGGTTTG	AAACAAAAAG	GAGGGATCAT	GCTCATGCT	480
AACGCTGAAA	TTGAAGTGG	TCAAAATGGT	GGAATCACTT	TTAGGGATAA	TGAAGGCCAA	540
ATTCAAGCGG	GCGCGTGGC	TTTACTGTAGT	TTTAGCGAAC	CTAAAAATCT	TAAAAAAATA	600
GGGCAAAACC	TTTATACCTA	TCAGGGCGAA	GGCGCTCATC	AAGTCTCTGA	CTCTGGTGGC	660
TTAAGGCAAT	CCATGCTAGA	AAAAAGCAAT	GTCAATCGGG	TGCGTGAGAT	GAGCACTTTG	720
ATTGAAATCA	ACCGCTTTT	GGACATGTAT	TCTAAAGTGC	TAACAAACCA	TCAAGATGAC	780
ATGAAACGCTG	AAGCGATTAA	CAAACCTCGCT	ACAAAAAGCT			819

## (2) INFORMATION FOR SEQ ID NO:1072:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1776 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1776

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072

GGAATGATAG	CGCTGAATTT	CAACCTCTTA	GATAAAAGAAA	AAACACGCC	CTTATTTGAA	60
AAAAGCCCGC	TAGATTCAAG	CTTAGAGCTA	TATAAAATA	GGAAATTCA	CATGCTCTAT	120
CCTTATTGAT	ATTATTTG	CTTGGGTAA	GGGGTGT	ATCGCTTGCT	TTTAGGCAAT	180
GAAAATTAA	AACGCTTGGT	GGTCATTGAG	CCTGAAATAG	AGGTGATTTT	CATTGTGCTG	240
AATCTTTGG	TTTTTCCAC	TGAGATTAA	GAAAATCGTT	TGATTTTATT	GCATGCAAGT	300
TTTTGCAATT	ACAACATGAT	TGCTTCATTA	TTTGATATGG	ATAAAAAGTC	TGTTTTATAC	360
GCAAGAATGT	ATGATTTAA	ACTTTTAAAC	GCTTATTATG	AACGATACTC	TCATCAAATG	420
ATAGAAATCA	ACCAGCATT	CACGCGCGCT	TTAGGATATG	GCGCTATTAG	CGTAGGCAAT	480
GACCTAAAG	ACGCACTCAT	AGGCATCAAA	CAGCATGTG	CTAATTGCG	TGAAGTCATC	540
AAAAGCCCTA	TTTGTGGA	TTTGTGAA	GCTTTAAAAA	ACAGAGACAC	CGCTTATTATC	600
CTTTCACCG	GGCCTAGTTT	AAATAAGCAA	CTCCCCCTTT	AAAAGAAAT	CGCTCCTTAC	660
GCAACGCTT	TTTGCATAGA	CGCTTCTTC	CCTATTCTAG	CCAGAGCCGG	TATCAAGCCT	720
GATATTGTGC	TGTCTTITAGA	AAGGGTGGAT	TTAACGGCGA	AATTCTATGA	AGAAACCCC	780
TTAGATTITC	AAGAAGGCGT	TATTTTGCT	CTGACTTCCA	TTGTGCATAA	ACGATTGATT	840
CAACCGATT	AAAAGGGGT	TAACCAATT	AGTTTCCGCC	CTTTGGCTA	TACCAACCTT	900
TTTGATTG	ACCAGTATGG	TTATGTGGC	ATAGGCATGA	GCGCAGCGAA	CATGGCGTAT	960
GAATTAGTGG	TGCATTCTCG	TTTCAAAAGG	TGCGTGT	TCGGGCAAGA	TTTGTAGCTT	1020
TCACAAAGCG	GTAACAGCCA	CGCTAGGGG	GGCATTTATG	GGCATAGAGA	GATCAAGCCT	1080
AAAAAGGATA	AAGACAAGAT	TTTTATAGAA	AAATACGGGG	GTAATGGGAA	AGTAGAAACC	1140

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ACTTTAGTGT GGAAACTTTT CTTAGAATTT TTTGAAAAAG ATATTTTAA	CACGCCCTAT	1200
AAATTAGAACG TCACTAACGC TACTGAGGG GGGCTAGGA TAAAGGGAC	TAAAGAAATG	1260
CCCTTAAAG AAGTGTGCGA AAAAATAGAC AAATCCAAGC CAAAGCCTCC	TATCAATCTT	1320
ATTATCCC A CCCAACAGA ACAGGCTAA AATTAAAGA TCGCCAAGAA	AAAATCCGAA	1380
GAGATCATCA AATACGCCAA TGAGAAAAA ACGCAAGTTG AAGAAGCGTT	TTTAAAGGTG	1440
GCAGAGTTT TAGAAAAAGT GGAAAAGCTT CATGAAAAAA ACAAAATTAGA	AGAGTTGGAT	1500
TTTGAAAGAT TAGAAAAATTG GAGCGCTGAA ATTGATAACG TAAAGAGCT	TTTTGATGAC	1560
AAACGATTCA ATTCTGATTT TATGGATGCC ATACAATCTT ACATTTTCCA	CCAGGAATTG	1620
CATATCGCTG AATATCGTGTG TAAAAAAAG AGTAATGAAG ACGGATTAAG	GGCTAAGCAA	1680
TTAGAATACA TTACGCGCA CAAATACTGG CTTTTAGTT TAGCGGGTGG	GATGGATTGC	1740
GTGATAGAAC CGATCAAAAT GGCTTGAAA GAATGG		1776

## (2) INFORMATION FOR SEQ ID NO:1073:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073

GTGCATTTA CGTGTATCTT TCTAACCTTA TTAAATGGA TTTGCCAGC CAAAAACAAG	60
CAGGCGTGCA AAAAGCCACC AACAGAGATCC ATTCAAGGTC TGCAAAACAT CCAGCAAAAT	120
ATCCCCCTC AAGTATTAAAC CCCTCAAATC CAAGCGGGTA TACAAGGGGT GATGCAAGGT	180
TTTGGGCTT TGAGCAGCAC TTTAGAAGCC CCCTTATTGT TTTCTAAGCA AAATGTGGTG	240
ATTGGGGCTT TTGAGCATTA TTATATCCCC TTATATGGGT GGGCAAGAT TCACGATGGT	300
GCGCATTGCC GAATTGAATG CAAAGACG CCAATGAAGT GTATCGCT	348

## (2) INFORMATION FOR SEQ ID NO:1074:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1131

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074

CGCATGAATT	TTTTTAAAT	CCTTTAATG	GAGTTAACAG	CCATTGTTTC	TCATAAGGC	60
GTTTTATTGA	TCCTTATAGG	CGCTCCTTA	ATCTATGGCT	TGTTATACCC	TTTGCCTTAT	120
TTGAAAGACA	TCGTAACGCA	GCAAAAATC	GCCCTTGAG	ATGAAGACAA	TTCCCTTCCTT	180
TCTAGGCAAT	TAGCCTTCAT	GGTGAAAGC	TCCAACGAGT	TAGAAATCGC	TTTCTTAC	240
CCCTCTATGC	TGGAAGCCAA	AAAGCTTTA	AAAGAAGAAA	AAATTATGG	GATCTTACAC	300
ATCCCCTCTC	ATTTGAAGC	CAATTTTAT	AAACAAGTGC	CTGTAACGAT	AGATTTTAT	360
GCAGACGCCA	ATTACTTTT	GATTTATGGT	CGCTTAGCGA	ATGCGGTGGT	GGGGAGCATC	420
AACGCCCTAA	ACGATGAAAT	CAGGTTCAA	CGCAACGCC	AAATAGAAGA	AGCTGAATTA	480
GGGACAGACG	CGATTAAGAG	TAAGCCTATC	GCTTGTATA	ACCCCTAGTG	GGGGTATTG	540
AATTACGCGC	TCTCTAGCGT	GTTCATTTTC	ATCTTACACC	AGGTGATGCT	CATTGCAAGC	600
ACCATGTTTA	CTAGCTCCAG	CGCTTGGAA	TTGGCCCTTT	TAGACAAAGAA	ACAAATCGCT	660
TTAAGGCTGT	GCGCAAGACT	CTTGGTGTTC	ATGGGGCGT	TTAGCGTTTT	TGTTTATGG	720
TATTTGGGG	CGCTGTTTC	TTTTATGGG	ATCGAACGGC	ATGGAAGCGC	TTTAAATGGTG	780
TTTTGAACA	GCTTGATTTT	CATGCTTGCG	GCCTTGAGTT	TGGGGTCGTT	TTTAGGGGCA	840
TGGATCAAA	ATGAAGCCCA	CACCACTCAA	ATCGTTTGA	TTTCCTTC	GCCCTTGATT	900
TTTATGATGG	GTTCATGTCG	GCCTTGTGAA	TCCTTGCCCT	CTTATTTGCA	AGCTTICGTT	960
CAAATAGTGC	CTGCTTATCA	TGGGATCAGT	TTGCTCGGGC	GATTGAATCA	TATGCATGCG	1020
GAATTATAG	ATGTTATAT	CCATTTTAC	CGCTTATTG	CGATTTTAT	CGTGAGTTT	1080
ATAGGGTGC	TGTTCAA	ACTAGCTTTA	AAGAAAGCTT	GTGAAAACGC	T	1131

## (2) INFORMATION FOR SEQ ID NO:1075:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...267

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075

ACCTTAAAGG	GGATTGTTT	GTTCAGATTG	ATAAGCGCAT	GGGTTTACA	AGACAAGTTC	60
TTGTTTGTG	TGTGTTTAT	ATTGCTTTT	TGTTTGGGG	TTTAGGCAC	GCAAATCTT	120
AAACAAGAGA	CCCCAAGACA	GCTCCCTATC	GTGGTGGTGG	ATTGGATAA	GACCACTACA	180
AGCCATCAAG	TGGCGTTGA	ATTAGGCGCA	ACGAGTGCAG	TTGAAATCAA	ATACCAAGTG	240
ACTAGCCTT	CAGAAGCTAA	ACGCTTT				267

## (2) INFORMATION FOR SEQ ID NO:1076:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076

AGCATGAAAA AAACAACCCCT CTTTGTATTG GGCTTATTAT TCAATAGCTC TTTAAGCGCT	60
GTGATGGGA TTTCCTAACAC CGAGCCTCTCT TCTTTGAATT TGGCTGAAGA TAGCCTGCCT	120
TTGAAACCATT CTAACGCCCA AAAACTCTCT TTAAAAAAACG CATGGAATAG GGTGTTGTCT	180
AATCATGAAG GCTTGCATGC GCAGAATACG CCATTAAGCG AGCGAGTAAA A	231

## (2) INFORMATION FOR SEQ ID NO:1077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077

GTAAGGAGAC AAACCTATGAA AAAGGTTATT GTGGCTTTAG GCGTTTGGC GTTCGCAAAT	60
GTTTTATGG CAACCGATGT TAAGGCTTT GTAAAAGTT GTGCCGCTTG CCATGGGGTT	120
AAAGTTGAAA AGAAAGCTTT AGGTAAAAGC AAAATCGTTA ACATGATGAG CGAAAAAGAG	180
ATTGAAGAGG ATCTTATGGC TTGTTAAAAGC GGTGCAACA AGAATCCTGT CATGACCGCG	240
CAAGCTAAA AATTAAGCGA TGAAGACATC AAAGCTTTAG CCATATACAT CCCCACCTCTC	300
AAA	303

## (2) INFORMATION FOR SEQ ID NO:1078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

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## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...477

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078

AGACCTATGC	TACATAAAAA	ATATCGCCT	AATGTTGGG	CCATTATCAT	GTCGCCAGAC	60
TACCCCTAAC	CATCGAAGT	TTTTATCGCT	GAGGCATAG	ACATTGAAGG	GGCGTGCGAG	120
TTCCCCAAG	GAGGCATTGA	TGAGGGAGAG	ACCCCTTAG	AAGCACTCTA	TAGAGAATTAA	180
CTAGAAGAAA	TTGGCACGAA	TGAAATAGAG	ATTTGGCGC	AATACCCTAG	ATGGATCGCC	240
TATGATTTC	CAAGCAACAT	GGAGCATAAA	TTCTATTCTGT	TTGACGGGCA	AAAGCAGCGT	300
TATTTTTAG	TGCGCTAAA	GCATGTTAAC	AACATTGATT	TGAACAAACA	CACGCCAGAA	360
TTTAGATCCT	ATCAATTCA	CCAGCTTAAG	GATTGCTTA	AAAAAATCGT	TCCCCTCAAA	420
CGCCAAGTGT	ACCGCCAAGT	CATCGCTTAT	TTTAAAGAAAG	AGGGGTATTT	GGGGTGT	477

## (2) INFORMATION FOR SEQ ID NO:1079:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...393

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079

TGCATGAATC	TTGTCTTTT	GTGGCCGCT	CTAGGAGGG	CTATAGGGAG	CTCGTTAAGG	60
TATTTTGCGG	GCAAAATGAT	GCCCCATAAA	TTTTTAATGT	TGAAAGTTT	CCCTTTAGGG	120
ACTTTTAGCG	TGAATCTCAT	AGGGTGT	ATCATCGCT	TTATGGGGCA	TTTGGCCGCT	180
AAAAAAAGTTT	TTGGTGATGA	TTTTGGGATT	TCCTTTGTAA	CCGGAGTTT	AGGGGGTTTT	240
ACGACCTTTT	CTTCTTATGG	GTTAGACACT	TTAAAACCTCT	TGCAAAATC	CCAATACCTT	300
GAAGCCATT	CTTATGTCTT	AGGCACTAAC	CTTTAGGGC	TTATTGGGGT	AGCTATCGGT	360
TGGTTTTGCGG	CTAAGAATT	TGTAGGGCGTT	AAT			393

## (2) INFORMATION FOR SEQ ID NO:1080:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

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## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...819

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080

TATTTATCAA	TCGTGGTGGAA	AGATCAGAAA	GGCATTTTCC	CTATCCAGC	GTCAAAAAGA	60
AAAAGCCAAA	GCTCTGTGAT	CATTGAAGAC	GTGTGCTTC	GCAAAGAGGA	TTTTGTAGAA	120
GGGGCAAAAG	CGATTGAGGG	GCTTTTAAAAA	AAACATGGCT	TTAAGGATAA	TGGCATTATT	180
TTTGGGCATG	CGTTAACGCG	GAATTTCAC	TTTGTGTTA	CGCCGATTCT	AGAAAATGAA	240
GCTGAAAGAA	AAGCGTTTGA	AAATTTAGTT	TCTGAGATGT	TTTTAATGGT	GAGCAAAAGC	300
TCTGGCTCTA	TTAAAGCCGA	ACATGGCAC	GGCAGGATGG	TAGCCCCTTT	TGTGGAAATG	360
GAGTGGGGAG	AAAAAGCTTA	TAAGATCCAC	AAACAAATCA	AGGAATTGTT	TGATCCTAAT	420
GGCCTTTTAA	ACCCCTGATGT	GATCATCAC	AAKGATAAAG	AAATCCACAC	TAAAAATTAA	480
AAGAGCATT	ACCCTATTGA	AGACCATTTG	GACATGTGCA	TGGAATGTGG	GTTTTGTGAA	540
AGGATCTGCC	CCAGTTAAAGA	TTTATCCTTA	ACGCCACGAC	AACGCATCGT	CATCCACAGA	600
GAGGTAGAGC	GTGTAAGAGA	AAGGGTAAGT	CATGGCATG	ATGAAGATCA	GGTTTTACTA	660
GATGAGCTTT	TAAAAGAGTC	TGAATACTTA	GGCGATGCCA	CTTGGCGGGT	GTGCCATATG	720
TGTTCCACTT	TATGCCCTT	ACGGATTGAT	ACCGGGAGTA	TCGCTTTAAA	TCATTATCAA	780
AAAAACCCCTA	AAGGCAGAAA	GATCTGCTTC	AAAGATTCT			819

## (2) INFORMATION FOR SEQ ID NO:1081:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...723

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081

CGATTTTTAC	AAAAGACTGC	GCAAATTG	GGAAATTAAAA	TGCTAGTAGA	AATAGAGAAAT	60
TTGACTAAAA	CTTATGGGAG	TTTAAAAGCG	CTAGACAATA	TCAGTTGAA	ACTACCCAAA	120
CAGCAATT	TAGGGCTTTT	AGGGCCTAAT	GGGGCGGTA	AAACCACTCT	GTAAATT	180
TTAGCCGGAT	TGAATTGAA	CTATCAAGGG	GAAGTGAAAA	TTTAAACCA	AAAGATTGCT	240
ATAGAGACTA	AAAAAACG	GGCGTTTTA	AGCGATGGCG	ATTTTTAGA	TCCTAAATTA	300
ACGCCTTTAA	AAGCGATCGC	TTTTTATAAG	GATTTTTTA	GCGATTTGA	TGAATCAAAA	360
GCCCTAAATT	TGTTAAAACG	CTTCAGCGTG	CCTTTAAAAA	GAGAGTTCAA	AGCCCTTTCA	420
AAAGGCATGA	GGGAAAAATT	GCAGCTGATT	TTAACCTAT	CACGAAACGC	TTCTTTGTAT	480
CTTTTGATG	AGCCGGTGGC	TGGGATTGAC	CCTATTGCAA	GAGAAGAGAT	TTTGAGTTA	540
ATCGCTAAGG	AGTTTAGCCA	AAACGCAAGC	TTGCTAGTCT	CTACGCATT	GGTGGTGGAT	600
GTGGAAAAGT	ATTTAGACAG	CGCGATTTTT	TTAAAAGAAG	CTAAAGTGGT	GGCTTTGGG	660
GATGTGGGGG	AATTAAAAAA	AGGGTATAGC	AGTTTGAGG	CAGCGTATAA	AGAAAGTTG	720
AAA						723

## (2) INFORMATION FOR SEQ ID NO:1082:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082

AAATCGTGGT	TTTTCTATGC	CCCTTTTAT	GGTTTGTGGT	GTTTAAAAAC	CCCTATCATA	60
GGGCATGGCA	TGAAGAAAAA	AGCAAAGTC	TTTGGTGTGTT	GTTTAAAAT	GATTCGTTGG	120
TTGTATTTGG	CGGTCTTTTT	TTTGTGAGC	GTATCAGACG	CTAAAGAAAT	CGCTATGCAA	180
CGATTGACA	AACAAACCA	TAAGATTTT	GAAATCCTTG	CGGATAAAAGT	GAGCGCCAAA	240
GACAATGTGA	TAACCGCCTC	AGGGAAATGCG	ATCCTATTGA	ATTATGACGT	GTATATTCTA	300
GCGGATAAGG	TGCGTTATGA	CACCAAGACT	AAAGAAGCGT	TATTAGAAGG	CAATAATTAAG	360
GTAAATAGGG	CCGAGGGCTT	GCTCGTTAAA	ACCGATTATC	TGAAATTGAG	TTTGAACGAA	420
AAATATGAGA	TCATTTTCCC	CTTTATGTC	CAAGACAGCG	TGAGCGGGAT	TTGGGTGAGC	480
GCGGATATTG	CTAGCGGGAA	GGATCAAAA	TATAAGATTA	AAAACATGAG	CGCTTCAGGG	540
TGCAGCATTG	ACAACCCCCAT	TTGGCATGTC	AATGCGACTT	CAGGCTCATT	TAACATGCAA	600
AAATCGCATT	TGTCAATGTC	GAATCCTAAC	ATTATGTCG	GCGATATTCC	TGTATTGTAT	660
TTGCCCTATA	TTTTCATGTC	CACGAGCAAT	AAAAGAACTA	CCGGGTTTTT	ATACCCCTGAG	720
TTTGGCACTT	CCCACCTTAA	CGGCTTTATT	TATTGCAAC	CCCTTTTATT	AGCCCCCAA	780
AACTCATGGG	ATATGACCTT	TACCCACAA	ATCCGTTACA	AAAGGGGTTT	TGGCTIGAAT	840
TTTGAAGCGC	GCTACATCAA	CCCT				864

(2) INFORMATION FOR SEQ ID NO:1083:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 447 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083

ATCGTTAGAA	AGAAGTTAAT	GTTAGAGATG	AGTTTGCAAG	CATTAATAC	ACAAGATTCT	60
TCTGTGATGG	CTCAATCCCT	GCTTGTCCAT	GCCTTTTTG	CCGCCTTGCT	CGCCCTAGCC	120
TTTATGATCA	ATCTTTACAC	CCTTTTTAAA	GAAAAGAATT	TCATCCAATT	GAACCGGAAA	180
ATCTATCTTG	TGATGCCAGC	GATTGATATT	CTTTTAAAGCA	TCGCTTTTT	GAGTGGGGTT	240
TTTATTTGGG	CGATGCAACA	ATTTGAATT	CTTTTGTAGCG	CTGTTGTCAT	GCTTTGGGG	300
TTGTGTGAA	TGCTCAATTG	AGAAATCAA	CGCCATAAAA	GGGTGAAATT	CGCTATCACT	360
AAAAAGAAA	GGATGAAACC	CTATATCAA	AAAGCTAAAA	TCCTGTATT	TTTAGAAACG	420

ATTCTTATCA TCGTGTTAAT GGGCATT

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## (2) INFORMATION FOR SEQ ID NO:1084:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084

CCAGAAGGAG GGAATGAAC	CAATGTGTTT GAGCCGGTA	TCGCTTACAA	GCTTTTCCAT	60
TCTTGTGA TTTTAGGGTG	CGCGATTGAA ACTTTAACGA	CTAAATGCGT	GGAAGGCATC	120
ACGGCTAATG AAAAGATTTG	CCACGATTAT GTTTTTAACA	GCATTGGCAT	TGTTACCGCG	180
CTCAACCCTC ATATCGGCTA	TGAAAAATCC GCTATGATCG	CCAAAGAAGC	CTTAAAAGC	240
GATCGCTCTA TCTATGATAT	CGCTTTAGAA AAGAAAATCT	TAACCAAAGA	GCAACTGGAC	300
GATATTTCAGCCAGAAAA	CATGCTAACG CCTCACGCTT	TCAAAAGCA	TAAAGAC	357

## (2) INFORMATION FOR SEQ ID NO:1085:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085

AAAAGGCTTA TGGTTTGTT	TCTATCCATT TTTAAAAAA	GCTTTAATGA	TTTTTTAAGC	60
GCTAGAACG TTTAATCAA	TCTTGGCCCT	ATCCTTTGA	TTTGGCGTT	120
ATCTTTTATT ACAATGGCGG	GAGTATGIG	AATTATGCGC	AAACTTTATT	180
TTGAATGATT ACGCTCATTC	TCAAGGCTTT	TTTGGCGGTG	TGTCGCATG	240
GCGTTAGTGT ATTTCCTTAT	TGAGTTAGT	CATCAATATT	300	
TTTGCCTCTA TTTCACAC	CCCTTTAGTG	TGCAACCAAA	ATATTATCCC	360
CATGTCGTT TAGAAGAATT	TGGCTCTATC	CTTTTTCTA	TTAAATATT	420
CTCACTTTA TGCTTTATT	TTAGCGGTT	TTAACGCC	TTTATTCAT	480

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GGGGTCTTTG GGGCTTTT TTCTATAGTC CGCATTCC TCTTTTCAA AAACACCAG	540
AGTTTGGATA TAGCCAGCAT GATTTTCAAC CATCAAAGCT ATCAAAATT ACTCAAACAG	600
CACCGATTGA AGCATTATCG TTTTCGTTT TTTCGCTATC TTTTTCCCTT GATTCTTTT	660
TTTAATTTT TTGCCACCTT GTGCCAAACC CTAATGTTAA CGCAC	705

## (2) INFORMATION FOR SEQ ID NO:1086:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086

GAATGTAAAG GAATGGAATT TATGAAAAG TTTGTAGCTT TAGGGCTTCT ATCCGCGGTT	60
TTAAGCTCTT CGTTGTTAGC CGAAGGTGAT GGTGTTTATA TAGGGACTAA TTATCAGCTT	120
GGACAAGCCC GTTGAATAG CAATATTAT ATTACAGGGG ATTGCACAGG GAGTGTTGTA	180
GGTTGCCCCC CAGGTCTTAC CGCTAATAAG CATAATCCAG GAGGCACCAA TATCAATTGG	240
CACTCCAAAT ACGCTAATGG GGCTTGAAT CGTTTGGGT TGAATGTGGG TTATAAGAAA	300
TTCCTCCAAT TCAAGTCGCT AGATATGACA AGCAAGTGGT TTGGTTTAG AGTGTATGGG	360
CTTTTGATT ACGGGCATGC CGATTTAGGT AAACAAGTTT ATGCACCTAA TAAAATCCAG	420
TTGGATATGG TCTCTTGGGG TGTGGGGAGC GATTGTTAG CTGATATTAT TGATAAAAGAC	480
AACGCTTCTT TTGGTATTTC TTGGGGGTG GCTATCGGCG GTAACACTTG GAAAAGCTCT	540
GCAGCAAACCTT ATTGGAAAGA GCAAATCATT GAAGCCAAG GTCCTGATGT TTGTACCCCT	600
ACTTATTGTA ACCCTAATGCG CCCTTATAGC ACCAACACTT CAACCGTCGC TTTCAAGTG	660
TGGTTGAATT TTGGGGTGAG AGCCAATATC TACAAGCATA ATGGCGTGGA ATTTGGCGTG	720
AGAGTGC CGC TACTCATCAA TAAATTGG AGCGCGGGTC CTAACGCTAC TAACCTTTAT	780
TACCATTTGA AACGGGATTA TTCGCTTTAT TTGGGGTATA ACTACACTTT T	831

## (2) INFORMATION FOR SEQ ID NO:1087:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2028 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...2028

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087

GCTTTGAAAG AATTAGAGCC	TTTGAGTTTT TCCTTCATT CGCCTAAAGG	GGCGTGCAGA	60
AGTTGTTTGG GTTTAGGGAC	AAAATTTAGC TTAGATAATT	GTAAGATTAA AGATCCTAAC	120
ACGCCCTTAA ATCAAGGAGC	GATTAAGATG ATTTTTGGCT	ATAACCGCAG TTATTACGCT	180
CAAATGTTG AAGGCTTTG	CACTTATAAT GGCATTGACA	GGCGCTTGT TITCAACGAA	240
TTGAACAAAG AGCAGCAAGA	CGCTCTTTG TATGGGAATG	GCACTGAAAT CAGCTTTCAT	300
TTTAAAAACCA GCCCCCTGAA	ACGCCCTTGG AAAGGCAATTA	TCCAAATCGC TTATGACATG	360
TTTAAAGAGC AAAAGGATT	GAGCGATTAC ATGAGCCAAA	AAACCTGTT TTCGTGTAAT	420
GGGCATCGCT TGAAAGCCTC	AAGTTTGAGC GTCCAAGTCG	CTGGCTTGAAT AATGGCGGAT	480
TTTTTAACTA AGCCCATTGA	AGAAGTCTAT CATTTTTTA	ATGATCCCAC GCATTITAAC	540
TATCTTAACG ACCAAGAAAAA	AAAAGATCGCT GAACCCATT	TAAAAGAGAT TTTAGAAAGG	600
GTGTTTTT TATACGATGT	GGGGCTAGGG TATTGACTT	TGGGGAGGGA TGCGCGAACG	660
ATTAGCGGAG GGGAGAGCA	AAGGATACCA ATCGGCACTG	AAATCGGGAG CGGTTTGACCA	720
GGGGTTTTGT ATGTTTTAGA	CGAGCCTAGC ATTGGCTTGC	ATGAAAAAAA CACGCTCAAA	780
CTCATCAACA CCCTTAGGAA	TTTACAAAAAA AAGGGGAAACA	CGCTCATTGT CGTAGAGCAT	840
GATAAAGAGA CGATTAAGCA	TGCGGATTTT GTTGTGGATA	TTGGGCCAAA GGCTGGAAGG	900
CATGGGGGTG AAGTGGTTT	TAGCGGGAGC GTAAAAGATT	TATTGCAAA TAACCATTCT	960
ACCGCTTGT ATCTCAACGG	CACTAAAAG ATTGAGCGCC	CCAAATTTGA ACCCCCTAAA	1020
GAAAAGCATT TTTAGAAAT	TAAAATGTC AATATCAATA	ACATTAAGAA TTTGAGCGTT	1080
CAAATCCCT TAAAACAATT	GGTGTGCATT ACGGGGGTGA	GCGGGAGCGG TAAAGCTCG	1140
CTGATTTCAC AACCCCTTTT	ACCCACCGCT CAAACCTTT	TAAACCATGC TAAAAAAAAT	1200
CAAAGCTTGA ATGGGGTGG	GATTGTAGGG TTGGAGTATT	TGGATAAAGT GATTATTTA	1260
GATCAAGCCC CCATAGGCAA	AACCCACCGA AGCAACCCCG	CCACTTACAC GGGAGTGATG	1320
GATGAAATCA GGATTTATT	TGCCGAGCAA AAAGAAGCTA	AAATTTTAGG CTATAGCACG	1380
AGCCGTTCA GCTTTAATGT	TAAAGGAGGG CGGTGTGAGA	AATGCCAAGG CGATGGGGAT	1440
ATTTAAATAG AAATGCACTT	TTTGCTGTAT GTGTTAGTCC	AATGCGATAG CTGTAAGGGC	1500
GCTAAATACA ACCCCCCAAC	TTTAGAAATC AAGGTGAAAG	GCAAATCCAT TGCTGATGTG	1560
TTGAACATGA CGGTGGAAGA	AGCTTATGAA TTTTTGCTA	AATTCCCTAA AATCGCTGTG	1620
AACTTAAAAA CGCTTATAGA	TGTGGCTTA GGCTATATCA	CTTGTAGGGCA AACGCTACG	1680
ACTTTAAGTG GGGGGGAGGC	TCAAAGGATC AAATTGGCTA	AAGAATTGAG TAAAAAAAGAC	1740
ACAGGCAAAA CCCTTTATAT	TTTAGATGAG CCTACCAACCG	GTTGCAATT TGAAGATGTG	1800
AATCACCTT TACAAGTCTT	GCATTCTTG GTGGCGTTAG	GCAATTCCAT GCTAGTGATT	1860
GAGCATAATT TAGACATCAT	CAAAACGCT GACTACATTA	TAGACATGGG GCCTGATGGG	1920
GGGGTAAAGG GCGGGAAAGT	CATTGCGAGC GGCACGCCCT	TAGAAGTGGC GCAAAATTGC	1980
AAAAAAACCC AAAGCTATAC	GGGAAAATTIT TTAGCTTGG	AATTGAAA	2028

## (2) INFORMATION FOR SEQ ID NO:1088:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 828 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...828

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088

GGCGCTTTG TAAAAATCAC	AGCGGATTAT TTTTCCCTA	TGGAAAACGT GTTTTACCGC	60
TCCATTACCA TGACGCTTTT	ACTCTTGCTT ATCTATCCTT	TCAAACCCCTA CCCCTTGAAAG	120
AGTTACAAAC AAGGCGTTT	AAAAAGCTC GCCTTGTAGGG	TCGTTGTGGG CGGCTTAGGCC	180

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ATGCTGGCGT	TTTTTATAA	TATTGAAAAA	ATTCGCTCG	CCACAGCGAA	CGCTTTCTCA	240
CAATCGCGC	CTATTTATAC	GGTGCCTCTT	TCCCCTTGTC	TTTTGAAAGA	AAAGCTAAA	300
AGAACGCGT	TAATTTCCGC	ATGCATCGGG	CTAGTGGGGG	TGGTGTGAT	TTCAGATCCT	360
AGCGTGGAAA	ATGTAGGACT	AGTGAAATC	ATTATGGCA	TATTGACCGG	GATCTTTGTG	420
TCTTAGCGT	ATATCACTT	AAGGGATTTC	AGGGAAATATT	ACGACAAGCA	GGCCGTGATT	480
TTAGCGTTCG	CCTTTGGCAT	GAGTCCTCTT	GGATTAGCGG	GCATGTTCAT	TGATATTCT	540
TTTTTATCCA	CAGCGGTICA	TATCCCTAGA	AAAGAGGATA	TTTTATGGAT	TTCTTTAATA	600
GGGATTAGCG	GGACTTTAGG	GCAGTATTC	TTAACCTATG	CTACATGAA	CGCTCCTGCT	660
GGGATCATCG	CCCCCATIGA	ATACACCCG	ATIGTTGGG	GGCTATTGTT	TGGCTGTAT	720
TTAGGCATA	CATTTTGGA	TCTTAAAAGC	TCTTAGGGG	TGGCTTTGAT	CTTATGTTCA	780
GGCTTGCTCA	TTGCCCTGCC	CGCTCTTTA	AAAGAATTAA	AAAAAATT		828

## (2) INFORMATION FOR SEQ ID NO:1089:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...807

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089

GTCATGCAAC	TAAGCCCCTT	ACAAAGCGCG	CTGTTATATT	TCCGTTACTT	TATTTATCCG	60
GAAAAAAA	CAAGGAGCT	TGATTTAACG	GATTAAATT	TTATTGTCAT	GGTTTTTTTA	120
GTCCTAGCTT	TGGGGCTGTT	GATGAGCGAA	GAAATTCTA	TCAGCTACAA	TGAAGCGAAA	180
GACTTTTT	ATAGCGATGC	GTGGTTTGTG	AAAATCGCTC	AAAAAGCGT	AGCCATTATA	240
GGCCAAAACG	ATTTGGCTTT	AAGATTGCC	TTTTTGATCG	CTCACGTCAT	CAACATGTT	300
TTATTCTACC	TCATAGGGCG	AAAGATTITA	AAAAGCCTA	AAGACGCTCT	TTATGTGGTA	360
TTGACTTACG	CTTTATTGCC	TGGGGTGAAT	CTCTTTGCGA	TTTACTGGC	AAAAGCGTG	420
CTGGTGTAA	GCCTTGGGCT	TTTGATTAGC	TATTGATA	TTAAAACCCA	AAAATCCCT	480
TATTTAACCC	TTAGCGCTTG	CGCGTTTTA	GACGGTGCCT	TCATCCCCT	TTTACTAGGG	540
GTTTTTGCCT	ACGCTTTAACG	AAAAGCCTAT	TTTAAGAGCG	CGATCTTGC	TTTGGTGGTT	600
TTAATTGTGA	ATACCGCTCT	TTTAGTGGG	GATTAAATA	AAGGCTTGCC	TAGGGGTAT	660
TTTATAGACA	CTTGCTTACA	ACTCATGCTT	TTGTATTGCC	CCTTATTGTT	CCTCTACTAC	720
CCTTATAACGC	TCTATAAAAGC	CCTTTTGGAT	AAAAGCCAT	CGTTACTAGC	CTTTATGGCG	780
CGAGCGGCTG	GCTTTCCCT	TTGCTT				807

## (2) INFORMATION FOR SEQ ID NO:1090:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090

AGCCCTTTTA TGGATAGAAA	ACTCTTAAAGA TTATACCAGC	CCTTAAACGC TTATTCTTAC	60
AATAGCGATT CGCTTTTTTT	ATACGATTTC TCACGCCCT	TTATCAAAAA TAGCGGCGCG	120
ATTTTAGACA TAGGCTCAGG	GTGTGGGGTT CTAGGCTTGC	TCTGCGCTAG AGACAACCCG	180
CTAGCGAGCG TTCACTTGT	GGAAAAGGAT AGCAAAATGG	CGTTTGCTC CCAAAAAAAC	240
GCCCCTAAAT TCCCTAACGC	TCAAGTGT	GAGAGCGATT TTTAGATT	300
ATTTTGATG ATGCGATTGT	GTGCAACCC	TTTTAGATT	360
CAAATTAAG GGCATGCGAG	CCTTTTATG CTTAGGATC	TATTAATCT	420
GTGAAAAAAT GCCTGAAACC	GAATTAGACT TCGCTTCTT	GGTGGCTAAA	480
TGCTTGGTCA TAGAGAGCTT	TTAAAGGTTAT	GCTATGAAGC CTTGTCGCTT	540
CAAAGTTCA AAGACAAAAA	AAAAAGCGTT	AAACTCACGC TAGAAACTTT	600
AGCGCTCTAA AAGTTTGCC	CGCCCATTTG ATGCTTGGAG	CGGCTAGGAA TAATTCCAAA	660
ACCAAAAGAAG TTTAAACAT	CCCTTTAAC	ACGCACAAATT CAAAAAAACCA	720
CTATCAAATT	TGTAACACTT ATTCTATCAA	AAAGCGACAAAC	
GAT		AGCGCTTTA	
			723

(2) INFORMATION FOR SEQ ID NO:1091:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1287 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091

TCTCGTTCTT TTAGGGGGCT	ATTATATTAT AATAAGATAA	ATTTGATTAA TAAGGATACA	60
GGCTTGCAG AAATTAATT AGACATTTAT	GCCACTTITAG	TGTGCATGGT TTTGGTGTG	120
CTTTTGGGGC GTTATGTGAT	TTCTAAAGTC	AAGTTTTAA GAGATTATGA	180
CCTGTTGTGG GTGGGTTTT	AGTCGTTTT	TTTATCATGT	240
TTTGGCTTC AGTTGATTC	TTCTTTAAA	TGCTGACTTT	300
ATTGGTTTGA GCGCGGATT	CAAATCTTTA	GGAAATGCT	360
TTGCTGGCTG TAGGGGGTT	TGTGGTGTG	TGGGGATTC TATCGCTAAC	420
CTTTAGGGG TCAATCCTT	AATGGGGCTT	TTAGGGGGAT CGATCGCTT	480
CATGGCACTA GTGGGGCATG	GGCTAATT	TTCACCCAAC CACCTTATCA	540
AGCTTGGAAAG TGGGCATGGC	GTGCGCGACT	TTTGGCTGG	600
GGGCCTGTG	CTAAATATT	TGAGCGGGGG GATTATTGGA	660
AAAGACACTT TAGAGGGCGT	GGTGTCTAA	GGTGGATTC AACCTAAAGA	720
ATCACTGCAT CCAGTTTGT	AGAAAACCTTA	CCCTAAAGA CACTAAAGAA	780
ACTTTTTAT CGCATTGAT	GCCTAAAAGT	GCTCTCATTC CAATAGCTT	840
TTTGTGGGGG TTATCTTAAAG	TTCACCTAC	CGACTTTCGT GTGGTGTG	900
AGAGAGGTTT CAGTTATAGG	TCGTTTTA	AAATCCATAG CGTGTGAC	960
AGCGTGAATT TATTGAAATT	GAATGTGAGC	TTGAGCTGT TTTAGCTTA	
GTTAAAACTC	GCTGTGCCCT	CGCTTTAATG	
	TAGCGGTTAT	TTTGAGCGTT	
			1020

796

CAAGTGGCGG TTATGATCCT TTATGTGGTG CTTGTAACCT TTAGGGTATG CGGGAAAGGAT	1080
TATGATGCGG CGGTGTTGTC CGCGGGCAT TGCGGTTTTG GCCTTGGAGC GACCCCAACG	1140
GCTATGGTGA ATATGCAAAC CATCACCAAC CACTATGGGC CATCGCATGT GGCGTTTATC	1200
GTCGTGCCCT TAGTGGGAGC GTTTTTGTT GATATTATTA ACGCTTTAGC GATTAAAGGC	1260
TTTTGCTTT TGCCTTTT CCCTAGT	1287

## (2) INFORMATION FOR SEQ ID NO:1092:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 573 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...573
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092

AAATTCGTT TGC GTT CAAT TTCAAGGATA AAGATGCTTT CAGTGTATGA AAAAGGGAAT	60
GCCCTAGACA AAAGGGTGCT TGAAGAATGG CTTTAAGCG AAGACATTTT AATGGAAAAC	120
GCCCCTATGG CTTTAGAAAG GGCGGTTTTA CAAACACGCTT CTTGGGCCGC TAAGGTCAATT	180
ATTCTTTGTG GGAGTGGGGA TAATGGAGGT GATGGCTATA CTCTAGCCAG GCGTTTAGTG	240
GGGCGTTTA AACGCTGGT CTTTGAAATG AAATTAGCAA AAAGCCCCAT GTGCCAATTG	300
CAAAAGAAAA GGGCTAAAAA AGTAGGGGTA GTCATCAAAG CATGGGAAGA AAAGAATGAA	360
GATTTAGAAT GCGATGTGTT AGTAGATTGC GTGGTAGGGA GCGCTTTAA GGGCGGATTA	420
GAGCCGTTTT TAGATTTGA AAGCCTTCT CAAAAAGCAC GCTTTAAAT CGCTTGCAC	480
ATT CCTAGCG GGATAGATTTC TAAAGGCAGG GTGGATAAGA GGC GTTTAAG CGGGATAACGA	540
CTATCAGCAT GGGCGCTATC AAGTCATGCT TAC	573

## (2) INFORMATION FOR SEQ ID NO:1093:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1323 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...1323
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093

**SUBSTITUTE SHEET (RULE 26)**

AATCCCCACA	ACTTGAAAGA	TAAAACCTTT	CAGGGGGGGT	TTGAACCTCT	TACGACCCCC	60
AAAGAATACT	CATGGGTGCG	GGTTGTTTA	AGCCTTTGT	TGGCGATTAA	CCTTTATTAA	120
GAATACITGA	ATCACCAAAA	GCTTGATTTC	TCAAAACCTA	CAAGCTTGAA	CGCTCAAATC	180
TTTATTACAAT	ACCCCTAAAAAC	GAAAGATCAA	AAAACCTATT	TTGTCTTAAA	ACTCCAATCT	240
AAGGGCATGA	TCTTTTACAC	CACCAATTAAA	GAGGCCCTTAA	AAAACCTCCA	ATACCCTAT	300
GCGCAATTTC	TTGGCAAGAT	CAAGCCTTGT	TCGTTCTTAG	AGTCTCTAAA	ATCATGCTTT	360
TTTCAAAACCT	ATTCTTTTTC	TTAACGCCTA	AAACAAGATT	TCAAATCGCA	TTTGCGCCAT	420
TTCATTTGACA	GCGCCCATTG	CAACGCCTTA	GTGGGTAATT	TGTATCGAGC	GTATTCTATA	480
GGGGATAGCT	TGAATAAAGA	CTTAAGAGAC	AGGGCTAACG	CGCTAGGGAT	CAACCACTTA	540
CTGGCCATTG	GCGGGTTTCA	TTTAGGGATT	TTGAGCGCGA	GGGTGTATT	TCTTTCTCT	600
CTTTTTTATA	CCCCCTTACA	AAAACGCTAT	TTCCCTTACA	GGAACGCTTT	TTATGATATA	660
GGGGCTTTGG	TGTGGGTTT	TTTGTGTTGG	TATTATTGTC	TATTAGATT	TTTACCCCT	720
TTTTTCAGGG	CGTTTTTAAT	GGGCTTATT	GGGTTTTGG	CATGTTTTT	TGGGTAAGG	780
ATTTTGAGTT	TTAAACCTTT	GGTTTTAGCG	TGCTGTATCG	CCATACCGTT	ACTCCCTAAA	840
TTGCTTTA	GGCGGGGGTT	TTTGCTTCT	TTTGTGTTGG	TGTGGTATAT	CTTTTTGTT	900
TTAAACACAA	CTCAAATTTT	TTTTAAAGAT	TCTTCTTTT	TCAAGCGATC	GTTCAGCG	960
ATCGCTTTAA	GCGTGTAGT	GTTTTGAAAC	ATGCTCATTC	TTGCGCATGC	CTTTTCCCT	1020
ATGTTTCGC	CCTACCAGCT	CTTTAGCATT	CCTTCTAGGCT	TGATTTTAC	TGTGTTTTC	1080
CCTTCTAGCT	TGTTCTTGCA	TGCGGTGGGT	TTAGGGCTTT	TATTGGATAA	TATTCTAAGC	1140
ATGCCCTTAA	CCATCCCCAC	GATTTGGTT	TCTTCGCCTT	TATGGCTTT	GGGGCGCAT	1200
TTGTTTTAA	CGATTTTAAG	CGTGCCTTT	TTTAAGGTTT	ATTAAGCAT	GAATGTTTG	1260
AGCATGGGCT	TTTCTTGTA	TTGTTGCTAT	CAATATATTA	TAATGCCTAG	TTAATTGTG	1320
GGT						1323

## (2) INFORMATION FOR SEQ ID NO:1094:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 906 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094

GAGGCCTTTA	AGGCGGATAC	GACTATCAGC	ATGGGCGCTA	TCAAGTCATG	CTTACTAAGC	60
GATAAGCTA	AAGACTATAT	AGGGGAATTG	AAAGTGGGTC	ATTAGGGGT	TTTTAATCAA	120
ATTTATGAGA	TCCCACAGA	CACTTTTTA	CTAGAAAAAA	GCGATTGAA	ACTGCCCTTA	180
AGGGATGAA	AAAACGCTCA	CAAAGCGAT	TACGGGCGAT	CGCATGTGCT	TTTGGGCAAG	240
CATAGTGGG	CGGGGTTGTT	AGCGCTTTA	AGCGCGTTAA	GTTCGGATC	TGGGGTGGTG	300
AGTATCCAAG	CGTTAGAGTG	CGAGATAACT	TCTAATAACA	AGCCTTCTAGA	ATTGGTTTTT	360
TGTGAAATT	TCCCTAAAAA	GCTCAGCGCG	TTCGCTCTTG	GCATGGGTT	AGAAAATATT	420
CCAAAGGATT	TTAAGAAGTG	GCTTGAATT	GCCCCATGCG	TTTTAGATGC	GGGCGTTTTT	480
TATCATTAAG	AAGTGTAC	AGCCTTAGAA	AAAGAAGTGA	TCTTAACCCC	TCACCCCTAA	540
GAGTTTTAT	CGTTATTGAA	ATCAGTGGGG	ATCAATATAA	GCATGCTAGA	ATTACTAGAC	600
AATAAACTAG	AAATCGCAAG	GGATTTTCT	CAAAATACC	CCAAGGTGGT	TTTGCTTTTA	660
AAGGGGGCTA	ATACCCCTAT	CGCTCATCAA	GGGCGGGTTT	TTATCAACAA	TTTGGGAGC	720
GTGGCTTGTAG	CCAAAGCAGG	CAGTGGCGAT	GTGTTAGCGG	GGCTGATTGT	AAGCCTACTT	780
TCTCAAAACT	ACACGCCCTT	AGACGGCGCC	ATTAACGCAA	GTTCGGCGCA	CGCCCTAGCG	840
GGTTTAAAGAAT	TTAAGAATCA	TTACGCTTTA	ACGCCCTAG	ATTGATAGA	AAAGATCAA	900
CGACTA						906

## (2) INFORMATION FOR SEQ ID NO:1095:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1125 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...1125
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095

CTCGCTTTAG CGTCAAAAGC GACCGGGTTT CCCATTGCAA AAGTGGCTAC CATGCTTGCG	60
GTGGCTTTA GCTTAGATGA ATTAAAAAAC GATATTACCA ACACCCCGAG GAGCTTTGAG	120
CCTAGTTGG ATTATATCGT GGTGAAAATC CCTCGCTTGT CGTTTGAAAA ATTTGCCGGT	180
GTTTCTAGCA CTTTAGGGAC TTCCATGAAA AGCATTGGAG AAGTGTGATGCC GATAGGGGGG	240
AATTCTTAG AAGCCTTACA AAAAGCGTTA TGCTCTTGG AAAACAATTG GCTAGGGTTT	300
GAATCGTTAA GCAAAGATTG AGAGGCAGATA AAAAAGGAAA TCCGCCGGCC CAATCCCAA	360
CGCTTGCTCT ATATTGCTGA TGCGTTGAGG TTGGCGTTT CTGTGGATGAA AGTGTGAA	420
TTATGCCAGA TTGACAGGTG GTTTTATCT CAAATTCAAA AACTAGTCAA AGCAGAAAGAG	480
GGCATCAATT CTAGCGTTT AACGGACGCC AAAAATTGAA GAGGGCTTAA AAATTAGGC	540
TTTACCGATG CCAGGATTGC CACTAAAATC AAAGAAAATG AAAATTAGA GGTCAGCCCT	600
TTTGAAGTGG AATTAGCTAG ATCTAATTAA CAAATCGCGC CCCATTTGA AGAAGTGGAC	660
ACTTGGCGGG CGGAGTTTTT ATCGCTCACG CCTTATTGT ATTCCACCTA TGCCCCCTAAC	720
CCTTGGCCCC CTATTGGAAA CAAACAGAA AAACAGAAA AGAAAATCCT AATCATAGGC	780
TCTGGGCCTA ACCGCATCGG TCAAGGCATT GAATTGATT ATTGTTGCGT GCATGCGAGC	840
TTTGTTTAA AAGATTGAA CATTAAAGC GTCATGCTCA ATTGCAATCC AGAAACCGTA	900
AGCACCGATT ATGATACTAG TGATACGCTC TATTGAAAC CCATACATTG TGAATGTGTG	960
AAGACTATCA TTCAAAGGGA GCGAGTGGAT GGCATTATCG TGCATTTGG GGGACAAACC	1020
CCTTAAAC TCGCTAAAGA TTTAGCCAAA ATGCAAGCCC CCATTATTGG CACGCCCTTT	1080
AAGGTGATTG ATATTGAGA AGACAGAGAA AAATTCCCT CTTTT	1125

## (2) INFORMATION FOR SEQ ID NO:1096:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 456 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...456

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096

CGTCCAGTCA TTAGCGCCAA AGAAGGGAGC GATCCAAGCT CTCTAGCTTA CAACACCATA	60
GAAAGCGCGA TCGCTAAAAA TATAGATGAA GTTTTTATAG ACACCGCCGG GAGGTTGCAC	120
AACCAGACCA ACCTCAAAA CGAGCTTTCT AAAATCGCGC ACACCTGCTC TAAAGTTTTA	180
AAAGACGCC CCTTTTACAA ATTCCCTTATT TTAGACGGCA CGCAAGGGAG TTCTGGGCTA	240
ACGCGAAGCGA AGATTTTCCA TGAGACTTGT GCGCTAGATG GCGTGATTAT GACTAAGCTT	300
GATGGCACTT CTAAGGGCGG AGCGATTTA ACCGTGCTGT ATGAGTTGAA ATTACCCATT	360
CTTTATTTAG GAATGGGCGA AAAAGAACAC GATTTGATCG CTTTGATGA AGAACGCTTT	420
ATAGAAGATT TGGTTGATGC GGTGTTGTG GAACAA	456

## (2) INFORMATION FOR SEQ ID NO:1097:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 693 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic).

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...693

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097

AATTTAACCA TTATAACCAT TAAAACGATT TTTAGAGATT TTTGTAAGA ACGCTTGAAA	60
AGGGCTAAAT CAAAAAAATAA AGTCAGGGAT AAATTGGCTT GCAAGCTTTT GTTTGGAAA	120
CTCAAAGATT ATCAAAATAT TTTATTGTAT AGCCCATTAG GGATGAGCT TGACATTAGG	180
CCTTTGATTGTT TGAAGTTAAG ACAAAAAAT AAGCGCGTGT GGTTGCCTAA AAGCATCAA	240
AAAGGGCTCT ATTITCTAA AGAGGGTTT ACTATCGCGC CCTTTAGGTT CCCATTAAGG	300
CGTTTGGGT GGTTTGTGA GCCGAGTTG TCGCGCTATT ATAAGCGGA ATTGGATTGT	360
ATTGTCGTGC CGATTTAGG AATGGATACA AGCTTTAGGC GCGTGGCTTT TGGGCTAGGC	420
ATGTATGATA GGAGTTTACC CCAATTATTC AAAAAGCAAC TAAAACGCC CTTAGTCATA	480
TTTGTAAAGTA GGGAGTTAGC GCTGGCTAAT GGTATTCTTA CAGACGCCA TGACATTGAA	540
GCAAATCTT ACATGAATGC TCGTATCGTT ATGAAGAATA ATAAAAGGAA ACATTATGAG	600
CAGCGGGTTA ATTACATTT CATTAGAAGT CTTGGTAGCG TGTGATCA CCGCTCTAAT	660
CATGTATTAT GTGATGAAAA AGATCTATTA CGC	693

## (2) INFORMATION FOR SEQ ID NO:1098:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 600 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

800

(A) ORGANISM: *Helicobacter pylori*

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...600

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098

AGAATAATAA	AAGGAAACAT	TATGAGCAGC	GGGTTAATT	ACATTTCATT	AGAAAGTCTTG	60
GTAGCGTGT	TGATCACCGC	TCTAATCATG	TATTATGTGA	TGAAAAAGAT	CTATTACGCT	120
AGAGGGCAAG	CCATTTAAA	AGGCCTTCA	GCCAAAGCTA	AATTAATGGA	ATTTCAAGCG	180
AAATCTTCG	TGGAAGCTGA	AGAAATGCGC	ATGAAAAGCC	AGGAATGCAA	GTTGCAACAG	240
CAATATGAAA	ATAAGAATT	GCAACTCCAA	ACCCATTG	ATAAAAAGA	AGCGCATTG	300
AAGCATTAG	AAGCGCAGCA	CAAAGAATT	GTAAGAGATG	AAAAACGCTA	TTTGGAAAAG	360
GAAAAAAAAG	AGCTTGAAAA	AGAACGCCA	ATTTTAAAC	AAGAGAGGGA	AAATTTAAA	420
AAACAGCGC	CCATTGTA	AGAAGCTCA	GCCAAAGCGC	TAGATGCGAT	GCTCAATTAC	480
ATGGCTTATA	CCAAAGATGA	AATTAAAGC	ATGATCTTAG	ACCAATTAGA	ACAGGAACTA	540
GAAGCGCAA	AGAGCGCCTT	GATCAGGGT	TATGAAGAAG	AAGCCTTAT	TATGTGTTA	600

## (2) INFORMATION FOR SEQ ID NO:1099:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1050 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1050

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099

ATAAGGTCA	CAAATGACAC	CCAAACCACC	CAAACACCAT	GGCACTCAA	CACCAGACGG	60
CCAAAACCCA	CCCCTAAACC	CATTAAAAAA	GAGGCTAAAA	AGGCTAAAGA	GAAAACAAC	120
AAGCATGCGC	ATTCAAAGCA	TGCGCACTCT	CCATTGAACG	AAAGGAGCGC	TAAAAAAGAA	180
ATTCCCTAAA	AAGAAATCCC	TAAAAAAGAA	ATCCCTAAA	AAGAAATCCC	TAAAAAAGAA	240
ATCCCCTAAA	AAGAAATCCC	TAAAAAAGAA	ATCCCTAAA	AAGAAATCCC	TAAAAAAGAA	300
GCAGAAAATG	AGAGTAAGAA	CCAAATCTT	ATAGCAGAAA	AAAATGATAC	TTGGATCAA	360
ACCAAGCGCA	AAAACACAA	AAAGATCGTT	TTGCACGCTG	GGCATGGGG	CAAAGATTGC	420
GGGGCGATGA	CCCGAATT	GGTGTGTGAA	AAGGACATTG	TTTAAAGT	GGTGAAGTT	480
TTGCATAAAG	AGCTTAAAAA	AAGAGGCTAT	AGCCTTTAT	TGACAAGGGA	TAAGGACATT	540
TACATTGATT	TAGTGGCCCG	AACGGAATT	GCAATAAAA	AAGGGGCGGA	TTTATTTCATC	600
TCAGTGCATG	CCAATTCCAT	CCCTAAACGC	TCCACCTCTA	ACGCCATGG	CATAGAGACT	660
TATTTTTTAT	CCACCGCAAG	GAGTGAAGG	GCTAGGAAAG	TGGCTGACCA	AGAAAATAAA	720
GACGATGTGA	ATTTAATGGA	CTATTTTCT	AAAAGTTGT	TTTAAATTC	ATTGAACACG	780
CAGCGATTGA	TGGTCTCCAA	CAAATAGCG	ATTGACGTG	AAATACGGCAT	GCTCCAAGT	840
GTCCGAAAA	ATTACCCCTGA	TGTGGTGGAT	GGGGCTGTTA	GGGAGGGGGC	TTTTTGGGTG	900
TTAGCCGGGG	CTTAAATGCC	TTCAATT	ATAGAAATTG	GTATAATT	CCATGCGATA	960
GAATCTAAC	GCATCCAAAG	CAAACCGTAT	CAAAATCT	TGGCTAAGGG	CATTGCTGAT	1020
GGCATTGATA	TTTCTTCAG	CAAGAATGAT				1050

## (2) INFORMATION FOR SEQ ID NO:1100:

**SUBSTITUTE SHEET (RULE 26)**

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100

AGAGTATCTA TGAATGTC	AA	558
GATTGTTGG AGAAACTTGG	AA	60
AGCATTGGTC AATTAGCGAT	CC	120
GGTGGGGTGA TGAGTAAAC	CC	180
TTAGCCGTC AAAGCGTAT	TT	240
GAGATGTATC AAAATCAATT	TA	300
TTCTTTATG AAAGTTTG	TT	360
GCTATAGCAG TCAATAACAA	TT	420
AAGCAAGAGT GCTGGGAATT	TT	480
CGTGGAAAAA CAGAAATT	TT	540
	TT	558

## (2) INFORMATION FOR SEQ ID NO:1101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1086 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101

AAGAGGGATC AAATGGCCGA	AGAAGAAAAG ACCGAACTCC	CTAGCGCGAA	558
AAAGCCAGAG AAGAAGCAA	TGTGCCTAAA ACCATGGAAG	TGGGGGGTT	60
TTGGCTGGC TAATGAGTAT	TTTTGTTTTT	TTTAGGGTTA	120
ATGTATCGCC ATGTGTTGAA	AGATTTCTCC	CTAGATTTA	180
CTGTTAACCC AGCTGGCTAA	AGACACCTTT	GCAAAGAAAG	240
ATGGTGGTGG CGTTTGTGTC	TAATGTCCTC	CGTTCAAGAG	300
ATTGAGGCCA AATTTCCTAA	CAATTGGCT	TGCCTGTTT	360
AAAAAGATCC TTGATGGGAG	ATCAACCCT	AATCATTITA	420
TTTTCATCT TTTCTTATT	TTAAAGTTT	GGCTCTTGC	480
TTAGGGAA TAAACCATG	TTTACGCTT	CCCTAAAGTC	540
	CGGCTCTTT	TTTTCTGGGG	
	GAATTGCAA		

802

GGCCAGTTGT TGTGGTTAA AAGCAAGCG TTATGGCTCA TTTCTTCGCT TTTATTTTTA	600
TTTTTGTCT TGGCTTTGT GGATTTAATC ATCAAACGCC GCCAATACAC TAACTCTTTA	660
AAAATGACTA ACAACAAGT TAAGGACGAA TACAAACAGC AAGAAGGAAA CCCAGAAATC	720
AAAGCCAAAA TCCGCCAGAT GATGGTAAAA AACGCCACGA ATAAAATGAT GCAAGAAATC	780
CCCAAATCCA ATGTCGTGGT GACTAACCT ACCCATTATG CCGTCGCTCT CAAATTTGAT	840
GAAGAACACC CTGTGCCTGT GGTAGTGCGT AAAGGCACGG ATTATTTAGC CATTAGGATT	900
AAGGGTATCG CCAGAGACCA TGACATAGAA ATTATAGAAA ATAAAACGCT CGCTAGAGAG	960
CTTATAGAG ACGTGAAATT GAACGCCACC ATACCAAGAAG AATTGTTGA AGCGGTAGCG	1020
ATTGTCCTCG CTCAAGTGGC TAAATTAGAG CAAGAACGCC AAAAACAAAA GATCATTAAA	1080
CCTCTT	1086

## (2) INFORMATION FOR SEQ ID NO:1102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...543

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102

GAAAATACTA TGCAAGATT ACAACATTTCA AAAAATGATA TTACGCTCAT TCTGTCTAAA	60
GACAGATTAG ATACTTATGA CAGCCTAGAG CAATACAAAG AAAATTTAAA ACTCATTTCT	120
TTCATCACGC CTAAAATCTC TAACCTAGAG ATTTATTTAC GCAACGCTTT AGACTATTGC	180
TTAACCCAAA TTAAGGGGAG CGAATGGGTG TTTAATGAAA ATTCTTTAAC AGATTTAATT	240
AACGAACAAA AAGAAAAGAA AAAAGAAATC ACACATTCTT TAATCTTATC TAAAATGCT	300
TTAGGGGAG TGGTTAGGCT TATTTTTGT TATAAGTTAG AGGGGGTAAT ATTAGATTG	360
AGAGCGTATC GTTGAGAGC TTATTATCAC GAAAATAAG ATACCTTGCT TATTAAGGC	420
AAAAAACGCC TTCTTTACAA TTATATTAAG GCCCATATTG CTTAAACTT GCTATGGACA	480
ATTAGAAATC GCACGTATCA TTGGGAAAT TTACTCAAA TCCAACCGAA CAACCGCCCCA	540
CAA	543

## (2) INFORMATION FOR SEQ ID NO:1103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

**SUBSTITUTE SHEET (RULE 26)**

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- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...567

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103

GCTAATGGAT GCGAAAAAAAG GATTTTCATG CTGCTTGCCTGCG CGGGAAAGGAA TGAGACTTTA	60
AAAAAAAGCGG TGCCATTGAG TGTGGGCTTG ATAGAGAGCG CGATCAATTG AACGAGAAATG	120
TGGCTTAAAC ACCCTGATAC AGAAAGCCTT ATTTCATAGG GGAGCGCGGG GAGTTATAGC	180
CCAGAAACGG AGATTTTGAG CGTGTGAA ACCATGAAAG GCTATCAAAT TGAAGAGAGT	240
TTTAGCCATT TAAACAGCTA CACGCCCTTG GATAATTCA TTCACATAGA AACTAAAGAG	300
CAGGCTCTTT TTGAAAGGGT GCGTGTGAAT AGCAGTAAC ACATCCACAC CAGCGAAATG	360
TTTGTAAAAA AAATGGTTCA AAAGGGCGTT TTATTAGAAA ACATGGAGTT TTTTACGCTC	420
TTAACGCTGG CTTAAATTTT TTCTTTAAAG GCTAAAGGGA TTTTTTGCGT GAGCAATCAT	480
GTAGGGCTTA ACACGCATAA GGAATTTAAA GAAAACCACG CCAAAGTCAA ACAGATTCTA	540
GAAAACATCA TTGATAGTTT GATAGTTT	567

## (2) INFORMATION FOR SEQ ID NO:1104:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1018 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1018

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104

TTTTAATGAG TTTTATAAGC TTGCAATCGC CTCTTGGCAA GAACCCCTAA GAGTGAGTAT	60
AGAATTTGTG GATTTGCCTA AAAAATCAT CGTTCCTCCG GCCCATGATT TGAAAGTGGG	120
GGAGTTTGGT TTGTTGGTTA CTCACTTTC AGATTATGAA ATCGTTAATT CTGAAGTGGT	180
CATTATTGCT GTTGAAATG GCGTCGCAAC GGCTAAATTG AAAGCGTTG AGTCGATGAA	240
ACAAGCCAT TTACCCACTC CAAGAATGGT CGCTAAAAAA GGGGATTTAG TCTATTCAG	300
GCAATTAAAC AACCAAGCGT TTTTGATCGC TCCTAATGAT GAATCTATG AGCAAATCAG	360
AGCGACTAAC ACCGATATTA ATTTCAATTAG CTCTGATTTG TTGGTTACTT TTTGAATGG	420
GTGGACCCA AAAATCGCTA ATTTAAGGAA AGCGTGAAT GTTTATAGCG TGGGGGTGAT	480
TTATATTGTA ACCACCAACA CGCTCAATAT TTTAAGTTGT GAGAGTTTG AAATTAGA	540
AAAAGAGAG CTGGATACAA GCGGCGTTAC TAAAACCTCC ACCGCCGTTT TTTCTAGGGT	600
TGAGGGCATT GATGCAGGCA CGCTAGGGAA ACTTTTTCA GGCAGTCAAT CTAAAATTA	660
CTTCGCTTAC TATGACGCTT TAGTGAAGAA AGAAAAACGA AAAGAACTAA GGATTGAAA	720
GAAAGAAGAA AGGATTGATG CTAGAGAAAA TAAACGAGAA ATCAAGCAAG AAGCCATTAA	780
AGAGCCTAA AAAGCCAATC AAGGCACAGA AAACGCTCCC ACTTTAGAAG AGAAAAACTA	840
CCAAAAGCA GAGCAGGAAAT TTGACGCTAA AGAAGAAAGG CGTCGTTCAA GAGATGAAAG	900
GAAAAAAACT AAAGCCACCA AAAAGCTAT GGAATTGAA CAAAGAGCGA GAGAACATCA	960
AGAAAGAGAT GAAAAAGAGC TTGAAGAAAG AAGAAAGCT TTAGAAATGA ATAAGAAG	1018

## (2) INFORMATION FOR SEQ ID NO:1105:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 852 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

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(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105

GGAGAAACAA CAATGAAACT GAGAGCAAGT GTTTTAATCG GTGTGGCAAT TCTGTGCTTA	60
ATTTTAACGTG CGTGCAGTAA CTATGCGAAA AAAGTGGTGA AACAAAAGAA CCATGTTTAT	120
ACGGCCTGTGT ATAATGAACG GATAGAGAAG TATAGTGAGA TCCCCTTAA TGACAAACTC	180
AAAGACACAC CATTCCATGGT GCAAGTGAAG TTGCCAAATT ACAAGGACTA TTTGTTGGAT	240
AATAAAACAAG TTGTACTAAC TTTCAAACCTT GTTCAACCATT CTAAAAAGAT TACGCTCATA	300
GGCGATGCCA ATAAGATCCT CCAATACAAG AATTACTTCC AAGCTAACGG GGCAAGATCT	360
GACATTGATT TTTACTTGCA ACCACATTG AATCAAAAGG GTGTGGGTGAT GATAGCCAGT	420
AACTACAATG ATAATCCCAA CAACAAAGAA AAACACAGA CCTTGTGATGT GTTGCAAGGA	480
AGTCAGCCAA TGCTAGGAGC TAACACAAAA AACTTGATCG GCTATGATGT GAGTGGAGCA	540
AACAAACAAGC AAGTGTCA TGAAGTGGCA AGAGAAAAAG CTCAGCTAGA AAAATCAAT	600
CAGTATTACA AGACTCTCTT GCAAGACAAG GAACAAGAAT ATACCACTAG GAAAATAAC	660
CAACGAGAAA TTTTAGAAAC ATTGAGTAAT CGTGAGGTT ATCAAATGAG GCAGAAATGTG	720
ATTAGTTCTG AGATTTTTAA GAATGGCAAC TTGAAACATGC AAGCCAAAGA AGAAGAAGTT	780
AGGGAGAAGC TACAAGAAGA AAGAGAGAAT GAATACTTGC GCAATCAAAT CAGAAAGTTG	840
CTCAGTGGTA AG	852

(2) INFORMATION FOR SEQ ID NO:1106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106

AGTTTATTGTC AAATGAAAAC ACTCGTAAAA AATACCATAT ATTCTTTTTT GCTATTGTCT	60
GTTTTGATGG CAGAAGATAT AAACAAGGGC TAAAGCAAC TGGATAACAC CTACCAAGAG	120
ACCAACCAAC AAGTGCTCAA AAACCTAGAT GAGATTTTTT CAACCACTAG CCCTAGCGCT	180
AATAATAAAA TAGGTCAAGA AGATGCTCTA AACATCAAA AGCGGGCCAT TGCTTTGAGA	240
GGAGATTTAG CGTTATTGAA AGCCAATTG GAAGCGGAATG AGTTATTTT CATCTCAGAA	300
GATGTGATTG TTAAGACTTA TATGCTAGC CCTGAACCTT TATTAACCTA TATGAAAATC	360
AATCCCTTAG ACCAAAAGAC TGCTGAGCAA CAATGCGGAA TATCCGATAA AGTTTAGTT	420
CTTTATTGTG AGGGGAAGCT GAAAATCGAG CAAGAAAAAC AAAATATAAG AGAGCGTTA	480

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GAAACTTCTC TAAAGGCATA TCAGAGCAAC ATTGGAGGTA CAGCTTCCTT AATCACTGCT	540
TCACAGACGC TTGTAGAAAAG CCTAAAAAAT AAAAATTCA TCAAAGGAAT CAAAAAGCTT	600
ATGTTAGCTC ACAACAAGGT CTTTTAAAT TATTTAGAGG AGTTGGACGC ATTAGAAAGA	660
TCCCTAGAAC AAAGTAAGCG ACAATACCTA CAAGAAAGGC AATCAAGTAA GATCATTTGTT	720
AAA	723

## (2) INFORMATION FOR SEQ ID NO:1107:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1617 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(iii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107

ATAAAATAAGA ACATGTTAA TATTAAGG ACTTTTTAA TAACGATCAT AAGTTTTTT	60
CTCATTGTC CTAATTGGTT GAAAGCTATT GATTTGCCA TTGTTCAAA TCTAAAATT	120
TACCAACAG TTTATTGCAT GCTGATACCG AGTTATGTT TAACCAACAA AAGTTTGCA	180
GATAATTGAG CAGGCTATAC ATCTATTGGT GCATCAGGGA GTGAAAGAG TTCAGGGCAG	240
GGTGTGATCG AACGCCTTAG CACACCTTA CCCACAAGTT TAGCCGCTAG CAATCTGGTG	300
AAATATTGAG ATACTTTAGG TCCCTTATGG GGATCAGCGT GGGCAACTG TGCTACAGCT	360
ATACAAGTT TTGCTCTAAC GCCATCAAGT GGCTGTAATT TTGCTGGAA CGCATTGATA	420
AATAAAAACA TAGATGTATC CATGGATAAGC GTACTAGACA ATTGAGCAA CAAGATTCA	480
AATTTTACCA AAGGGCGGTGT TGAGGACAAT GTGAAAGGC ATATTCTTT ACAAAATAATT	540
GGCTCAATAA CCGCTCAAGC TTCTACGAAT ATTACAGCTG ATGGTTAAT TTGGCTGATT	600
GGTAAAGAAT TCACTGCAA TAAACTGCAA AACAACACTA TAGCCATGCT TGCTTTGCC	660
GCATTAAGAT CTGTTGTCAGGAGGCCAG GCTGCTGTT TCCTGATA TGGTGTAGTC	720
AATCTGCCTG ATATTATCAT AGGGCAAGGG TCATATCTG ATTGTTGTTTC TTACCTAATT	780
TATATTGTT TTGGGATTIT TGTGTTATGA ATTGAGAGA TATTGAAAC	840
GGCATTCAAGA TTAACATAGG TTTGAATAC ATGCGATTG TTGGGGGAC ATTATTCAA	900
ATGGCGATGG TCTCTTTAT CGCCTATGCA GGTTTGGTT ATCTTATAA ATATCTTTAT	960
TCTATTATT TTGGTTTAGC AGGTGCTTTT GGGCTGAATC AAGTTCTTT TTGGGCTTTA	1020
GATTTAGTGC TGAATTACAC TGTTAATTCA ATTTCACCTG CGGTAAAGAGC TGTTTTTCT	1080
AATGTTGGCA ACAACGCTCC TAGTTTGTCA CAAGGCTTGC AAGTGGCAGG TATTTCTTTA	1140
TTCGCTATT TTATGCAAGT AACTATCATT ATGAGAATAA GCACTGTTGT TGTGAAACCT	1200
TTGATAGCGG GGGCTTTAG CCGTATTGTT TTCCCTATTG CAGTATGTTT GATCGTGCTA	1260
GATTTGGTCA AAGATTCTAT GAAAAACATA TTGATATGGT TTATTAATAA TCTGTTTATC	1320
TTGGTTCTAG CTATTCCTAT TTTGCTCTT GGTGTTTGG CATTATTGGC ATTCAATTG	1380
ACCATAACGC CCTCTGTTGC TATACAAAAC ATCAATCAAG GGGGATTGGG TATCGATTCA	1440
ACTATTGCGA GTTGATCAC TCTATTATT TTAAAGGTT TCATAGAGAC GATTATTGAG	1500
AGCGTCATG CGATCGTTAA CACCAATTTC AGCTCTGCT CTATGGATGG TAGCAGAATG	1560
GATAGAGAAA GAGATGCCCTT AATGGGGAGA AGAGTTGGTG GATCTATGTT TAAAGGA	1617

## (2) INFORMATION FOR SEQ ID NO:1108:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 768 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

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(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108

CTCCATAGAA TTATCTCCTG CGATAGCGCT TGGAGGACTA ATCTTGTGT GCGGACCAAT	60
AAAGCCTTGT ATCAATTCA TTTGAGGATA GCCCAAAAAG ACAATTTCGC TTCAGCGTAT	120
CTAACAGTCA ATTAGAATA CCCACAAAGA CACGAAGTCT CTAGCGTTAT TGAAGAGGAA	180
TTAAAAAAGA GAGAAGAACG AAAGAGGCAG AGAGAATTGA TCAAGCAAGA AAATCTAAC	240
ACCACAGCCT ACATCAATAG AGTAATGATG GCGAGCAATG AACAGATTAT CAACAAAGAA	300
AAAATAAGAG AAGAAAAAAC AAAATTATA CTAGATCAAG CAAAGGGCGCT AGAGACCAA	360
TATGTGCATA ATGCGTTAAA AAGAAACCCCT GTGCCCTAGAA ACTACAATTAA CTACCAAGCG	420
CCTGAAAAAC GCTCTAAACAA TATTATGCC TCTGAAATT TTGATGATGG CACATTCACT	480
TATTTGGTT TCAAAACAT CACTCTCCAA CCTGCTATT TTGATGGTCA ACCTGATGGG	540
AAATTGAGCA TGACTGATGC CGCCATTGAT CCTAACATGAA CTAATTCAAGG ATTGAGATGG	600
TATAGAGTTA ATGAAATTGC AGAGAAGTTT AAGCTCAITTA AAGACAAAGC CCTTGTAACA	660
GTGATCAATA AAGGCTATGG GAAAAATCCA TTGACAAAAA ATTACAATAT CAAAAACTAT	720
GGTGAATTGG AGCGTGTGAT TAAAAAGCTC CCTCTTGTCA GAGATAAA	768

(2) INFORMATION FOR SEQ ID NO:1109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109

ACTAGTTCTT TCAAAACCAA AATGAAACGA CCGATCAGCA AATTGAAACA AAACCTTTTA	60
CAATTCAAAC ATTCTTTCAA CAAACATTAA GATAAGTACA GCCTTTATTA TAGGCTGTTTC	120
AATATCAGCT CTATCGTTAT AGGTTTTTA ATAGCGCTTT TTCTTATGG GGCAGGGGTG	180
ATTTTAGTTT ATCCAATATT ATTCTTGTGT GCTCTTATAA TAAAACCTAG CTTTTTTTAT	240
TACACTACTT ATCTTTTGCT ACTCGTTCT CTCAGCATAA TAAGCAAATA CTATCTCTA	300
AGCCACGCAA ATTTCACAAT GAAGCTAACG ATGCTTATGA CTCAATGGCA AAATTGGTTC	360
TTA	363

(2) INFORMATION FOR SEQ ID NO:1110:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 393 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...393
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110

GTATGCTATT	GTA	AAATGCT	TCC	TACTAAA	ACACGCCATTA	GAGATCCGAA	CAAGCAAGAA	60
CTTACACAAC	CAA	AAATAAA	AGG	ATTGAGT	ATGGGAAAAA	TTTAGCTTC	TTGTTGGGT	120
GGCGGAACAA	ATC	TTTTTAC	AGG	TTTATCC	AGTGATTGT	TTCTATGAT	ATTAATTTT	180
TTGTTCTTCC	TGATGTTAAT	GATGGGACTT	AATGAACCAT	TAGGGAAAAA	ATTTAACTTG	240		
CCTATGGACA	ATATCAAGAA	TTTATGGCA	GAAGTCCTGA	AGAATGGATT	CGATAGTATC	300		
AAAACATGG	GATCTGCTTT	GGTTGGTAAT	GGTTGGTA	GCAGCAAATC	AGACAAAACC	360		
ACTAATAAA	TGAGTGTCCC	ACAAGTAAGA	CTC			393		

## (2) INFORMATION FOR SEQ ID NO:1111:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 891 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...891
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111

GAGGAATTGT	TGATGGGCA	GGCATTTTTT	AAAAAAATTG	TTGGCTGTTT	CTGTCTTGGT	60
TATTTATTTT	TATCTAGCGC	AATAGAAGCA	GTAGCACTTG	ACATTAAGAA	TTTAATCGT	120
GGTAGGGTGA	AAGTGGTGAA	TAAGAAGATT	GCTTATTG	GAGATGAAAA	ACCTATTACG	180
ATTTGGACTT	CATTAGACAA	TGTTACCGTG	ATCCAACCTG	AAAAAGATGA	AACTATTCT	240
TACATCACAA	CAGGTTCAA	TAAAGGTG	AGTATTGTG	CTAATTCTAA	TCATATATT	300
ATTCACCTA	AATCGTAAA	AAGTAATCTC	ATGTTGAAA	AAGAACAGT	GAATTTGCC	360
CTAATGACAA	GAGATTACCA	AGAATTTTA	AAGACAAAAA	AACTTATCGT	AGATGCGCCT	420
GACCTAAAG	AATTAGAAGA	ACAAAAAAA	GCTCTAGAAA	AAGAAAAAGA	AGCTAAAGAA	480
CAGGCCAAA	AGGCACAAAA	AGATAAAAAGA	AAAAAAAGAA	AGGAGGAGCG	TGCAAAAAT	540
AGAGCCAATT	TAGAAAATCT	CACTAACGCT	ATGAGTAACC	CACAAAATT	GAGCAATAAC	600
AAAAATCTTA	CGAATTGAT	CAAGCAACAG	AGAGAAAATG	AATTAGACCA	AATGGAACGA	660

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CTAGAGGACA TGCAAGAGCA GGCTCAAGCT AACGCACTCA AACAAATTGA AGAGCTAAC	720
AAGAACAAAG CTGAAGAGGC AGTTAGGCCA AGAGCCAAGG ATAAAATCAG TATTAAGACA	780
GATAAAATCTC AAAAAAGCCC CGAGGATAAC TCCATAGAAT TATCTCCTGC GATAGCGCTT	840
GGAGGACTAA TCTTGTTGTG CGGACCAATA AAGCCTTGTA TCAATTCAATT	891

## (2) INFORMATION FOR SEQ ID NO:1112:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 765 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...765

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112

AGCTGTCGCA TGTTAGGGAA AAAAAACGAA GAAGTCTTGA TTGATGAAAA TTTGGTTGGG	60
GGTGTGATAG CCCTTGATAG ATTGGCAAAA CTCATAAAGG CCAATAGGAC TTTCAAAGG	120
GCTTTTATC TCTCTATGGT GCTCAATGTC GCCGCTGTAA CGAGTATTGT GATGATGATG	180
CCTTGAAGA AAACAGATAT ATTGTTTAT GGCATTGATC GATACACAGG AGAATTAAA	240
ATCGTAAAC GCTCCGATGC TAGGCAAATC GTCAATTCTG AAGCCGTTGT GGATAGTGCA	300
ACTTCAAAAT TTGTCTCATT GCTGTTTGGT TATAGCAAAA ATTCTTTGAG GGATCGAAG	360
GATCAACTAA TGCAGTATTG CGATGTGACT TTCCAAACCC AAGCAATGAG AATGTTCAAT	420
GAAAATATCA GACAATTCTG AGATAAAGTC CGAGCAGAAG CTATCATTAG CTCCAACATA	480
CAAAGAGAAA AAGTCAAAAA TAGTCCCTTA ACGAGATTAA CATTTTTCAT TACCATCAAA	540
ATCACGCCCTG ATACAATGGA AAATTATGAA TATATCACTA AAAAACAAGT AACTATTAT	600
TATGATTTTC CTAGAGGTAA CTCTTCTCAA GAAAATCTTA TCATCAACCC TTTGGCTTC	660
AAAGTGTTC ACATTCAAT CACGGATTAA CAAAACGAAC AGACAGTAAG CGAAATTTC	720
AGAAAGATTA AAGAAGTGGG ATCAAAAAAT AAGGCATTAA ATAAA	765

## (2) INFORMATION FOR SEQ ID NO:1113:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 750 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...750

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113

AAGCGCCTAA TTCAAAGAGA TGAGACAATC GCAACTCAGA GAGAGAATGG TATAATATCA	60
AAACAAATTTC TCAATTAAAT TCTTGAAAGG AGTTTCTGTA ACGATACAAC AGAGCACCAT	120
GGATCCAATC CGCTAACGC CCCACCACCT AGCAACTCAC AGAGCAACGA TCTCTTAAAT	180
TTGCTAGACT CGTTATATCC TAAAGGGAGT TTAGGGAAAC AAAGATTTCA CGAAGCTTTA	240
AAGAATCAAG AAGAGTTGAA AAATATCCTA ATAGAAATAG AAAAGCTACC GCAAGAAAAA	300
AGGTATGAAC TTCTGATGCA GATAGGACAA GCCAAACAGA GAATAATGGG AGCATACGCT	360
CATTCAATTCT TAGGATATAT AGGGGGACTA GAGCATCTGT TAGGATTGTC TATGGGTGGG	420
ATATTTGTTT TGTTGCAAT CTATTTGTA TTTTTAGAA CTAGCAAAAA CACAGAGCTA	480
GTGGAAAGTC TAAAAACAAA ATTAAAACCTT CAGTATTTTT ACTATGCCCT TGCTGTGGGT	540
GCGGTTTTGT TTTTGGATT AGAAACAATT AGATCGATTT ATGAACTATA TATCTTAGGA	600
ATTGGTACCA CTAACGACAA GGTGCTCTT GTTTGAAAA ACATTTGCTT CATAGGTATG	660
GGCTATTGTA TTATAAAGT TATTAAGTT ATTGGTATAA AAAATTTTAT CAATGGTCTT	720
TTCGCTTCAA AGAAACAAGG CGGTGCAGAA	750

## (2) INFORMATION FOR SEQ ID NO:1114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1146

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114

GGTTACAAAA ACTATAAGAT GCTTGCAGAA ATCGTTTTA GCTCATTGGT TGCGTTTGGA	60
GTTTTGTGG CTAATGTGGA GCAGTTGGT TCATTTTCA ACGAGATAAA AAAAGAACAA	120
GAAGAAGTGG CCCAAAAAGA AGACGCTCTT AAAGCTCGA AGAAGCTCTT AAACAATACG	180
CATGATTCT TAGAAGACTT GGTTTTAGA AAACAAAAA TCAAAGAGCT TGTGGATTAC	240
AGAGCTAACG TTCTTTAGA TTAGAAAAAC AAGTACAAAAA AAGAAAAAGA GGCTCTAGAG	300
AAAGAGACAA GAGGTAAAG CCTTACTGCT AAGTCAGG CTTATGGTGA TCTAGAGCAA	360
GCCTTAAAG ATAACCTCTT TTATAAGAAA CTTCTTCTTA ACCCTTATGC TTATGTTTA	420
AACCAAGAAA CATTACGCA AGAAGATAAG GAGCGTTGAG GTTATTACTA CCCCCAAGTG	480
AAAAGAGCA GTATTTTAA AAAACTACC GCTACCACTA AAGATAAGGC TCAGGCTTIG	540
CTTCAAATGG GTGTTTTTC TTAGATGAA GAGCAAAACA AAAAGCGAG CCGATTAGCT	600
TTATCTTACA AGCAAGCGAT TGAAGAATAT TCCAATAACA TTTCTAATTT ATTGAGCAGA	660
AAAGAATTGG ATAATATAGA TTATTACTG CAGCTTGAAA GAAACAAATT TGACTCCAAA	720
GCAAAAGATA TTGCTAAAA AGCCACCAAC ACGCTTATT TTAACTCGGA ACCCTTGGCG	780
TTTAGCATGG CGATTGATAA GATCAATGAG AAATCTAA GGGCTATGAG AGCTTTTCT	840
AACTTGTGAA AAAATGTCAA AGATGATGTG GAGTTGATAA CTTTACTAA AACCTTCACC	900
AATCAAAAT TGAGTTGCG ACACAAACAA AAATTGTGTT TGTGTTTT AGACAGCTTC	960
AATTGATA CCCAATCCAA AAAATCTATA TTAAAAAGA CTAATGAATA CAATATCTTC	1020
GTAGATAGCG ATCTTATGAT GAGGCACAAA ACAACTATGC AAAAGAACAA CTACAAGATA	1080
TTTAAATTCT TCAAAACAGT GGTTTCTGCA TACCGGAAACA ATGTTGCCAA GAATAACCCC	1140
TTTGAA	1146

## (2) INFORMATION FOR SEQ ID NO:1115:

## (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 927 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115

AAATTTAGTG AAGTATATTT TATAATGAAA ACTAAGGCAG GCTTTGTAGC TCTTATAGGC	60
AAACCAAACG CTGGAAAAAG CACTCTTITA AACACTTTAT TAAACGCTCA TTTAGCCCTT	120
GTTTCGCATA AGGCTTAATGC GACTAGAAAA TTIGATGAAAT GCATCGTGCC TTTTAAAGAC	180
AAAGAAGGGT ATGAGAGCCA AATCATTTTT TTAGACACTC CAGGGCTCCA TCATCAAGAA	240
AAATTACTCA ACCAGTGCAT CCTCTCACAG GCTTAAAAG CGATGGGCAG TGCTGAATTG	300
CGCGTTTTTG TGGCTTCTGT GCATGATGAT TTGAAAGGGT ATGAAGAGTT TTTGAGTTTG	360
TGCCAAAAAC CCCATATCTT GGCTTGAGT AAGATTGACA CAGCCACGCA TAAGCAGGTT	420
TTACAAAAAT TACAAGAGTA TCAAAATAT TCATCGCAAT TTTAGCTCT AGTGCCTTTG	480
AGTGCAGAAA AATCTCAAA TTTAAACCGG CTTTAAAGAT GCATCAGTAA GCATTTAACG	540
CCTAGCGCAT GGCTTTTTGA AAAGGATTG ATGAGCGATG AAAAATGCG CGATATTAT	600
AAGGAAATCA TTAGGGAGAG TTTGTTGAT TTTTGAGCG ATGAAATCCC TTATGAAAGC	660
GATGTGATGA TTGATAAAATT TATAGAAGAA GAACGCATAG ACAAGGTGTA TGCGGCCATT	720
ATCGTAGAAA AAGAAAGCCA AAAAAAAATC GTGATAGGTA AAAACGGGGT GAATATCAA	780
CGCATCGGGA CTAACGCGCG ATTGAAAATG CAAGAAGTGG CGGAAAAAAA GGTTTTTTTA	840
AACTGCAAG TGATCGCTCA AAAATCATGG AGTAAGGAAG AAAAAAGCTT GCAAAACTA	900
GGCTATATCT ATCAAAGGAA TAGGGAT	927

(2) INFORMATION FOR SEQ ID NO:1116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1176 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116

TTCTGTCTC TAAGTCTCAT AGAAAGGGAC TTGAAAACTA TGGCAAAGAT ATTAAAACCT	60
AATTAGATA GAGATGAGTT AACACACCT TATAAGGCAA ATCTTGCTTA TGCTAAAAC	120
ACGCATGAGC ATTATTTCAA ATTTAAAAAA GATGTAGACT ACAAAACTCTT TAATCCTAGC	180
ATTATGCATG AGCAATGTT TATAAGCTTT GTAGCGGAC AAGGAGCTAA AAGATTATTA	240

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TACATACTCT ACAAGCTCGC	ATTTAATGCT AAGTCTAATA	AGATTGCCCT AGATAGACAT	300
TACGCCAAA TGTTTTGCA	AGTTGTAGCA AGAACTCTAA	TAAGAATGT CAATATATTA	360
GAAGAGCAAG GTTTTATTGA	AGTCATTAAC CGAAAACAAA	GATACTTGTG TGTGTATCTT	420
AAAGATTACA GAGAATTAGA	ATGCTTAGTG AAGAGCAAGA	TGGCTAAGTA TGTGATGTAT	480
TTAAGACAAT TCCTTGATTA	TTTGGATAGA AAAAGGCCTT	ATGGCTTGTG TTTTACGCTT	540
AAAAACCTAG CCTTGCTAA	GACCAAAGAA AGCTTACCCA	GACATTTAAA CGATAAAGAC	600
TTAAGAGTT TTAAACAAAC	ACTCTTAGAC TATAAGCCAG	CTACAAGCTT TGAAAACGC	660
AATAAGTGA TTCTACTTAT	TGTAATACTT GGGGACTTA	GAAAATGCGA AGTGTAAAC	720
ATAGAATTAA AACACATTCA	AGTAGAAGAG CAAACTACT	CTATTTAAAT TCAAGGTAAA	780
GGTAGAAAAG AGAGAAAAGC	TTATATTAAA AAGAGTTGTG	TAGAACCAAG CTTGAATGCT	840
TGGATTAGTG ATGATTACAG	ACTAAAATAT TTCAATGGAG	CATACTCTT TAAAAGGAT	900
AACCAAAAT CACAAAATTC	TTTAACGCTT TATAATTITA	TCCCCTTAAT CTITAAATTA	960
GCCCAATCA AACATTACAA	ACAATATGGC ACAGGCTTAC	ATCTATTTAG GCATAGTTT	1020
GCAACACTCA TTATCAAGA	AACCCAAGAC TTAGTTTAA	CTTCAGGGC GTTAGGGCAT	1080
AGCTCCTTAC TCTCTACTAA	GATTTATATT CATACCACAC	AAGAGCATAAA CAAGAAAGTG	1140
GCTCTGTGT TTGATAGTTT	GATAGAGAAC AAGAAC		1176

## (2) INFORMATION FOR SEQ ID NO:1117:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117

AAAAGAAAGG AACATTGCAT	GAAAAATTAA AGGCATTTA	GAAAGCTTAT CGCCTTTTA	60
GGTTTTTCAC CTCTTTTATT	ACAAGCGGAT ATGACTACCT	TTTTAATTC CATTGAACAA	120
CAGCTCACTA GCCCTACGGC	TAAAGGCATT TTAATGGTTA	TTTTTTAGG ACTTGCTATT	180
TTTATATGGA AAAACTTAA	TAGATGGAAA GAAATTAA	TGACCGTGCT TGCTTTAAAA	240
GAAGTCCCCA TGCAATTAGT	TGCTATTCA GTTTCTAAC	TCAAAGAAAT CAGCTCCAAA	300
AAAAAATTTC TTGGCTCAA	TGCTAAAGAGT	TTTTTACTCT CAGGATTGTG GCCTTTATT	360
ATGATACCTT GGCTAGATAT	TTTGAACCT	TTTGTGCTT ATGTGTGCTT TCTCTTAATT	420
TTTACCATAG CGGAGTTCTT	TGATGAAGAT	ATAAGTGACA TTTAATCGC TCATTCCAAA	480
ATTAAAACCA AAGCTAATT	CTTACGCT		510

## (2) INFORMATION FOR SEQ ID NO:1118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118

AAGCTCTCGCA	ACTTTAGCTA	TAATCAAACA	GAAAAAAATT	GGGAAAACCA	CTTTAACTTA	60
TTTTCAGTAG	GAATAGGCAT	GGCAGAAAGA	CAAGAAAATA	CCCGCGAACCA	ACCCCCAAAAA	120
AAAAGCAAAG	CCCTTTTATT	TGTCATTATT	GGAAAGCGTGC	TAGTGATGCT	TTTATTGGTG	180
GGGGTGATTA	TCATGCTGCT	TATGGGGAAT	AAGGAAGAAT	CTAAAGAAAA	CGCTTCTAAA	240
AACACCCAAG	AAAGTCCAAGC	TAATCCTATG	GCGAACAAAGA	ATCAAGAACG	CAAAGAAGGC	300
TCTAATATCC	AGCAATATTT	GGTGCTTGGG	CCTTTGTATG	CGATTGATGC	GCCTTTGCG	360
GTGAATTG	TCTCTCAAAA	TGCCAGACGC	TACCTTAAGG	CTTCTATTTC	GCTAGAATTG	420
ACCAATGAAA	AGGCTTGAA	TGAAGTCAAG	GTAAAGACA	CGGCGATTAA	GGACACGATT	480
ATAGAAATTTC	TATCGTCTAA	AAGCGTGGAA	GAAGTGGTTA	CTAACAAAGG	CAAAAACAAG	540
CITAAAGATG	AAATTAAGAG	CCATTGAAAT	TCGTTTTGA	TTGATGGCTT	TATTAAAAAT	600
GTCTTTTCA	CTGATTTCAT	TATCCAA				627

(2) INFORMATION FOR SEQ ID NO:1119:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 549 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119

GGAAGGCATGA	TGACGGAAAT	GGAAATTAAAG	CTCATTAAAAA	TAGACACAAG	CCATTATTTT	60
GAAAAAAAC	CAGGCTTGGG	GGAGAGAAATG	GATTATGCGG	GTCGTTGTTA	TTATAATAAA	120
TTCCAAAGAG	TGAATGCCAT	GCTCACAAAGC	TCGCTCATTC	AAAAGCATTT	GAAAAGGGAG	180
ATAGAAATCG	CGCACAAACCT	CATTITGCGT	AACGATAAGG	TGAAAACAT	CGTGTGTTGAT	240
TATAATGGGA	GGAAATCCGGA	GCGTTTTAT	CATAAGGCAG	AGTTATTGCT	TCGTGAGGAA	300
GGTTTTATGA	ATTTTACCGC	TTATAACACG	AAGACGCCAG	GGCATTGCA	TTTGTATGTG	360
CATAAGGGGC	ATACGGAATT	AGGCGAGGGT	GAAAGGCTGA	TTAAAACTTT	ATCCATGAAA	420
TTAGCGCAAG	GGTTCGCTAA	AGAATGGAGG	TTTTTCCCTA	GCAATGAATG	GCCTAAAGGAA	480
TTAAATATT	TAGCTTTACC	TTATGAAGTG	TTTGCAAAAG	AGCGCGGGAG	CTCTTGGCG	540
						549

(2) INFORMATION FOR SEQ ID NO:1120:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 825 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...825
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120

CCATTTTGA AAGGATTTT GATGTCAGAA AAAGAAAAGAC TGAATGAAGT GATCTTAGAA	60
GAAGAGATA ATGGGAGTGG TACTAAAAAG GTGTTTTGA TCGTGGCCAT AGCCATTATC	120
ATTTTGGCGG TGCTTTAAT GGTGTTTG AAAAGCACCA GAGTCGCTCC TAAAGAGACT	180
TTTTACAAA CCGATAGTGG CATGCAAAAA ATAGGCAACA CTAAAGATGA GAAAAAAGAC	240
GATGAGTTG AAAGCTGAA TATGGATTCT CCCAAACAAG AAGACAAGTT AGACAAAGTG	300
GTGGATAATA TTAAAAAACCA AGAGAGTGA AATTCTATGC CCATTCAAAC CGATCAAGCT	360
CAAATGGAGA TGAAAACAAC AGAAGAAAAA CAAGAATCTC AAAAGAATT AAAAGCTGTT	420
GAGCTTATTG CCATGAGCAC TCAAAAAAGAA TCTCAGGCTG TGGCTAAAAA AGAAACCCCC	480
CATAAAAAGC CTAAAGTAGC GCCAAAAGAT AAAGAAGCGC ATAAGATAA AGCTAAGCAT	540
GCAGCTAAAG AGCCAAAAGT CAAAAAAAGAA GCTCGTAAAG AAGTTTCTAA GAAAGCTAAT	600
TCTAAACCA ATCTTACTAA AGGGCATTAT TTGCAAGTGG GGTTTTTGC GCACACGCC	660
AACAAAGCCT TTTTACAAGA GTTTAATCAA TTCCCCATA AAATTGAAGA TAGGGGGGCT	720
ACTAAACGCT ACCTCATAGG CCCTTATAAG AGCAAGCAAG AAGCCTTAAT GCATGCCGAT	780
GAAGTCAGCA AGAAGATGAC TAAACCGGTT GTCATAGAAG TCGCG	825

## (2) INFORMATION FOR SEQ ID NO:1121:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 567 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...567
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121

TCAAGGCTTC AAAAGCCAT ATTAAAAGA GTTGAGATGT TGGAAAAACT GATTGAAAGA	60
GTGTTGTTTG CCACTCGTTG GTTGCTAGCC CCTTTATGCA TTGCCATGTC GTTACTGTTG	120
GTGGTTTGTG GCTATGTGTT CATGAAAGAG TTGTCGCACA TGCTCAGCCA TTTAGACACC	180
ATTAGTGAAA CGGATTTGGT TTTATCAGCC TTAGGTTTAG TGGATTGTT GTTCATGCC	240
GGGCTTGTGTT TGATGGTGCT TATGAAAGT TTGTTCTAA ATTAGACAAG	300
GTGGATGCTA CGGAATTCAC TTGGCTAAA CACACAGATT TTAACGCTTT AAAATTAAAAG	360
GTTCCTCTCT CCATIGTAGC CATTTCGGCG ATTTCTGTC TCAAAACGCTA CATGAGTTA	420
GAAGACGTTT TATCCAGTAT TCCTAAAGAC ACGCCCTAT CGCATAACCC TATTGTTG	480
CAAGTGGTGA TCCATTTGGT GTTGTGTGT TCAGCGCTGT TAACCGCTGT TACCAATAAC	540
ATCGCTTTT CGCAGAAAGA AAGGCAT	567

## (2) INFORMATION FOR SEQ ID NO:1122:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 711 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...711
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122

GGTTTGAAC	ATATTGATT	GGCGTTACTT	GTCGGTAGTGG	TAGCCTTTGG	GATTAGGGGG	60
TTTATCATG	GCTTCCTGAG	TGAAATAGCA	GGCACCTTGG	GGATTGTGCT	TGGCGTTTAT	120
TTGGCGTCTC	GCTATTCTGT	GGCTGTTGGG	AATTATTTT	CAGAGCAATT	GTATGATTAA	180
AGAAAATGAAA	CCATGACCAA	TCTCATGGT	TTTTTACTGG	TGTTGGCGTC	CATTGGGTG	240
TTTTTTTATG	CTCTTGGAGT	GTTGCTAGGC	AAGATGTTAG	TCTTTAGCGG	TCTAGGCATT	300
ATAGACAAGG	CGTTAGGGTT	TATTTTTCA	TGTTTGAAGA	CTTTTTAGT	GCTTTCTTTC	360
ATCCTTTATG	CGCTCTCTAA	AATGGTTTA	ATGAAAGACG	CTAACGCCAA	TTTGCAAGAA	420
AAGAGCGCTA	TTTTCCCCAC	CATGAAAAGC	GTCGCTAGTA	AGATCATGCC	CCTTGATGGC	480
GTCAAACATG	TGGAGAAAAAA	CCTTAAAGAC	AACCTGAAAG	AAATGAGCGA	TGAAGTTAAA	540
AATAAAGGAT	CTATTGATAA	CGCCAAAGAA	TCTTTTAATA	AGGCTACGGA	TAAGGGCGTA	600
GAAGCTTTAA	AAGAAAAGGC	TAAAGATTIG	CCTAAAAACA	TGCTAGAGCC	AAAACACAAT	660
AAACCCAACC	AAACCCCACC	AATCCCAACC	CCATCTAATA	AAGAACCCCT	A	711

## (2) INFORMATION FOR SEQ ID NO:1123:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1185 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...1185
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123

AGCTTATGGG	TTGAAAACCC	TATATTACTA	TCACACTCAC	AAGTCTATAG	CCCCCCAAAGA	60
TGCTGGTTT	TTAAACCCCC	TAGAAACAGC	GCTTTTGCTT	TGGTTTTTT	CGTGGGGCG	120
TTATTGTTT	ACTGGTGCGC	TTTAAGGCTT	TCGCATTCCG	ATTTCACTTA	TTTATTGCC	180

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TTAACATTG	TTTAGTAGC	GTTAGTTAT	GGGGTTTAT	TTTATTGTT	GCTCTATTT	240
GAAAACCCCT	ACTTCAGGCT	TTTGAGTTT	TTAGGCTCTA	GTTCATGCCA	CCCTTTGGA	300
TTTGATTGGT	TAGTCCCGGA	TAGCTTTT	TCTTATAGCG	TGTTTAGGGT	GGATAAAATTA	360
TCTTTAGGGC	TTATTTTTT	AGCTTGCAATT	TTTTTGAGCG	CTCAAAATCT	TAAAAATAC	420
AGAATGATAG	GGGTTTATT	GCTGCTTGGC	GCCTTGGATT	TTCATTTTTT	AAAATAAGC	480
GATTAAAG	AGGTTGGAAA	TATTGAATTA	GTCTCTACAA	GAACGCCCA	AGATTGAAA	540
TTTGACTCAA	ATTACCTTAA	TAATATTGAA	AACAACATTC	TTAAAGAAAT	CAAACTCGCT	600
CAAAGCAAGC	AAAAAACCTT	GATTGTTT	CCAGAGACCG	CTTACCCAT	CGCTTTAGAA	660
AACTCCCCTT	TTAAACCCCA	ACTAGAAGT	TTAACGCGCA	AGATCGCCAT	TTTAATAGGG	720
ACATTGCGCG	CTCAAGGCTA	TAGCCTTAT	AACAGCTCGT	TTTATTTTC	AAAAAAAAGC	780
GTTCAATCG	CTGATAAAAGT	GATCTTAGCC	CCCTTTGGCG	AGATAATGCC	TTTACCGGAG	840
TTTCTTCAA	AAACCCCTTGA	AAAGCTCTT	TTTGGCGAGA	GGCCTTATTT	ATACCGCAAC	900
GCTCCCCATT	TCAGCGATT	TACATTAGAC	GATTTCACCT	TTCGCCCCTT	GATTGCTAT	960
GAAGGCACCTT	CCAAACCCGC	TTATTCAAGC	AGCCCTTCAA	AAAGTTTTAT	CCTAATGAGC	1020
AATAACGCAT	GGTTTAGCCC	AAGCATTGAA	CCCACCTTAC	AAAGAACGCT	TTTAAAATAC	1080
TACGCAAGGC	GTATGATAA	AATCATCTT	CACAGCGCGA	ACTTTCAAC	TTCTTACATT	1140
TTAAGCCCTA	GCTTATTGGG	CGATATTCTT	TTAGGAAAC	GATCA		1185

## (2) INFORMATION FOR SEQ ID NO:1124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124

GAAACGATCA	TGATTAAAGC	GATTGATATT	TCTCATGCTT	TTGAAAAACC	TCTTTATAAT	60
GGCGTGAATT	TGCGCATTAA	ACCCAAAGAA	AGCCTGGCGA	TTTGTAGGCGT	GAGCGGGAGC	120
GGTAAAGCA	CGCTTTTAAAG	CCATTGGCC	ACCATGCTAA	AACCGGATAG	CGGAACAGTC	180
AGTTTGTAG	AACACCAAGA	TATTTATGCC	CTAAATCCA	AAAAGCTTTT	GGATTGCGG	240
CGCTTAAAG	TGGGCATCGT	TTTCAATCG	CATTCTTT	TTAAGGTTT	TAGCGCTTTA	300
AAAAACTTGC	AAGTCGCTTC	AATCCTAGGC	AAGCAAGAAA	TAATCATTC	CCTTTAGAA	360
CAATTAGGCA	TAGCCCACAC	CCTAAACAA	GGCGTGGGCG	AATTGAGCGG	CGGCCAGCAA	420
CAACGTTAA	GCATGCCAG	AGTGCTTCT	AAAAACCCC	AAATCATTAT	CGCTGATGAA	480
CCCACCGGGA	ATTAGACAC	CACTAGCGCT	AATCAAGTCA	TCACCATGCT	GCAAAATTAC	540
ATTACAGAAA	ACGAAGGGGC	GTAGTCCTA	GCCACGCGATG	ATGAGCATTT	AGCCTTCACT	600
TGCTCTCAAG	TCTATCGCCT	AGAAAAAGAA	TCTTGTATTA	AGGAAAAA		648

## (2) INFORMATION FOR SEQ ID NO:1125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

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- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...183
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125

TCGCTCGCCC C	CTAAATTAAA AGC GTTTTT AAGGTAGCGT TATCCTGTAA GCGGGTGATA	60
AAAATCACAG GCGTAGAGAT TAAAAAAATCG TTTCATGATGC GCTTGAATAA TTCCAAGCTA		120
TTCATTCAG GCACTTGCAC GTCTAAAAGC AAGAGGTTAA AGCGCTCAAC AGAGAGCCTT		180
TCA		183

## (2) INFORMATION FOR SEQ ID NO:1126:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 900 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...900
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126

TTTGCCTTGC ATAAAAAAAGT TCTGTTGGCT TTAAC TGCCA GCTTGATTTG CCAAGAGTCT	60
TTGTCGCTA AGGATAAAGA CTACACTTG GGCAAGGTTT CTACTGCCG TAAAAAGGAT	120
AGATCTGACT ATTCTGGCA GGTCAATTG GGTATAGCG GGATTACCGC GCCTAACAGT	180
TGGCAAGATG AAGAAGTGAA AAAATACACA GGAAGCCGCA CGGTGATCTC TAACAAAGCG	240
CTCACCCAAC AAGCTAACCA AAGCATTGAA GAAGCTTTAC AGAATGTCCC CGGTCTGCAA	300
ATAGGAATG CCACAGGTGT GGGGGCTATG CCTACTATCC AAATCCGTGG CTGGAGCG	360
GGGGGTTTCAG GGCGATAGCGA TGCGACGCTC ATGTTAGTTA ATGGTATTCC TGTTTATATG	420
GCCCCTTACG CTCACATTGA GCTGACATT TTCCCTGTAA CCTTCAAGC CATTGATGCC	480
ATTGATGTGA TCAAAGGTGG AGGCAGCGTG CAATATGGC CTAACACTTA TGGGCTATT	540
GTCAATATCA TCAC TAAACC TATCCCTAAT CAATGGGAAA ACCAAGCGGC TGAAAGGATC	600
ACTTATTGGG CTAAGGCTAG AAACGCTGG TTTGCCGCTC CCCCTGATAA ACCCGCGAT	660
CCTTCTTCA TCAAGTCTTT AGGCAACAA CTCCTCTATA ACACATTATGT GAGGACCGGA	720
GGGATGATCA ATAAGCATGT GGGTATCCAA GCGCAAGCTA ACTGGGTTAG AGGCCAAGGC	780
TTTGGGACA ATAGCCCCTC TAGTATTCTA AACTATTGGC TGGATGGGGT CTATGACATC	840
AATGAAAGCA ATGGGATTAA AGCCTATTAC CAATACTACG ATTTTGCTAT CGCCCAACCG	900

## (2) INFORMATION FOR SEQ ID NO:1127:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 825 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

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(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127

GTGTCATAAC TAGTTATAAT AGAACCTTAC ACTTTTACA	AAAGGGAGGA	GAGTGTCA	60
TTGGGGAGCG TCAAAAAAAGC GGTTTTAGG GTTTTGTT	TGGGGCGTT	GTGTTTATGC	120
GGGGGGTTAA TGGCAGAGCA AGATCCTAAA GAGCTTATAT	TTTCAGGTAT	AACTATTAC	180
ACGGATAAAA ATTTCACTAG AGCTAAGAAA TATTTTGAAA	AACTTGCAA	ATCAAACGAT	240
GCTGATGGCT GTGCAATCTT AAGAGAGGTT TATTCTAGTG	GTAAAGCCAT	AGCGAGAGAA	300
AACGCAAGAG AGAGCATTTG AAAAGCTCTT GAACACACCG	CTACTGCTAA	AGTTTGTA	360
TTAAACGATG CTGAAAAATG CAAGGACTTA GCAGAGTTTT	ATTTTAATGT	AAACGATCTT	420
AAAATGCTT TAGAATATTA CTCTAAATCT TGTAAGTTAA	ATAATGTTGA	AGGGTGTATG	480
CTGTCAGCAA CTTTTTATAA CGATATGATA AAGGGTTGA	AAAAAGATAA	AAAAGATCTA	540
GAATATTATT CTAAAGCTTG CGAGTTAAAT AACGGTGGAG	GGTGTCTAA	ATTAGGAGGG	600
GATTATTTTT TTGGTGAAGG CGTAACAAA GATTTCAAAA	AAGCTTTG	ATATTCTGCC	660
AAAGCTTG TGCTAAAGGG TGTTACGCTC TAGCAGCGTT	TTATAATGAG	720	
GGTAAAGGCG TGCCAAAGGA TGAAAGCAA ACGACAGAAA	ACCTTGAAAA	GAGTTGCAAG	780
CTAGGATTAA AAGAACATG CGATATTCTC AAAGAACAAA	AACAA		825

(2) INFORMATION FOR SEQ ID NO:1128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128

ACCCGAAAT CATCAGCATC CATGTCAGAAA	AATGAAAAAC	ACCCCCATAG	GGTGTGCAA	60
CTCATTTAAA GTTCAGGCAT CACGCCAGGC	ATTGTCTAA	ACCCCCACAC	GCATGAAGAA	120
AGTATTAAT ACTTGCTAGA AAGCGTGGGG	CTAGTGTCTT	TAATGAGCGT	GAATCCGGGC	180
TTTGGGGGC AGAAGTTTT AGATCTAGTG	CTAGAAAAGT	GCTTGAAGT	TAAGAAACTG	240
ATCAAACGCT ACAACCCTAG CTGTCCTTTA	GAAGTGGATG	GGGGCGTGAA	TGATAAAAAT	300
ATCTTTGAAC TCCAACAAGC GGGCGTGGAT	GTGGTGGTTT	CAGGGAGTTA	TATTTTGAA	360
TCCAAAGATC GTAAGCTGGC TATTGAAGGC	TTACAGAATG	TCAGACAAACC	TCTTGCA	417

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## (2) INFORMATION FOR SEQ ID NO:1129:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 945 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...945

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129

AAACTTTTAA GAGTTTACA TAAGATGATT	AAAAAAGCGG CTAACCCCCC	TTTTTTTAAA	60
ATTTGTTTC AAGCTTTAAG CTACAATATA	CGCATGAAAG ATTTAACAA	GACTATCGGC	120
GTGTTTGTGC GGCCCACTCA TCATCAAAAC	GCTTTTTTA AAGAGCTAGA	GCAGGGCTAAA	180
GAATGGGTTT TAACGCTTTT AGAAGATGAG	GGGTTTGAAA GCTTTATGAT	TGATAGCCTT	240
GATGGGGCAA AAGATGCACA ATTGATAAAA	AAAGCTTACG CGTTTTGTG	TTTAGGAGGC	300
GATGGCACGA TTTTAGGGGC TTAAAGAATG	ACGCATGCTC ACAATAAGCC	ATGCTTTGGG	360
GTGAGGATTG GGAATTAGG GTTTTTGAGC	GCGGTTGAAT TGAACGGGTT	GAAAGATTTC	420
TTACAAGATC TCAAGCAAAA CAGGATCAA	TTAGAAAGAGC ATTGCGTTT	GGAGGGCCGT	480
ATTGGAAACA CCTCTTTTA TGCGATCAAT	GAAATCGTGA TCGCTAAAAA	AAAAGCTTTA	540
GGGGTTTATAG ACATCAAAGC GTGCGCGGGC	CATAGCCCT TTAACACTTA	TAAAGGCAT	600
GGGCTTATCA TTGCCCCGCC CCTAGGCTCA	ACCGCTTATA ATTGAGCGC	TCATGGGCC	660
ATTGTGCATG TTAAAGGCCA AAGCTATAATT	TTAACGCCCT TGCGGATT	TTCTTTAACG	720
CAACGCCCTT TAGTGTAGG GCGGAATT	TGCTTGAGTT TTGCGCTCA	TGAAGACGCT	780
CTTGTGGTTA TTGATGGCA AGCCACCTAC	GATTAAAAG CCAACCAACC	CCTATACATT	840
CAAAAAAGCC CCACGACCAAC CAAGCTCTTA	CAAAAAAATT CAAGGGATTA	TTTAAAGTG	900
CTTAAAGAAA AGCTGTTATG GGGGAAAGC	CCTAACAAAAA AAAGA		945

## (2) INFORMATION FOR SEQ ID NO:1130:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 654 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...654

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130

CGCTACAATA CCCCATGCA AAAAAAGATT	TTTTTACTAG AAGACGATTA	CCTTTAAAGC	60
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GAGAGTATCA	AGGAGTTCTT	GGAGCATTAA	GGCTATGAAG	TGTTTGC	GGCGA	120	
AAAGAGGCTC	ATGAAAGGCT	CTCTGTTGAG	CGCTTTAAC	TCTTGCT	AGACGTGCA	180	
GTGCCTGAAA	TGAATAGCTT	GGAAATTATTC	AAGCCATCA	AAAACGATT	TTTAATCTCT	240	
ACGCCTGTGA	TTTTTATCAC	CGCCTTACAG	GATAACGCTA	CCTTAAAAAA	CGCTTTAAT	300	
TTAGGGCGA	GCGATTATTT	GGAAAAGCCT	TTTGATTGAG	ACGAATTGGA	AGCGCGCATT	360	
AAAAGGTTT	TCAATGATGA	TCCGATAGAA	ATCATGCC	ACATT	CCACCAACAC	420	
GCTTGAACG	TTAAAGGGAA	AAAGGAATTC	TTAGGCC	AAACCGCCC	ACTTTAGAA	480	
TATTTTTAG	AGCATAAAGG	GCAAATCATC	AGCTCTCAAG	CGTAGAAAA	CAACTTATGG	540	
GAGCAAGCGA	TTCATGATTC	CACCTTACGC	ACTTACATTA	AAGTGTGCG	CAAGCTTTG	600	
GGTAAAAATT	GCATAGAAAC	GCATAAGGGG	GTGGC	TATC	GCTTAAACCC	ACTA	654

## (2) INFORMATION FOR SEQ ID NO:1131:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1074 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131

TGTGGCGCTA	ATCGCTCAAA	AGGGCGTGG	GGTTTTAGTT	CAAATGCGC	GGCGCGAAT	60
AGCGGTTATA	GTAAACGAAGC	GTATGAAAGC	GTGGGGGCTA	AAATCGTGG	TICTAAAACG	120
GCGTGGGGC	AGGATTTGGT	GGTCAAATGC	AAAGAGCCTT	TAGAGCATGA	ATACCCTTGT	180
CTCAAAGAAA	AAGCGACTCT	GTTTAGTTAT	TTGGATTAG	CGTATCAAAA	AAGCTTGTGT	240
GAAATGTTA	TIAATAAAAAA	AATCACTTCT	ATTTGCACTG	AAACCATATG	CGGGCCTAAA	300
AACGACTACC	CTATTTAGC	GCCTATGAGC	GTGGTGGCTG	GGAGGTTGGC	TGCGCATT	360
GTCCACGATT	ATTACTGGC	TTTAGAGCAT	GTAAAGGGT	TTATGGCTAA	GGGGGTCA	420
CTAGGGGTT	TGTCGGGTG	GCAAAGGGCT	AAAATCGTCG	TAATTGGAGG	CGGTGTGGTT	480
GGCATGGAGA	GGCGCAAAGT	CTTAAGCCAA	ATGGGGCTA	AAAGTAACGAT	TTTAAATT	540
GACTAACGCTA	AATTACAAAAA	CCACCCCTTAT	TATCATTGT	ATGATTTAGA	AGTCTTAAGC	600
GTGAATGAAG	CCAATATCAT	TCAAGCTTAA	AAACGGGGCG	TGGGGCTAGT	GGGAGGGCTG	660
CTGGGTACAG	CGAGCCAAAC	CCCTAAAGTC	ATCTTAAAGAA	GGCATT	ATACATGCAG	720
ACACAAGGGG	TAGTCATTGA	TGTGGCTTGC	AGTTTAGGGG	GGTCATAAG	AGCCATACGC	780
CAAGCAAGCC	ATTCATACCC	GGTGTATGT	GAAGAAAGTT	TGGTCATT	TGGCGTGC	840
AACATGCCAG	GGATTGTCG	TAAAACGAGC	TCTACGGCTT	ATAGCCATGC	GAGTGTGC	900
TATTTGTGT	ATATTAGA	GCATGGCTTG	AAAGGTTTTT	TAACAGCCAA	CACTAAAATC	960
GTGGCGAAC	CGCTTGGAGG	CTTGAGCGCT	TATAACGGCT	ATATCACCC	AGAAGGCATC	1020
GCTAAAGCGT	TCAATCTGGC	GTTCAATCG	CCTT	TTAGAAA	TTTAAAGGA	1074

## (2) INFORMATION FOR SEQ ID NO:1132:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 489 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

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- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...489
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132

AAGGGTAAAA	GGGTAAAAAA	CATGCGAGAT	TTCAATAACA	TTCAAATCAC	ACGCTTAAAA	60
GTGCGTCAAA	ATGCCGTTTT	TGAAAACGT	GATCTGGAGT	TTAAAGATGG	CTTGAGCGCG	120
ATTAGTGGGG	CTAGTGGGGT	GGGGAAAAGC	GTCCTTATTG	CGAGCCTTTT	AGGGGCGTTT	180
GGGCTTAAAG	AGAGCAACGC	TTCAACATT	GAAGTCCAAT	TGATCGCGCC	TTTTTTAGAC	240
ACGGAAGAAT	ACGGCATTIT	TAGAGAAGAT	GAGCATGAAC	CCTTAGTTAT	TAGCGTGAATT	300
AAAAAAAGAAA	AAACACGCTA	TTTTTTAAC	CAAACAAGCC	TATCTAAAAAA	CACGCTCAA	360
CGCTTATTAA	AGGGGCTTAT	TAAACGCTTA	TCTAACGACA	GATTCAAGCCA	GAATGAACTC	420
AACGATATTAA	TAATGCTCTC	CTTATTAGAT	GGCTATATCC	AAAATAAAAAA	TAGGCCTTTA	480
CCCCCTTT						489

## (2) INFORMATION FOR SEQ ID NO:1133:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 891 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...891

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133

TCAAATCATA	AAAGGGTTTT	TATGGATTAC	AAACGTTTTA	AAGGCAAGCA	TCCGAACATC	60
GTATAGAAA	TCATCAGTCT	TTTAAAGAAA	GGGGTTAAAA	AAGCCAAGA	GATTTAGAA	120
AAGCCGGACG	CTGGGAGTTA	CACTCAGTTA	AAAAACAGCA	GCGGGGATAC	GCCTATTAAA	180
GCGGATTTAG	CCCTAGATAA	TTTTTAGAG	GAAACTTTTT	TGAGTTAGA	GAATGTGAAA	240
AGCGTTTTA	GCGAAGAAAA	AGAACCGCT	TTACTAAAG	AAAACGGCT	TTATTTGATC	300
GCTTATGACC	CCCTAGATGG	GAGITTCAGTG	ATGAGGGCGA	ATTTCTTAGT	AGGCACGATT	360
ATAGGGGTTT	ATGAAAAGGA	TTATAAGGCG	CAAATTTAG	TTGCAAGCCT	TTATGTGGTT	420
TTTGGGCATA	AAATAGAATT	GGTGGTGGCT	TTAGAAGAAG	TTTATCGTTA	CGCTTTTTAT	480
CAAACAAAGT	TTCATTATAT	AGAACCCATC	TTTTAGAAA	ATAAGGGTAA	AAATCATCGCT	540
AGCGGAGGCA	ATCAAAGGA	TTTTCTTCTTG	GGCTTAAAAAA	AGGCTTTAGA	AGGGTTTTTT	600
GCAGAAAATT	ACCGCTTGGC	ATACTCAGGA	TCTATGGTGG	CTGATGTCCA	TCATGTGTTG	660
GTTAAAAAGG	GCGGAATGTT	TTCTTACCCG	CAAAGAAAT	TGCGAAAGCT	TTTGTGAAGTC	720
TTTCTTTAG	CCTTGATGGT	TGAAAAAGCT	AAAGGGGAAG	CGTTTTATT	TGATAAGGGG	780
GTTAAAAAGC	TTTGCTAGA	TCAAACGCTA	GAAAGCTACC	ATGAAAAAAG	CGAATGCTAT	840
TTAGCCAGCC	CCCATGAAGC	TCAGATTTA	AAAAACATT	TAAAGGGAGA	A	891

## (2) INFORMATION FOR SEQ ID NO:1134:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 789 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...789
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134

ACTTTTTTAA TTATTTTTTG GGTATTCTTT TTAAGAATTA AGCATTATGT TAAGGAATTA	60
TCCATGAAAA AATTTTTTTC TCAATCTTGT TTAGCTCTTA TTATCTCTAT GAATGCGGTA	120
TCTGGCATGG ATGGTAATGG CGTTTTTTA GGGGCGGGTT ATTGCAAGG ACAGGCGCAA	180
ATGCATGCGG ATATTAATTC TCAAAAACAA GCCACCAACG CTACGATCAA AGGCTTTGAC	240
GCGCTCTTGG GGTATCAATT TTTCTTGA AAACACTTTG GCTTACGCCT TTATGGTTT	300
TTTGAATACG CTCATGCCAA TTCTATTAAAG CTTAAAAACC CTAACATAAA TAGCGAAGCG	360
CGCGAAGTGG CCTAGTCAAAT TCTTGGGAAA CAAGAAATCA ATCGTTTAAC AAACATTGCC	420
GATCCCAGAA CTTTTGAGCC GAACATGCTC ACTTATGGGG GGGCTATGGA CGTGATGGTT	480
AATGTCATCA ATAACGGCAT CATGAGTTTG GGGGCTTTG GCGGGATACA ATTGGCCGGC	540
AATTCAATGGC TTATGGCGAC ACCGAGCTTT GAGGGCATTG TAGTGGAAACA AGCCCTTGTG	600
AGCAAGAAAG CCAATTCTTT CCAATTTTA TTCAATGTGG GGGCTCGCTT AAGGATCTTA	660
AAACATTCTA GCATTGAAGC GGGCGTGAAA TTCCCCATGC TAAAGAAAAA CCCCTACATC	720
ACTGAAAAAA ATTTGGATAT AGGGTTTAGG CGCGTGTATT CGTGGTATGT GAATTACGTG	780
TTCACTTTC	789

## (2) INFORMATION FOR SEQ ID NO:1135:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 702 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...702
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135

TGGATTGACG CTAAAAATAA AGAAGAAGCC ATCATTCAAG GCTACACTAT CATTGATCCA	60
AGCACCGTTA TTGCGACGCA CACCAAGCGAA TTAGTGAAAA AATACGCTGA AGATTTTATC	120
ACCAAAGATG AAGTGAAATC CCTTTTAGAG CGCTTGGCTA AAGACTATCC TACGATTGTA	180
GAAGAGAGTA AAAAAATCCC CACCGGTGCG ATCCGCTCAG TCTTGAAGC CTTGTTGCAT	240

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AAAAAAATCC	CCATTAAGGA	CATGCTCACT	ATTTGGAAA	CGATTACTGA	TATTGCTCCA	300
TTGGTCAAA	ACGATGTGAA	TATCTTAACC	GAACAAGTGA	GGGCGAGGCT	TTCTAGGGTG	360
ATCACCAACG	CTTTAAATC	TGAAGACGGG	CGTTTGAAT	TTTAACCTT	TTCTACCGAT	420
AGCGAACAAAT	TTTGCTCAA	AAATTGCGA	AAAAATGGCA	CCTCTAACAGAG	CTTATTACTC	480
AATGTGGGCG	AATTGAAAAA	ACTCATTGAA	GGGGTTCTG	AAGAGGCTAT	GAAAGTCTIG	540
CAAAAGGGA	TCGCTCCGGT	GATTTGATT	CTAGAGCCTA	ATTAAGAAA	AGCCCTTCT	600
AATCAAATGG	AGCAGGCTAG	GATTGATGTG	GTCGTCTAA	GCCATGCGGA	ATTAGATCCT	660
AACTCTAATT	TTGAAGCCTT	AGGCACGATC	CACATTAACT	TT		702

## (2) INFORMATION FOR SEQ ID NO:1136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136

AAAAAAAAGA	CCCTAACAT	TTCACAATTA	GGAAAAACCA	TGCATGTTGC	TTGTCTTTG	60
GCTTTAGGGG	ATAACCTCAT	CACGCTTAGC	CTTTTAAAG	AAATCGCTTC	CAAACACCAA	120
CAGTCCCTTA	AAATCCTAGG	CACTCATTG	ACTTTAAAAA	TCGCCAAGCT	TTTGAATGTC	180
GAAAACATT	TTGAAATCAT	TCCCTGTTTT	GAAAATATCC	CTGCTTTTA	TGACCTTAAA	240
AAACAAGGCG	TTTTTGGGC	GATGAAGGAT	TTTTTATGGT	TATTTAAAGC	AATTAAAAAA	300
CATCAAATCA	AACGTTTGTAT	TTTTAGAAAAA	CAAGATTTA	GAAGTTTCT	TTTATCCCAA	360
TTTGTTCCTA	TAACCACTCC	AAATAAAGAA	ATTAAAAACG	TTTATCAAAA	CCGCCAGGAG	420
TTGTTTCTC	AAATTATGG	GCATGTTTT	GATAACCCCTC	CATATCCCCT	GAGTTTAAAA	480
AACCCCAAA	AGATTTTGAT	CAACCCCTTC	ACAAGAGAAA	ATGATAGGAA	TATTTCTTTA	540
GAGCATTAA	AAATCGTTTT	AAAACCTTTA	AAACCTTTT	GTGTTACGCT	TTTAGATTT	600
GAAGAACGAT	ACGCTTTT	AAAAGACAGA	GTCGCTCATT	ATCGCGCTAA	AACCAGTTA	660
GAAGAAGTTA	AAAACCTGAT	TTTAGAAAGC	GATTGTATA	TAGGGGGGA	TTCGTTTTTG	720
ATCCATTG	TTTACTATT	AAAGAAAAAT	TATTTATCT	TTTTTATAG	GGATAATGAC	780
GATTTCATGC	CGCCTAATAG	TGGGAATGAG	AATTCTCAA	AAGCCCATAA	AAGCCATTTC	840
ATAGAACAGG	ATTTAGCCAA	AAAATTCCGC	CATTGGGGC	TATTA		885

## (2) INFORMATION FOR SEQ ID NO:1137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137

AACACACAGC GCCAAACACT CCCCCTAGTC AAGTCCCGCC CACACCCCCT AGTCAAAATT	60
TACCTAAAAC AAATGTGTGG AATGGGGTTT ATTGGCTTCA AAAACAAAATCT TACTCAAACA	120
AAGGCATTTA TTATATTGAT CCCAATCTTT CAGGACAGAG CGGTCAAAGC GGCAACACGC	180
TCAGCACCTA TACAGCTAAT TTGT	204

(2) INFORMATION FOR SEQ ID NO:1138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...4239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138

ACGCTAATAT CAATTTTCAG CGCAAGCCAG GCTGATTTTG GAGGCAACAC GACTATTGAT	60
ACAGCAAGCT TTAATTTTGA CAGCGCAAGT TCATTGAATT TTAATAACCT TACGGCTAAT	120
GGGGCGTTAA ATTTTAATGG TTATGCGCCC TCTTTAACTA AGGCTTAAAT GAATGTCAGC	180
GGGCAGTTTG TTITAGGGAA TAATGGGAT ATTAATTAT CTGACATCAA TATCTTTGAC	240
AACATCACAA AATCTGTAAC TTACAACATC TTAAACGCTC AAAAAGGGAT TACTGGCATT	300
AGTGGGGCTA ATGGCTATGAA AAAATCCTT TTTTATGCCA TGAAAATCCA AAACGCTACC	360
TATAGCGATA ATAACATGAT CCAAAATCCTG TCGTTTATAA ACCCTCTCAA TTCTTCTCAA	420
ATCATTCAG AGAGCATTA AAATGGGGAT CTAACCATAG AAGTTTAAAC TAACCTAAC	480
TCGGCTTCCA ACACTATTTT TAATATCGCT CCTGACCTTT ATAATACCA AGATTCTAAC	540
CAAAATCCTA CCGGTATAG CTATGATTAT AGCGACAATC AAGCAGGCAC TTATTACTTG	600
ACAAGCAACA TAAAGGTCT TTTCACCCCT AAAGGCTCTC AAACGCTCA AACCCCAGGC	660
ACTTATAGCC CATTAAACCA GCCTTTGAAT AGTTGAATA TCTACAATAA GGGTTTTCT	720
AGCGAGAATT TAAAAACGCT TTGGGGATC CTTCTCTAAA ATTCCGCCAC CTTAAAAGAA	780
ATGATTGAAT CCAACCAACT AGACAATATC ACTAACATTA ATGAGGTGT GCAACTCTTA	840
GATAAGATTAA AAATCACCCA AGCGCAAAG CAAGCGCTCC TAGAAACGAT CAACCATTG	900
ACTGACAACA TCAATCAAC CTTTAAATAC GGGAACTCG TTATAGGCCTC TACCCAAGAT	960
AATGTTACAA ACTCTACTAG CTCTATATGG TTGGGGCA ATGGCTATAG CAGCCCTTGC	1020
GCGCTAGATA CGGCCACTTG TTCTCTTTT AGAAACACTT ACTGGGGCA ATTATTAGGC	1080
TCAACTTCCC CTTATTTAGG CTACATTAAC GCTGATTTA AAGCTAAAG CATTATATT	1140
ACCGGGACAA TTGGAAGTAG TAACGCTTTT GAAAGCGGAG GGAGCGCGGA TGTAACCTTT	1200
CAAAGCGCTA ATAACCTAGT GTTGAATAAA GCTAACATAG AAGCTCAAGC CACAGACAAT	1260
ATCTTTAATC TTTGGGTCA AGAAGGGATT GATAAAATCT TTAATCAGGG GAATTTAGCG	1320
AATGTTCTTA GTCAAATGCC TATGGAAAAA ATCAACGCAAG CGGGGGTTT AGGGAACTTT	1380
ATAGAAAACG CTCTAACGCC TTTGAGTAAG GAATTACCCG CTAGCTTGCAG AGATGAAACC	1440
TTAGGCCAAC TTATAGGTCA AAATAACTTA GATGATTAT TGAATAATAG TGGAGTCATG	1500
AATGAAATCC AAAACATTAT CAGTCAAAAA CTAAGCATTT TTGCAATT TGTACCCCA	1560
TCCATCATAG AAAACTACCT TGCTAACGAG TCTTTAAAAA GCATGCTAGA CGATAAAGGG	1620
CTTTGAATT TTATCGGTGG GTATATAGAC GCTTCTGAAT TAAGCTCTAT TTTAGGCCTG	1680

ATTTTAAAGG ATATTACTAA	CCCCCCTACA AGCCTGCAA	AAGACATTGG TGTGGTAGCG	1740
AACGACTTGT TGAACGAGTT	TTTAGGACAA GATGTTGTCA	AAAAGCTAGA AAGTCAGGC	1800
TTGGTGAGTA ATATCATCAA	TAATGTTATT TCTCAAGGCG	GGTTGAGCGG CGTTTATAAT	1860
CAAGGTTTAG GGAGCGTGT	GCCCCCTCT TTACAAAACG	CCCTCAAAAGA AAACGATTAA	1920
GGCACTCTT TATCGCTAG	AGGCTGCTAT GATTTTGGC	AAAAAGGGTA TTTTAACCTT	1980
TTAACAAATG GCTATGTTTT	TGTCAATAAC AGCTCTTTA	GTAACGCTAC TGGGGTAGT	2040
TTGAATTTCG TCGCCAACAA	GTCTATTATC TTTAATGGCG	ATAATACGAT TGACTTTAGC	2100
AAGTATCAAG GCGCATTGAT	TTTGCTTCT AATGGTGT	CTAATATCAA TATCACCAC	2160
CTAACGCCA CTAATGGCTT	AAGCCTTAAT GCGGGTTTGA	ATAATGTGAG CGTTCAAAAA	2220
GGAGAAATT GTATCAATT	AGCCTAATTGC CCTACAAACCA	AAACAGCTC TCCTGCAAAC	2280
TCTACGTAA CCCCCCTAA	TGAGTCTTT AGCGTGCACG	CTAATAATTTC CACTTTCTTA	2340
GGCACAACTAA TCTCTAATGG	GGCTATTGAT TTGCTCTAAG	TAACAAATAA TAGCGTTATA	2400
GGCACGCTCA ATCTCAATGA	AAATGCGACC TTGCAAGCTA	ATAATTTAAC GATCACCAAC	2460
GCTTTAAACA ACGCCTCTAA	CTCTACGGCT AATATTGATG	GTAATTTCAC CTTAAACCAA	2520
CAAGCGACTT TAAGCACTAA	CGCTAGTGGT TTGAATGTCA	TGGGAAATT TTAAATAGCTAT	2580
GGCGATTTCG TGTTTAACCT	CAGTCATCTA GTTGTCTCAT	CTATTATCAA TACTCAAGGC	2640
ACAGCGACGA TCATGGCCAA	TAATAACCT TTGATCCAAT	CTAACGCTTC TTCACCCAGAA	2700
GTGGGTACTT ACACCGCTGAT	TGATAGGCT AAAGCCTATT	ATTACGGGTAA ACAACCCAA	2760
ATCACAGGAG CGAGTAGCCT	GGATAATTAC CTTAAGCTT	ATGCGCTCAT TGATAATTAA	2820
GGCAAGCACAA TGGTGTGAC	TGACAACCGC TAAACCTATA	ACGGGCAAGC CGTGAGCGTT	2880
AAAGATGGCG GTTTAGTTGT	AGGCTTTAAG GACTCTCAA	ATCAATAACAT TTACACTTCC	2940
ATTCTTTATA ATAAAGTGA	AATCGCTTT TCTAATGATC	CTATCAATAA CCCACAAGCC	3000
CCCACCTTAA ACAATATAT	CGCTCAAATT CAGGGCGTTC	AAAGCGTGGAA TAGCATCGAT	3060
CAAGCTGGGG GAAATCAAGC	GATTAATTGG CTCAATAAAA	TCTTTGAAAC TAAAGGAAGC	3120
CCTTTATTCTG CTCCCTTATA	TCTAGAGAGC CACTCCACAA	AAAGATTTAAC CACGATCGCT	3180
GGAGATATTG CTAAACACTT	AGAAGTCATC GCTAACCTTA	ATTTTAAAAAA TGACGCCACT	3240
AATAATTCTA AGATCAACAC	CTACACCCAG CAAATGAGTC	GTTCAGGCCAA GCTCTCTGAC	3300
ACTTCAACTT TCGCCCGTTC	TGATTTCTTA GAACGCTTAG	AAGCCTTAA AAACAAGCGA	3360
TTCGCTGATG CGATCCCTAA	CGCTATGGAT GTGATTTAA	AATACTCTCA AAGGAATAGA	3420
GTTAAAATA ATGTGTGGGC	GACAGGAGT GGAGGGCTA	GTTCAGCTTAA TGGAGGTACT	3480
GGAACCTTAT ATGGTATCAA	TGTAGGCTAT GATAGGTTA	TTAAGGGCGT GATTGTGGGA	3540
GGITTAIGCCG CTTATGGGT	TAGCCGTTG CATCCTAAC	AGGCTCTAGC 3600	
AATGTCATG TGGGGCTTTA	TAGCCGAGCG TTTATCAAA	AAAGCGAGCT AACCATGAGC	3660
TTGAATGAGA CTTGGGATA	CAATAAAAATC TTCTACACT	CCTATGACCC CCTACTCTCA	3720
ATCATCAATC AGTCTTACAG	ATACGACACT TGGACGACTG	ACGCTAAAAT CAATTATGGC	3780
TATGATTTCA TGTAAAGA	AAAAGCGTT ATTTTAAAC	CCCAAGTAGG CTTAAGCTAT	3840
TATTACATTG GTTTGTCTGG	TTTAAGGGC ATTATGGATG	ATCCTATTTA CAACCAATT	3900
AGAGCCAATG CTGACCCCTAA	TAAAAAAATCC GTTCTAACGA	TCAATTTCGC CCTAGAAAGT	3960
CGGCATTATT TCAATAAAAAT	CTCTTATTAT TTGATGATTG	CGGATGTGGG CAGAGACTTA	4020
TTCAATTAAAT CTATGGGGGA	TAAAATGGT CGTTCATCG	GTAATAACAC CCTAAGCTAT	4080
AGAGATGGTG CGAGATACAA	CACTTTGCT AGCATTATCA	CAGGGGGGA GATAAGATIG	4140
TTCAAAACCT TTTATGTGAA	TGGTATGCCTA CGGGCTAGGT	TTGGGCTTGA TTATAAAGAT	4200
ATTAATATTA CCGGAAATAT	TGGTATGCCTA TATGCTTT		4239

## (2) INFORMATION FOR SEQ ID NO:1139:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...579

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139

AGGGATAACA TGGAGCTTAT	TTTAGGCTCT CAATCCAGCG	CTAGGGCGAA	TCTTTTAAAAA	60
GAGCATGGGA TTAAGTTGAA	ACAAAAGCG CTCTATTTC	ATGAAGAAAG	CCTAAAAACC	120
ACAGACCCA TAATTTGCGC	GGGAGTTTGT CTATTTGGCG	TGCAAGGGGA	AATTAGAAAA AGCTAAAGAG	180
TTACTTGCGA ATAATTTGCGC	TATCGTGGTG GCTGATAGCC	TGGTGAGCGT	GGGTAATCGC	240
ATGCAACGAA AAGCTAAAAA	CAAGCGAGAA GCCCTTGAAT	TTTTAAAACG	CCAAAATGCC	300
AATGAAATAG AGGTTTTAAC	TTGCTCTGCA TTGATTTC	CTGTGTTGGA	ATGGCTGGAT	360
CTATCGGTTT TTAGAGCGC	TTTAAAGGGCG TTGATTGCA	GCAGAAATAGA	AAAATATTAA	420
GAGAGCGGTT TATGCAAGG	AAGTGCAGGC TGTCGCGTT	TAGAGGACTT	TCATAAGCCT	480
TATATTAAAA GCTCAAGCAA	GAATTAAAGC GTGGGTTGG	GGCTGAATGT	GGAAGGCTTG	540
TTAGGGCAC TAAAATTAGG	GGTTAAACTT TCATTATTA			579

## (2) INFORMATION FOR SEQ ID NO:1140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...504

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140

AGAATGGCTC TTTTGGTTC	AAAGAGTAAG ATGTTAGAAA	CTTATGCACT	AAAAAGTGGG	60
GCTGTTTTTA TCTCTGATGC	GCATTTTTTG	CCAAAAAGCC	CTCATTTAAT	120
AAAGAACTTT TAAGCGCCAA	ACCCCCGCAA	GTCCTTTCA	TGGGCGATAT	180
CTTGCTGGCT ATTTACCCCT	AGATAAAAGAG	CAGCAAAAAA	TCATTGATTT	240
TTGAGCGAAA TTTCACAAGT	TTTTTACTTT	GAAGGCAACC	ATGATTTTTC	300
GTATTCAATT CCAAAGTAAT	GGTTTTTGAG	CGCCAAAACC	AACCCGCATT	360
GATAACAAAC GCTTTTGCT	AGCCCCATGGG	GATTATTCA	TCACTAAAGC	420
TACATCACCG AGCTCACTTC	CACTGGGCT	AGATTTTTT	GTATGAATT	480
AGTTTAAAA CCTTATACCC	TTTT			504

## (2) INFORMATION FOR SEQ ID NO:1141:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 960 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

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## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141

AATGATGATG AGAATAAAAGT AATTGAATTA AAAACAAAGGA ATAACATGCG CATCGTATTT	60
ATGGAAACGC CTAGTTTTCG TGAAGTGATC TIAAGGGCGT TGGTTGAAAA TGAAGATAAA	120
AAGATAGAAG TGGTGGGGCT ATTCACTCAA AGGGACAAAC CTTTTGGCG CAAAAAAAGAA	180
TTGAAGGCC CAGAGACTAA AACATACATT TTAGAAAATC ATTAAATAT TCCCATTTC	240
CAGCCCAA GTTTGAAGA GCCTGAAGT CAAATCTTAA AAGGTTTGA GCCTGATTT	300
ATCGTGGTGG TGGCTTATGG TAAGTTTG CCTAAAGAGG TTTAACCAT CGCTCCTTGC	360
ATTAATTTCG ATGCGTCGTT ATTGCCAAA TACAGGGGG CTTCGCCAT TCATGAGATG	420
ATACTCAATG ACGATAGGAT TTATGGCATA AGCACCATGC TTATGGATT GGAAATTGGAT	480
AGCGGGGATA TTTTAGAAAG CGCTTCTTTT TTAAGAGAAG ATTATTTGGA TTTAGACGCT	540
TTAAGTTAA AATTAGCGCC CATGGGGCG ACTCTGCTTC TTTCAACGCT CAAAAATTTC	600
CATTCATCA CAAGAAACCC TCAAGATCAC ATCGAGGCTA GTTTTTGTAA AAAAATCGCC	660
AAGGCCATG GTTGTAGTGGG TTTAAAGAC GCTAAAAACT TGTTTTAAA ATCGCTTGC	720
TTTAAATCTT GCCCAGAAAT CTTTTAGAA AATAGCCTTA AACTTTTGA AGTGGAGTTA	780
GTGGAGAATG AAAAGAGCCA CAAGGAAGGC GAGATTTAG CAATTGATGA AAGAGGCCTT	840
CTTGTAGTTT GTTTGAAGG CAGCGTGCCT ATAGCAAGGT TGCAAGCGGT GGGTAAAAG	900
CCTTTGAAG CGAAGGATTA TTTGAATGGC AGGCCTTGA AAGTGGCCGG TATTCTAAC	960

## (2) INFORMATION FOR SEQ ID NO:1142:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...513

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142

AAAAGCACAA GGAAAACAAT AATGGAAGCG CAATTACGAT TTACGGGTGT TGGAGGGCAA	60
GGCGTGTGT TAGCGGGAGA GATTTAGCT GAGGCTAAGA TCGTGACCGG GGGCTATGGC	120
ACTAAGACTT CCACCTACAC TTCGCAAGTC CGTGGAGGTC CCACTAAAGT GGATATTTC	180
TTAGATAAAAG ATGAAATTAT TTTCCTTAT GCTAAAGAGG GCGAGATTGA TTTCATGCTT	240
TCAGTCGCTC AAATCAGCTA CAACCAAGTTT AAAAGCGACA TTAAAAAAAGG CGGTATCGTT	300
GTCATTCGATC CCAATCTAGT AACCCCCACT AAAGAAGATG AGGAAAAATA CCAGCTTAT	360
AAAAATCCCTA TCATTAGTAT CGCTAAAGAT GAAGTGGGTAA ACATTATCAC GCAATCTGTG	420
GTGGCGTTAG CCATTACCGT GGAGCTGACT AAATGCGTGG AAGAAAATAT CGTTCTAGAT	480
ACCATGCTTA AAAAAGTTCC CTGCAAAAGT CGC	513

## (2) INFORMATION FOR SEQ ID NO:1143:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

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(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...1284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143

GCATGTTTAA AACAAAGAAA TATTACTAAT ACGCAGATAT TGCATATCGG TGATAATTCT	60
TGGGCAGATG ACAGCTATGCC TAAAAGTTTA GGCATAGCAA CGCTATTAG AAAAACCGTG	120
TTGAAACAAT TAGAAGAAGT TTTTCCTAAA TACAAACAT TTAATCCAAC CAGTGTGCG	180
CAAAGTTTAA TTTAGGATC TTATGCGTT TTTTATAAAA ATTATATTCA AAAACATGAA	240
AAATTGATT ATTGGTTCTC TTAGGAGCG ATGCAGGCAG GAATTGCAGC CGTTGCTTAT	300
TGCCAGTTIA TCTATAAGGA GATTCACAAA AGAAATATTG ATACITTTAGT GTTGTGCG	360
CGAGATGGTT ATTATTGCA AAAAATTTTT AATATTTTAT ATCCAAATTG ATATAAAACT	420
ACTTATGCT ATGCTCCCAG AAATTAAAAA AAAGCGGTAT TTTTAGAAGT CGTAGAGGGC	480
GAGAGTTGG AAATTGGCG TATTTTAGAA GGCGAAGAAG AAGTTAAAAA GAAGCAAATC	540
ACCACCAACC AACAGGCGTA TGTATATCTC TATAGCAATT TTGAAACATTG CCGCCATTAA	600
CGGTTAAAT GTTGTAGATAA TTACAGAAAA TACTTGTTTT CATCAAATTG AGAAGGAAAT	660
ATCGCTATTG TAGATACGAT TACTTTAGGC TATTCTTCGC AAGGGTTAAT CCAAAAAGCT	720
TTAAATAAAG AAGTTTTTGG GTGCTATGTG GATCTCCTAA GAATTTAAA TTATGATTGC	780
GTGAGTTCT TACCTTTTC ACACCTAAA CCCGTTTATT TTCTATAATTG GGATTTTATG	840
GAGTTTTGCA TAAACAGGCC TGAATACCTT ATTAAAAATG TAGAAAATGG CGTICCAATC	900
TATCAAAAG ACGTTTCATC TTGIGAAAAA CACCGCTCTA AAGCTTATGA AAAAATAGTA	960
GAAGGGGCTG TTGGATAATGC TTCATATTAA AAGAAAGTC AAATTCTTT AGACATTCAT	1020
GATGTGATAG AATGGGTGAA TTCTTCATT GACAATCCTA GTATTCAAGA TCAAGAGCAA	1080
TTCAGACAAA TTATTTCTC TCCAGACGGC ACGCATAAAA ACGCTCTGCC CTTGTTTGC	1140
AACGATGTTT CTITGTTGTC TTGTATTITA AAGCCTTCAC AAAGTTATAG CGTATTAAAAA	1200
AGGAGTCTTA GGACAAACAA GCAAGAGAGG TTGTTTAAA TATIGTCTCT AATTAAAAAA	1260
ATCTATGGGA AGTTAAAAAA GAAA	1284

(2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144

GGGTTATTAG CTTGTTTGCT GGTCTTACTC AATCTAAAGA TTACGCCGAA TTGATGTGG 60

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CCTTTAGATA TTATTGTGGT	TGTGGCATGG GTGTTATGGG	GGGTTAATAT	GTTTGGGAGC	120
ATGAGCGTTA GAAGAGAGAA	TACTATTAT	GTGCTTTGTG	GGTATTACAT	180
GTGGGTATAG CGGTGATGTA	TATCTTCAAT	AACTTTCTA	TCCCCACCTA	240
GATATGGGA GCGTTGGCA	TTCTATTCT	ATGTATTCA	GCAGTAATGA	300
CAATGGTGGT GGGGGCATAA	TGCGGTGCGCT	TTTGTCTTTA	CGAGTGGGGT	360
ATTTATTATT TCTTGCTAA	AGAGAGCGGC	CAGCCTATCT	TTTCTTACAA	420
TTTCTTTTT GGAGGTTGAT	GTTTGTGTTAT	ATTTGGCCGG	GCGGGCACCA	480
TCCACCGTGC CTGATTGGT	ACAAACCCCTT	TCTAGCGTGT	TTTCAGTGGT	540
CCTTGTGGG GGACACGGAT	TAACATGCTT	TTAACGATGA	GAGGCCAATG	600
AAAGAAAGCC CTTTGATCAA	GTTTTAGTT	TTAGCCTCAA	CTTCTACAT	660
CTAGAAGGCT CAATTCAAGC	CATTAAAAGC	GTGAACCCCT	TAGCCCACCT	720
ATTATAGGGC ATGTGCATGA	CGGCGTGCCT	GGGTGGGTAG	GCTTCACTTT	780
ATGTATCACA TGACCCCTAG	GCTTTCAAA	AGAGAGATCT	ATTCAGGAAG	840
TTCAATTTT GGATCATGAC	TTTAGGGATT	GTGCTTTACT	TTTCGTCCAT	900
GGGATCAGC AAGGGATGAT	GTGGAGGGAT	GTGGATCAA	ACGGGAATCT	960
TTCATGACA CGGTTAAGGC	GCTAATCCCT	TATTACAATA	TTAGAGGCCT	1020
ATGATTTTA TTGGATTAT	TATTTTGCT	ACAATATCT	TTATGACAAT	1080
AAAAAATTAG AGCGTGAGCC	CAATTACGCC	ACGCTATGG	CCAGA	1125

## (2) INFORMATION FOR SEQ ID NO:1145:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 903 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...903
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145

GGTTTGTGATG ACGATATGGA	AATTAGAAAAC ATCAAAGAGT	TTGAAAAAGC	TTCCAAAAAA	60
CTCCAAAAAAG ACACTTTAA	GATCGCTCTC	GCTCTTTGT	TCCTCATTTG	120
CTCGCTCTCA TTTTTGGCA	GGCTAATTCT	AAGGGATTGT	TGCTCATCTT	180
ATTGGGGGGT ATATGGCGAT	GAATATTGGC	GCGAACGATG	TGCTCTAATAA	240
TCCGTAGGCT CTAAAGCCAT	TAGCATGGGT	GGGGCGATTT	TGATCGCTGC	300
ATGCTAGGAG CGATCATTTG	TGGGGGGGAA	GTGGTTCTA	CGATTAAGGG	360
TCGCCTGAAT TTATTAACGA	TGCGCATGTT	TTCATTAATG	TCATGTTGGC	420
AGTGGGGCGT TATGGTTGCA	TGTAGCCACT	TTAATAGGG	CTCCCGTTTC	480
TCCGTAGTGG GAGGGATTAT	GGGGGCTGGA	ATGGCAGCAG	CTGGAATGTC	540
TGGCATTTTT TATCGGCAT	TGTGGCTAGT	TGGGTATCT	CGCCCTTTAAT	600
ATAGCCATGT TTTCATTTAAT	GCTCATTAAA	AAGACTATCG	CTTATAAAGA	660
AGCGCGGCGTT TAAAGGTCGT	GCCTTATTG	GTGGCGTTGA	TGAGCTTAGC	720
TATTGATCG TGAAGGTTT	AAAACGCCTC	TATGCGGTGG	GTGGTAAAT	780
TGCGGTGTG TCCTTGCCT	TTTGATTTT	ATCCTTTTA	AAAGATTG	840
GCCCCGCAAT TAGAAAATAG	CCACGAAAGC	GTCAATGAGC	TTTTTAATGT	900
TTT				903

## (2) INFORMATION FOR SEQ ID NO:1146:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1296 base pairs

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(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146

AGAATGAAGC	TTAAAAAAAC	CCTGACTTAT	CAACACCACG	CCTATTCTTT	TTTAAGCGAT	60
AACACGAATG	AAGTTTTAGA	AAACCCAAA	GAAATCCTTT	TTGTCAAAC	GCCTTTAAC	120
AAAAAAATACG	CCCCTTTAAT	CGCAGAAAAA	AACCTGGCTA	TTTGGATT	TAACGAGCTT	180
AAAACACT	TTGATTITAA	GATTAAGATT	GTAGGGATTA	CAGGCACTAA	TGGTAAAACG	240
ACCACAGCGA	GCTTGATGTA	TTCCTTGCTC	TTAGATTGTA	ATAAAAAGAC	CGCTCTTTA	300
GGCACAAAGAG	GGTTTTTTAT	CGACGACAAA	CACATCAAAG	AAAAGGGCTT	GACCACGCC	360
ACTCTTTAG	AGCTTATAG	CGATTGGAA	GAAGCGATTC	GTAAAATG	CGAATACTTC	420
ATTATGGAGG	TGAGCTCCA	TGCGATTGTC	CAAAAACGCA	TGCGTGGGCT	TGAITTCGCT	480
CTTAAATTTC	TCACCAATAT	CACAAGCGAT	CATTAGATT	TCCATCAAA	TATAGAAAAT	540
TACAGGGACG	CTAAAAACAG	CTTTTTAAA	GATGAGGGCT	AAAAAGTCAT	CAACAGAGAT	600
GAAACAAACG	CCCTTTTAA	CCCCATTAAC	GCGCGACTT	ACGCACTGGA	TAAAAAAGCG	660
CATTGAAAT	TTCAGGCCTT	TTCGCTCAAC	CCTTCATTA	GCGCGTCTTT	ATGCTACCAA	720
CACGATTTAA	GAGATCCAA	TCTTAAAGAA	ACCGCCCTGA	TCCATTCCCC	CCTTTTAGGG	780
CGTTACAACC	TTTATAATAT	TTTAGCGGGC	GTTTTGGGG	TTAAATTGCT	CACTCAATTG	840
CCTTTAGAAA	CGATCGCACC	GTTATTGGAA	AACTTTTATG	GGGTTAAGGG	GCGTTTGGAA	900
ATTGTACATT	CTAAACCTTT	AGTGGTCGTG	GATTTGCC	ACACAACAGA	CGGCATGCAA	960
CAAGTTTTG	AAAGTTTAA	AAATCAAAG	ATCACCCTC	TTTTGGGCG	AGGGGGCGAT	1020
AGGGATAAAA	CCAAGCGCCC	TAAAATGGGA	GCGATAACGA	GTGTTACGC	GCATCAAATC	1080
ATCTTAACCT	CAGACAATCC	TAGAAGCGAA	AACGAAGAAG	ACATCATTAA	GGATATTTTA	1140
AAAGGCATCA	ATAATTCTTC	TAAAGTCATT	GTAGAAAAAG	ACCGAAAAAA	GGCCATTGAA	1200
AACGCTTTAG	AAAATTTAA	AGACGATGAG	GTGTTGTTGA	TTTACGCAA	GGGCATGAA	1260
AACATTCAAA	TCTTAAAGA	CAAAACGATT	TTTTTT			1296

(2) INFORMATION FOR SEQ ID NO:1147:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 981 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147

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AGATTATTAT	CTCAATTAA	AACAAGGATA	AACATGCAAG	AATTCAAGT	TGTGGTGCGAT	60
TTTATAGAAA	GGGATTTTT	AGAAAACGAT	TTTTAAAGC	TCATCAATAA	GGGGGCTATT	120
TCCGGGGCGA	CGACTAACCC	TAGTTGTTT	TGCGAACCGA	TCACAAAAAG	CGCGTTTAT	180
CAAGATGAAA	TCGCTAAACT	CAAAGGCAA	AAAGCTAAAG	AAATTATGA	AACTCTGGCA	240
CTAAAGGATA	TTTTACAAGC	CTCTAGCGCG	TTAATGCCCT	TGATGAAAAA	AGACCCTAAC	300
AACGGCTACA	TCAGCCTAGA	AATTGACCCC	TTTTAGAAG	ACGATGCGAT	AAAAGCATT	360
GATGAAGCCA	AGCGGTTATT	CAAAACATTA	AACGCCCCA	ATGTGATGAT	AAAAGTCCC	420
GCGAGTGAAA	GCGCTTTGA	AGTCATTAGC	GCTCTGGCTC	AAGCCTCTAT	CCCCATTAAAT	480
GTAACTTTAG	TCTTTTCGCC	AAAATTGCC	GGTGAATCG	CTCAAATCTT	AGCCAAAGAA	540
GCACGAAAAA	GAGCGGTCA	TAGCGT	GTCTCACGAT	TTGACAAAGA	AATAGACCCA	600
CTAGTGCAC	AAAATTGCA	AGCTCAAAGT	GGGATCATGA	ACGCTACC	GTGTTATTAT	660
CAAATCAACC	AGCATCTAA	TAAGCTATAA	AGCACCTTT	TTGCATCCAC	CGGGCTTAAA	720
TCTAATTCTT	TAGCTAAAGA	TTACTACATT	AAAGCGCTGT	GTTTTAAAAA	CTCTATCAAC	780
ACAGCCCCC	TAGACGCCCT	AAACGCTAT	TTGCTTGACC	CAAACACCGA	GTGTCAAACC	840
CCTTAAAAAA	TCACAGAAAT	TGAAGCGTC	AAAAAAGAAT	AAAAAACGCA	CAATATTGAT	900
TTAGAAAACA	CCGCCAAAAA	ACTCCTAAA	GAAGCGTTGA	TAGCGTTCAA	ACAATCCTT	960
GAAAAGCTTT TAAGCAGTTT T						981

## (2) INFORMATION FOR SEQ ID NO:1148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148

GGGTTTAAAG	TGGCTTTGTT	TAGATTGTG	GGGTGGTATT	ATTTCAAATA	CTTTTTAA	60
GTGCTTTAG	CTTGGAAATT	GTTTTTGTA	GCCATGACA	GCCTGAAATA	CGCCGATAAA	120
ATGCCCTGATT	CTGCGAACAT	GATCATTATA	TTTTTCACCT	ATGATATTIT	ATTCGCTCTC	180
AATTACACCT	TGCCCATTT	CTTGCTTTA	GCGATGGTT	TATTTTATAT	CACCTTCATT	240
AAATCCAACC	AATACACCGC	CCTGCTCTCT	ATGGATT	CCAAATGCCA	GATTTTAAGC	300
CCTTTTTT	TGATTAGCCT	GT	CTGTTTATG	TGGGGTTGAA	CGCGACTCCT	360
TTTGTGTATA	TGAAGAAAAA	AACGCAAAT	TTAATTATA	AAAGACAATC	TTTGAGCGTT	420
TCAGAGCATT	TGTTAGTGA	ATACAACGAT	GATTAGCTGT	ATTTGATAA	GATTAATCCC	480
TTAATGCAAA	AAGCCAAAAA	TATCAAGGTT	TTTCGCTTAA	AAAGATAAAAC	TTTGAATACT	540
TATGCTGAAG	CTAAAGAAGC	TTTTTTGAA	GACAAATTAT	GGATTTTACA	TGACACTACT	600
ATCTATGAGA	TGCCCTTGAG	TTTGAAC	GGCGCGAACG	CTTAAACAC	CACGCATTTA	660
GAAACCTTTA	AAACGCTAA	AAATTCCGC	CCTAAAGTTT	TAGACACCAT	TTATCAAAC	720
AAGCTCGGG	TTTCTATCAC	AGACGCTTT	TTATCCTTGC	ATGCTTTAGT	CGGCCAAAAC	780
GCGGACACCGA	AAAAAGTGCG	CTCGTTT	TATGTTGTTG	CGATTTTGCC	CTTTTTGTG	840
CCGTTTTAA	CGCTTTAAT	CGCTTATTT	TGCGCCAGTC	TCGCCCGCTA	TGAAAACCTG	900
GCTCTTTAG	GGCTAAAGTT	TATCATTATC	ACGCTCGT	TTTGGGGGCT	ATTCCTTGCT	960
TTAGGGAAGT	TCAAGCATTTC	AGGGATACTC	ATTCTGAA	TAGCGTTCT	ATCGCCCTT	1020
TTCGTATTTC	TAGCTCTCGAG	TCTTTGGTAT	TTTAAAAAC	TTAATAAGAG	ATTG	1074

## (2) INFORMATION FOR SEQ ID NO:1149:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1377 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...1377
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149

AAGAGAAAGAG	TGGTGAAATT	CTATACTTAT	AGTGGGGAAA	CGGCCGCTGA	AGCTTTAAAG	60
ATCGCTCAAA	GCCACCATGG	GGTGGATACG	CTGGTGTGTA	AAACCCAAGA	AATCCGTAAA	120
AAAACGCTCA	CTTCCTCTGG	GCTTTATGAA	ATCGTGTGTTG	CGGTTGAAGA	AGAAGAAAAC	180
AAAAAGCCC	CCCTCATTCC	AGAGACTTGTG	TATGATGAAG	AATTGAATGA	AGAAGACGTG	240
GTCATGCAGC	TTTCAAGCAC	CGTAGAAGAA	ATGCCAAAC	TCCCGGGGT	TTCATCTAAC	300
CAGCGCAACT	ATACTTTTTC	AAAAATAAG	ACTCTTTAG	AAAAGACGC	TCCATTAGAG	360
GATACGCCCT	TAGAGGCTAA	TAAGCAAGAC	GCCTTGTG	AAAGCTTAAA	AGATGAAGCC	420
AACCATAAAA	AAGAAAGAGA	AAAAAGAGAA	GTCAAACAAG	AAAGAGAAAT	TAAAGATATT	480
AATGCGCAAC	TAAGTAAAAT	CAGAGACAGC	TTAAAACTCA	TTCAAAACAT	GTGTTGGGAT	540
GAGAAAACC	CTAATCTGT	CAATATCCCT	CAAGAATTG	CCGAAATTAA	CAAACTAGCC	600
AAACAAAGCG	GCATGAAATC	CACTCATTTA	GATGAAATCA	TGCAATTAAAG	CCTGGAATTG	660
ATGCCCTTAC	GCATGCGGGAA	AAATTCCGTA	ACGATCAAGC	GCTATTTAG	AGAAGTGTG	720
CGTAAATAA	TCTCTGTGCG	CCCTGAAGAT	TTGAAATTGA	GGCAAAAACG	CATTAAATG	780
CTTGTAGGGC	CAACAGGCGT	GGGGAAAACG	ACGACTTGG	CTAAATTAGC	CGCACGCTAT	840
TCTAGAATGC	TGGCTAAAAA	ATACAAGGTG	GGCATTATCA	CTTTAGACAA	TTATCGCATT	900
GGGGCTTTGG	AGCAATTGAG	TTGGTATGCT	AATAAAATGA	AAATGAGTAT	AGAAGCGGTG	960
ATTGACGCTA	AGGATTTTGC	AAAGAAATT	GAAGCTTGG	AATACTGCGA	TTTTATTTA	1020
GTGGATACGA	CAGGGCAATTC	GCAATACGAT	AAGGAAAAAA	TTGCCGGTTT	GAAAGAGTTT	1080
ATAGATGGGG	GTATATAATAT	TGATGTATCC	TTAGTGCTTT	CGGTTACAC	TAAGTATGAA	1140
GACATGAAAG	ATATTTATGA	TTCTTTGGG	GTGTAGGGG	TTGACACTTT	AATCTTTACG	1200
AAATTAGATG	AGAGTAGGGG	GTAGGGAAAT	TTGTTTTCTT	TAGTCATGA	AAGCCAAAAG	1260
CCTATCAGTT	ATCTTTCTGT	CGGCCAAGAA	GTGCCTATGG	ATTGAAAGT	GGCTACTAAT	1320
GAGTATTTAG	TGGATTGCAT	GCTAGATGGC	TTAGTAACC	CTAATAAGGA	ACAAGCA	1377

## (2) INFORMATION FOR SEQ ID NO:1150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1065 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature

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## (B) LOCATION 1...1065

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150

ATCATGGCTG ATATTTAAAG CCAAGAAGAA ATTGATGCAG TTTTAGAAGT CGTTGATGAG	60
AATGTGGATA TTCAAAATGT CCAAAAAAAA GATATTATCC CCCAACGCAG CGTAACCCCTC	120
TATGATTTCA AGGCCCTAA TCGTGTGAGT AAGGAGCAAT TGCGCTCTTT TAGGAGCATC	180
CATGATAAAA TGGCTAGGAA TCTTTCCAGT CAAGTCTCTT CTATCATGC G TTCTATTGTA	240
GAAATCCAGC TTCATAGCGT GGATCAAATG ACTTATGCCG AATTTTGAT GAGTTTGCT	300
AGCCCTACGA GTTTTAATGT CTTCATGCATG AAGGCTATGG GGGGAACGGG GGTGTTAGAG	360
ATTAATCCTA GCATCGCTTT CCCTATGATT GACAGACTAT TAGGGGTAA GGGGAGCCGC	420
TATGATCAAA ACAGGGAGTT TAGCGATATT GAATTGAAT TATGGGATAC GATTTTACGC	480
CAGGTGAIGC AAATTTAAAG AGAAGTGTGG TCGCCGTG TGGAGATGTA TCCTACCAT	540
GACGCTAAAG AATCCAGCGC GAATGTGGTC CAAATCGTCG CTCAAAATGA AATTTCTATC	600
ATGGTGGTT TAGAGATTAT CATTGGCAT AGCCGTGGGA TGATGAATAT TTGTTACCCG	660
GTGATTTCCA TTGAGAGCAT TCTTTCTAAA ATGGGAGTA GGGATTTCAT GCTTTCAGAA	720
ACGAACCTCA AAAAGAGCCG TAATAAGGAA TTGCAAGCAC TATTGAGCGG GGTGAGCGTG	780
GATATGATGC TGTTTTGGG CGCGGTGAA TTGAGTTGAG AAGAAATGTT GGATTTAGAT	840
GTGGGGATA CTATCCGGTT GAATAAAAGTC GCTAACGATG AAGTGAGCGT GTATGTACAT	900
AAGAAAAGC GTTATTTAGC GAGCGTGGG TTCAAGGGT ATAGGAAAAC CATTCAAATT	960
AAAGAAGTGG TTATAGCGA AAAAGAACGC ACTAAAGAAA TTITAGAAAT GCTAGAAGAA	1020
CAGCGCAGAG GCAAAGTGGG CGATATTATC AAGATAGAAG AAGAG	1065

## (2) INFORMATION FOR SEQ ID NO:1151:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...891

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151

GGAPACAAGCA TGAGTAATCA ACCGAGCCAT TTGGATAATT TTATGAACGC TAAAAATCCC	60
AAAAGTTTTT TTGATAATAA GGGGAATACC AAATTCATCG CTATCACAAG CGGTAAAGGGG	120
GGCGTGGGAA ATATCAACAT TAGCGCTTAT TTAGCTTACT CTTTATACAA GAAAGGTAT	180
AAGCTAGGGG TATTGATGC CGATATTGGT TTAGCGAATT TAGATGTAT TTTTGGGTG	240
AAAAACCCATA AAAATATCTT GCATGCCCTA AAAGGCGAAG CCAAATTGCA AGAAATCATT	300
TGCGAGATTG AACCCGGGCT TTGCTTAATC CCTGGGGATA GCGGCGAAGA AATTTAAAA	360
TACATCAGCG GCGCGGAAGC TTGGATCGA TTCGTAGATG AAGAGGGGGT TTAAAGCTCT	420
TTAGATTATA TTGTGATGAG TACGGGTGCT GGGATTGGG CCACTACGCA AGCGTTTTG	480
AATGCGAGCG ATTGCGTGGT GATTGTTACC ACACCCGATC CTTCAAGCGAT TACCGATGCG	540
TATGCCATGCA TAAAATCAA CTCCAAGAAT AAAGATGAAT TGTTCTTAT CGCTAACATG	600
GTAGCCCAAC CTAAAGAAGG CAGGGCGACT TATGAAAGGC TATTCAGGT GGCTAAAAAC	660
AATATCGCTT CATTAGAATT GCACTATTG GGGCGATTG AAAACAGCTC CTTATTGAAA	720
CGCTATGTGA GGGAGCGAAA GATTGAGG AAAATAGCCC CTAACGATTG GTTTTCGCAA	780
TCCATTGACC AGATAGCGAG CTTTGTAGTT TCTAAACTAG AAACCGGCAC TTTAGAAATA	840
CCAAAGAAG GTTTAAAAG CTTTTTAAAG AGGCTTTGAG AGTATTGAG	891

## (2) INFORMATION FOR SEQ ID NO:1152:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1593 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152

ATITCGGAGT	TTAACCCACCG	CAGTGCCT	TTAACATTA	ATTATGTGAA	TACCATT	60
AAAAAAAGCTT	ATCAAAATTC	ACCCACCGCT	TACTTGGAGC	AAAAATACCC	TAAAAC	120
AACAATAAAC	ATGTTACAGA	GGGCTATGTT	AAAGTCTCTT	TAGTGGCTGA	TGAAAAAAGAA	180
TTGTTATTAG	AACAAATCTT	ACAAGAAGCT	CAAACCTTT	TAGAACATCG	TATTGATCCT	240
AAAGACATTA	CCATTGTTG	CGCCACCAAT	AAGGACCGCTT	TAGAAATCAA	AAATTATTG	300
CAAGAGTATT	TGAGCGCAAT	TCGCCCAGC	ACGGAATCTA	CGCGAAATT	GTCTCAATTG	360
GTAGAGTCTA	AAATCATTAA	GAACGCTTTA	GAATACGCTT	TAGCGGAAGA	ACCTTACAAG	420
CCCTTTTATA	AACACAGTGT	TTTAAAAC	GCTGGATACT	TGCATGATGA	TGTGATCGCT	480
TTACCTGGTT	TTAACCCCTAA	AAAAGAGAGC	GTGGCAAGCT	TTGTGTGGAA	AATTATGGAG	540
CAGTTAAC	TTTATGAAGA	GCCTGCGCAA	AGCTGTTG	AATTAGCGGT	TGGGTGCGAA	600
GACGCCGATG	GATTTTAGA	AAAATTAGAG	GCTAAAGAGA	TCGCTTCTTT	CAATCCAAA	660
GGCGCCGAGA	TCACTGACCAT	TCATAAATCT	AAAGGCATGC	AATTCCCTTA	TGTGATCTG	720
TGCGAACGCT	TGGCAATCC	TAATTCAAGC	CATGCCAATC	AACCTCTTGA	AGAATATGAC	780
GGCACAGAGC	TTGCGCGCT	TTATTACAGA	ATGAAAATC	GTGAGGTGGT	GGATAAAGAT	840
TACGCCAGGG	CTTTAGACAA	AGAAGAAGCG	GCTAAAGATC	ACGAAGAAAT	TAATGTCAT	900
TATGTCGCAT	TCACTAGGGC	TGAGTTAGGG	CTGATTGTCG	TGGCCAAAGA	CAAGAAAGAA	960
AGCAAAAAG	AAAGCAAAAA	CAAAAAAATG	CACCAACAAT	TGGAACCTCGC	ACCTTTAGAA	1020
GAGGGAGAAA	TCGCGCCGGT	TATTCTCCT	CAAAAGAGC	CTTTAATGAC	AAGCGTTGTC	1080
ATCAAGCCCC	ATGCTATGG	CGAGCAACT	CAAGAAATAG	AAGAAGAGTC	AGATAGCGAT	1140
TATGAAAAGA	ATAACGACCA	GGAAGCGATC	AATTGGTA	TCGCCCTTGCA	TAAGGGATTG	1200
GAATACCAAT	ACGCTTACAA	CATTCTAA	CAAAGCGTT	TAGAATATT	AAACTACCAC	1260
TATGGTTTT	ATGGTTGGA	TTACCAAGCG	TTAGAAGAAA	GTTAGAGCT	TTTTGAAAAC	1320
GATCGAGGG	TACAAGCCCT	TTTTAAAAT	CATGCCCTAA	AGGGTGAAGC	GGCTTTTTTA	1380
TTCCAAGGG	TTGTGTCTAG	GATTGATGTT	TTATTGTGGG	ATAGAGGGCA	AAATTGTAT	1440
GTTTTAGATT	ATAAAAAGCT	TCAAAATTAC	CAGCAAAGCC	ATAAAGCGCA	AGTGTCTCAT	1500
TACGCTGAGT	TTTGCGAAC	TCAAGCCCCC	CATTAAAGA	TACAAGCGGG	CATTATTTAC	1560
GCTCATAAA	GACTGCTTGA	AAAATTATGG	GTT			1593

(2) INFORMATION FOR SEQ ID NO:1153:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 759 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153.

TTATCAACCG	CTTATCAGGC	GGTAGAACCT	CATTGGTTC	TGAAAGCTGT	TCTAGTCCTG	60
GAGCGATCAC	CATCTTCACC	AGAAATAAAA	GGTATTTGGG	ATAGGGATTA	CCACACGCC	120
ATCACCAAGTT	CTTTCACCCCT	TGATGTGAGC	TATGACAACA	CCGATGATTA	TTATTTCCCT	180
AGAAATGGGG	TTATCCTTGT	TTCCTATGCG	ACAATGTCTG	GTTCGCCAAG	CTCTGGCAGC	240
CTCAATTCTT	GGAACGGGTT	AGGCGGGAAAT	GTCCCTAACCA	CCAAAGTTTA	TGGTAAATTG	300
GCCGCTTACC	ACCATTTGCA	AAAATATTTA	TTGATAGATT	TGATCGCTCG	TTTTAAAACG	360
CAAGGGGGCT	ATATCTTTAG	GTATAACACC	GATGATTACT	TGCCCTTAAA	CTCCACTTTC	420
TACATGGGGG	GGCTAACACCAC	GGTGAGAGGC	TTTAGGAACG	GCTCAATCAC	ACCTAAAGAT	480
GAGTTTGGCT	TGTGGCTTGG	AGGCGATGGG	ATTTTTACCG	CTTCTACTGA	ATTGAGCTAT	540
GGGGTGTAA	AAGCGGCTAA	AATGCGTTTA	GCCTGGTTTT	TTGACTTTGG	TTCTTAACC	600
TTTAAAACCC	CAACTAGGGG	GAGTTCTTC	TATAACGCTC	CCACCACGAC	GGCGAATTT	660
AAAGATTATG	GGCTGGTTT	GAAAGGGCGA	CTTGGAGGGC	TTCTACAGGC	720	
TTACAGATTG	AATGGATTTC	CCCCATGGGG	CCCTGGGT			759

(2) INFORMATION FOR SEQ ID NO:1154:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 258 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154

GCGACGGATCA	TGCTTGATAAA	ACGCATTAAG	ACGCTTTAC	TTTTTTTGG	TCTTAATATG	60
GTCGTGTTGA	GCCTGAGTTT	TACCAATAAG	CCTCATTGT	TTTTTTGGTT	TTTAGTGTAA	120
GGTTGTTATT	TAGTTTATGA	GTGGCAAAG	AAACAAAAAA	AAGATTITCA	AAGCGCTAAA	180
AGTTTGAAAT	TTGACAGCGT	TAGCGAATTA	GAAAAGGATT	TGAACATGGA	AGTAACATAAT	240
GATGAATGGG	ATACCCAT					258

(2) INFORMATION FOR SEQ ID NO:1155:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 816 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155

TCACGGAGTG TTGAAATGAA CTACCTAAT CTACCTAACCA GCGCTTTAGA GATAAGCGAA	60
CAGCCAGAAG TGAAAGAAAT CACTAACGAG CTTTTAAAGC AATTACAAAA CGCTTTAAGG	120
ACCAACGCGC ATTGTTAGCGA GCAAGTGGAA TTAAGCCTTA AATGCATCGT TAGGTTTTA	180
GAAGTGTCTT TGAGTTTCTGA TTTTTTAAG AATGCGAATG AGATTGATAG CAGTTTAAGA	240
AATTCCATTG AGTGGCTGAC TAACGCCGGC GAGAGCTTGAA ATTAAAAAAT GAAAGAATAC	300
GAGCGCTTTT TTAGCGAGTT TAATACGAGC ATGCATGCCA ACAGAGCAGGA AGTAACCAAT	360
ACCTTAAACG CTAACGCCGA GAACATTAAA AGCGAAATTA AAAAGCTAGA AAATCAATTG	420
ATAGAAACCA CGACAAGACT TTAAACGAGC TATCAAATCT TTTTAAACCA AGCCAGAGAT	480
AACGCTAACCA ACCAAATCAC AAAAACACAA ACCCAAAGCC TTGAAGCGAT TACACAAGCT	540
AAAACAACG CTAATAATGA ATAAGCAAC ACTCAAACGC AACGATAAC TAATATCACC	600
GAAGCGAAAA CGAACGCTAA TAATGAAATA AGCAACAATC AAACGCAAGC GATAACTAAC	660
ATTAACGAAG CCAAAGAAAG CGCTACAAACG CAAATAACG CCAATAAGCA AGAAGCAATA	720
AATAACATCA CGCAAGAAAA AACCCAAGCC ACAAGCGAGA TCACCGAAGC GAAAAGACC	780
GATCATTATC AAAACATTGA TTTTTTGAG TTGAA	816

(2) INFORMATION FOR SEQ ID NO:1156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156

GGATTGTCGG TGTTAGAACG CTATGCGAAT GAAGAAATGA AAGCCCTATG GAATGAGCAA	60
ACCAAATTG AAACTTATTG GGAAGTGGAA AAAGCTGTCG TTAGGGCGTG GAATAAGCTT	120
GGGCAAATTC AAGATAGCGA TTGTGAAAAA ATCTGCTTAA AAGCGGCATT CAATCTTGAA	180
CGCATCAAG AAATTGAAAA AACCACTAAG CATGATTTAA TCGCTTTCAC TACTTGCGTG	240
GCTGAAAGCT TGGCGAAGA ATCCCGCTTC TTTCATTATG GGATCACTTC TAGCGATTG	300
ATTGATACGG CTATGGCGTT ATTGATGACCC AAAAGCTTAA AACTCATTCA AAAAGGGCTT	360
AAAAACCTCT ATGAAACCCCT TAAAATAGG GCTTTAGAGC ATCAAGACAC GCTAATGGTG	420
GGCAGAAGCC ATGGGGTGTGTT TGGCGAACCC ATCACCTTGT GTCTAGTTTT AGCTCTTTT	480
GCTGATGAAA TCAAACGGCA TTTAAAGCC CTGGATTAA CGATGAAATT TATCAGCGTA	540
TGGCGATCA GTGGGGGTCT CGCGAATTTC GCGCACGCC CTTTAAATT AGAAGAATTA	600
GCGTGGGAT TTTAGGCTT AAAACCGCT AATATCAGCA ATCAAGTCAT TCAAAGAGAC	660
CGCTACCTA GGCTTGCATG CGATCTGGCT CTTTAGCGA GCAGTTGTGA AAAATCGCT	720
GTCAATATCC GCCATTGCA ACCGAGTGA GTCTATGAG TGGAGAAGC TTTTCAGCA	780
GGCAAAAGG GAAGCTCTGC GATGCCCTCAT AAAAGAAACC CCATTTGAG CGAGAATATC	840

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ACCGGGCTTT	GCAGGGTGAT	TCGCTCTTT	ACTACCCCCA	TGCTAGAAAA	TGTCGCCCTA	900
TGGCATGAAA	GGGACATGAG	CCATAGCTCT	GTGGAGCGTT	TTGCGCTGCC	TGATCTGTTT	960
ATCACCAGCG	ATTTCATGCT	CAGCCGTTTG	AATAGCGTGA	TTGAAAATCT	GGTGGTTTAT	1020
CCTAAAAACA	TGCTTAAAAAA	TTTAGCTTTG	AGTGGGGGGC	TAGTCTTTTC	GCAACGGGTG	1080
TTATTGGAAT	TGCCTAAAAAA	AGGTTTGAGC	AGAGAAGAAA	GCTATTCTAT	CGTGCAAGAA	1140
AATGCGATGA	AAATATGGGA	GGTTTTGCAA	CAAGGCGCTT	TTAAAAAACGC	TGATGAAAAT	1200
TTATTTTAA	ACGCCCTACT	TAACGATGAA	CGCTTGAAAA	AATATTGAA	TGAGAGCGAA	1260
ATCAGAGCAT	GTTTTGATTA	CAGCTATTAC	ACTAAAAATG	TGGGGCGAT	TTTTAAAAGG	1320
<b>GTGTTTGGAA</b>						1329

## (2) INFORMATION FOR SEQ ID NO:1157:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 291 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...291
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157

AATGATAGTG	GCTCAAAACA	TTTCATCTTG	CCTTTTTAA	CGCTCCTTTT	GCAAATGTAT	60
TTGAGCCGCA	CACGAGATA	CATGGCCGAT	AGGGGGCGG	CGTTTTAAAT	GCATGACAAT	120
AAGCCCATGA	TCAGAGCCTT	ACAAAAGATT	TCTAACGATT	ACACCAACAA	CGATTATAAA	180
GAAATAGATA	AAAATAGCAC	CCGATCAGCG	GCCTATCTTT	TTAACGCTGA	AATGTTTAGC	240
ACCCACCCCTA	GTATTAAAAAA	TCGTATCCAA	TCCTTAAGAA	AGCGTGTGAT	C	291

## (2) INFORMATION FOR SEQ ID NO:1158:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 540 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...540
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158

ATGGAAAAAT	TTTTCAACCA	ATTTTTGAA	AACATCGGCG	AAGACAAGAA	TCGAGAAAGGT	60
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TTGAAAGAGA CGCCTAAAAG GGTCAGAGA TTATGGAAT TCTTGTATAA A-----	140
GAAGATCCTA GAGGGCTT AAAAGCGCG TATTTCAAG GCGTTTGCAG TGAAATGATA	180
GTGGCTAAA ACATTGAAATT TTACTCCACT TCGGAGCACC ATTTGCTCCC TTTTTTGCGG	240
AATATTAGCG TCGGATATAT CCCTAAGGA AAGATTGTAG GCATTAGCGC GATCGCTAAA	300
CTCATGGAA TTTATAGCAA ACGCTGCAA ATCCAAGAAA GGCTGACAC TCAAATGCA	360
GAAACTTTG ATGAAATCAT AGAGCCAAGG GCGGTGATCG TGGTTTGTGA AGCCAAGCAC	420
TTGTGCATGA CGATGCAAGG GGTGCAAAAG CAAAATGCGA TCATTAACAC AAGTGTGTTA	480
AGAGGCCTCT TCAAAAAAGA CCCTAAACAG AGAGCTGAAT TTATGCAACT CTTAAATCT	540

## (2) INFORMATION FOR SEQ ID NO:1159:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159

GTTATAATTCTAGGCATGAG TAACCCTAAT TTATCCTTTT ATTGTAATGA GTGCAGCGT	60
TTGAAAGCT TTTTAAAAAA CCATTATTTA CACCTGAAG GCTTCCACCC TTATTTGGAA	120
AAAGCCCTTTT TTGAAATGGT GCTTAATGGG GGCAAAAGGT TCCGCCCAA GCTTTTTTA	180
GCCGTGCTTT GCTCTTTAGT GGGTAAAAAA GATTATTCTA ACCAACAAAC AGAATATTIT	240
AAAATCGCTT TAAGCATTGA ATGCTTGAC ACTTATTCGC TCATCCATGA CGATTTGCCT	300
TGCATGGATA ACGCTATTTT AAGAAGAAC CACCCCACTT TACACGCCA ATACGATGAA	360
ACACACGGG TTTTATCGG CGATGCGTC AACACCTATT CTTTGAAATT GCTCTCAAAT	420
TCTTITACTAG AAAGCGGTAT CATTGCGAA TTAGTCAAA TCTTAAGCGC TAATGGGGGG	480
ATTAAAGGCA TGATTTTAGG GCAGGTTTG GATTGCTATT TTGAAAACAC CCCCTTAAAT	540
TTAGAGCAGC TCACCTTCCT ACACGGCAT AAAACCGCTA AATTGATTAG CGCAAGCCTG	600
ATTATGGGGC TTGTTGCGAG CGGCATTAAC GATGAAGAGC TTTTAAAATG GCTTCAGGCT	660
TTTGGGTTAA AAATGGGTCT TTGTTTCAA GTGCTAGATG ATATTATAGA CGTTACACAA	720
GATGAAAAAG AAAGCGGTAA AACCAACGCAT TTAGACAGCG CTAAAAACAG CTTTGTGAAT	780
TTATTGGGGC TAAAAAAGGC AAGCGGTAC GCCCAAACCTT TAAAAACAGA GATTTTAAAC	840
GATTGAATG CATTAGAACCT TACTTATCTT TCATTCGAAG AAAATTAAA CGCATTATTG	900
AACACTCTAT TTAAAGGCAA GACA	924

## (2) INFORMATION FOR SEQ ID NO:1160:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1041 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160

CTTCTCAATA CATCAAAGAA AAAGCGAACAT TTGAATTGGA ATTTTACTTG CCTAAAGGGA	60
GTTATGCGAG CGCGCTGCTC AAAGAAATCA AGCATGAGAA AGGAGAAAAT AATGACGAAT	120
TTTGAAAAGA TTATCGCGCA AAACAGCCCTC AAAACGAACG CGGTTTTAAC CACTTACTGC	180
GCGGATTTTG CTTTTATTGG GTTGTGGTG GATGCTATTAA GAATCAACGC TAATGATTTA	240
GGTAGAGCCC TTTTTAAACT CATGACTTTT CAAATTTTTC CTACGATTAC TATTGTCATG	300
TTTGTTGGTGG CTTTTGTAT TATTCTTGTGTT TGTATCCAAA ATTTTAGCTC TATCATGTTA	360
AGCGCCGATG AATACAAGCT TATTGACCCA AGCAAGGTTT TAAGCTCTAA AGAAAATCAA	420
ATCCATCGCC TTTTGTAGA GCTTTTAGAA GAGGCTAACG TTCATTTGAA GCCTAAGCTT	480
TATATCATTTA CATGAACGCT TTTGGAGCG GGTGGGATGAA ATCTAATTC	540
CTTATCGCTC TTACAAGCGC TTTAATAGAG AGGTTAGATA GAGACGAATT AAAAGCCGTG	600
ATCGCTCATG AGCTCAGCCA CATAAGGCCAACGACATCC GCTTGACCAT GTGCGTGGGG	660
ATTTTGAGCA ATATCATGCT ATGGTGGCT AATTTAGCG TGTTTTTTT CATGGGGAAAT	720
CGCAAGAATA CGGGGGCGAA TTTAGCCCGA ATGATTTTAT GGTTTTTACA GATCATCTT	780
CCTTTTTAA CGCTCCCTTT GCAAATGTAT TTGAGCCGCA CACGAGAAATA CATGGCCGAT	840
AGCGGGCGGG CGTTTTTAAT GCATGACCAAT AAGCCCATGA TCAGAGCCTT ACAAAAGATT	900
TCTAACGATT ACACCAACAA CGATTATAAA GAAATAGATA AAAATAGCAC CCGATCAGCG	960
GCCTATCTT TTAACGCTGA AATGTTAGC ACCCACCCCTA GTATTAACAA TCGTATCCAA	1020
TCCTTAAGAA AGCGTGTGAT C	1041

(2) INFORMATION FOR SEQ ID NO:1161:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 195 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161

ACACAGCCAC ACAAAAACAA GAGATTAAC AAGAGATTAAC AAGAGATTAA AAACAAGAGA	60
TTAAACAAGA GATTAACAA GAGATTAAC AAGAGATTAAC AAGAGAAACT AAACAAGAGC	120
AAGAAAAAGA AAATAAGCCT AAACAAAACA GTGTCCTGCC CGTTCAAAAC GATCAAAAAA	180
CCCCCACAAAC CCCCT	195

(2) INFORMATION FOR SEQ ID NO:1162:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 414 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

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- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...414
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162

GGGGTAAACA TGCTTATTTT	AGGACACCCCT TTAATCCCTA	GCGCTCGTT TGTTTCATT	60
AAAAACACCG ATGCTATTCA	TTCCAGCGCC AATAACGATA	TAGTGTGTTT TGAAGCAAAC	120
CCCCAAAATT TGGATTAGC	CCAATATTGC TGTGAAAATG	GCGTCCATT TAGCGTGATC	180
TTTTTATCGC ACAAGATAGA	GACGGACACC TTTTTTTAT	TCAACGCTTT CAAACCGCTC	240
TATTGTATT TTAAGGATAT	TAAGCAAGCC ATACTCGCCC	AACAAACACGC CACTAATTAC	300
TTGTTAGATA GAAAATCTT	GTTTTCTATG GATTTTAACG	ATACAGAGTC ATGGGAGATT	360
TGGCTAAAAA ATCAAATAGA	TGGTGTCTATT	TCTAAAGATT CACTCCTTTT GAAA	414

## (2) INFORMATION FOR SEQ ID NO:1163:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 402 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...402
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163

TTTAAATGCA ATCTTAAAG GAGAACTGCT	TGAAACTAC TGGTAGTAGA	TGATAGCTCA	60
ACTATGAGAA GAATTATTAA AAACACACTT	TCACGCTTAG	GCTATGAAGA	120
GCTGACCATG GGGTGGAAAGC	TTGGGAAAAAA	CTAGACGCTA	180
ATTACGGATT GGAAACATGCC	TGAAATGAAC	ATGCGGACAC	240
GATAACCGAT TTAAGGAAAT	CCCTATCATT	TAAGGTGCTT	300
GTCATTACGA CTTTAAAGC	ATGATCACCA	TCGTTAAAAA	360
CTTTTGAAG AAAAATTAGA	GGGCCTGAAT	GGTGCCTGCG	402
	AACTACATTG	TAAAGCTGAG	
	TGAAACCTTT	TACCCCCCAA	
	GGTGTCTTTA	GGGACAAACG	
	AT		

## (2) INFORMATION FOR SEQ ID NO:1164:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 840 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

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- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...840
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164

CGGGTTATGG	CGGTGCGAAT	CATGGCGACG	GTATGGACAA	ACTCATGCAA	GGAATTGGGA	60
CTCGTATCGC	TCTTTTAAG	CTTGTGGTG	CTAGTGGTGG	TGGGGCGTTT	TTTCATTAAG	120
GGGGCGTTT	ATGGGCTAA	AAATGGCGTT	TTGGGCATGG	ATTGAGCGGT	GTCTTTGGG	180
GCGTGTGCGG	CGTTTGTGTA	TCCTCTTAT	GCGATGTTGG	TGTCTCAAGA	GACCTATTT	240
GAAGCGAGCA	GCACGATTT	AACGCTTGT	TTTGGCTCTA	AGTTTTGGG	ATTAAGGCT	300
AGGCTGTGTTG	CGAATGAAAA	ATGTCTGCC	CTAGAACGCA	ATGAAATCCA	TAGCCTGATC	360
GTTGTAGAAA	ACGGCAAGCA	GATAGAAAAA	CACCTAAAG	ATGTGGCGAT	AGGCTCGGTT	420
GTTTGGGTGC	CAACGGGGC	AAAATCGCT	TTAGATGGCG	TGCTTTAAA	TAGCCTGAGC	480
GTGGATGCGT	CTTGTGATCAG	CGGGGAGTT	AAGCCTTGG	AATTGGGGGT	TAATGATCCA	540
ATTTAGGGGG	GTATGTGAA	CGTGGGGCTG	CCTTTTAGCT	ATCAAGTGAG	CGCGACCTT	600
CAAAGTCAC	GCCTTTCTAG	TTGCTAGAA	ACTTTAAAAA	AGAGTTTTT	AGAAAAGCCC	660
TTAATTGAGA	GCAGCGCGAA	AAAATCGCG	GATATTTTT	CTAAAGCGGT	GTTCTTTTA	720
GCCTTGTGA	GCTTTTATT	GTGGCAATT	GGTTTGGGGG	GTAAATTGTA	AAAAGCTTA	780
ATGGTGTGTA	TTAGCGTGCT	AGTCATAAGC	TGCCCTTGCG	CGTTCGCTCG	GCTACGCCA	840

## (2) INFORMATION FOR SEQ ID NO:1165:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 588 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...588
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165

CGTGTAGTC	ATAAGCTGCC	CTTGGCCGTT	CGCTCGGCTA	CGCCCCATAGC	GTTAGTGATA	60
GGGGTGTITA	AAAACCCTTT	GATCGTGT	AAAGAAGCGT	TGTTTTAGA	AACCTCTGGCT	120
AAAGTAAAAA	AAATCTTAT	AGACAAAACC	GGCACCCCTCA	CGCAAAAAGA	AGTCCTTTA	180
AAAGAAAAAA	TCATTCACTGA	AGAATTGAT	GAAAGGCTTT	AAAAGAGCCT	TTTAAAAACT	240
AGGGAGCATT	TAGCCCATAA	TGCGATTCTT	AAAACATTAG	ATGGCGATGA	GGTTGATTTG	300
GAAAAGATAG	AGTTTTTCGC	TCATGGCCTG	AAAGCGAGCT	ATCAAAACGA	AACCTTGCTA	360
GTGGGGAGTT	TGAAATTGTT	AAACGCTATG	GGGGTTGATT	AAAAGTTAA	AGAGAGCGCT	420
AATATCATGG	TAGGCTTGC	AAAAAATAAG	ACCTTATGCG	CGTTATTCTAT	TTTACAAGAG	480
CGTTTGAAAG	CTAACGCTAA	AGAAGTCATT	CAGGCTTTAC	AAAATCAAGG	CTTGGAAATTA	540
GAAATTGAA	GGGGGATAA	TGAAAGCTCG	GTAAAGGAGT	GGCGAAA		588

## (2) INFORMATION FOR SEQ ID NO:1166:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2001 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...2001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166

ACCCCAACCA AAGCCCCATAA AATCGTCAA GAGCAGGTTA CTTACCCGTT GGTTTCTACT	60
TTCATGACTA TCGCTAACAT TGACACGGTT AGAGGGATTCTAGCTATGA AAGCGGCTTG	120
ATTTACATCA TTTTAAAGA CGGGCTAAAT TTGTATTGGG CTAGAGATAG GTTTTAGAG	180
CAATTAACAA GAGTAAGCAA TCTGCCTAACAGCGCTAAAG TGGAAATAGG GAGCGATTCC	240
ACTTCTATTG GCTGGGCGTA TCAATACGCT TTATCTAGCG ATAGCAAGAA TTAAAGCGAT	300
TTGAAAGCTT TGCAAGATTT CTATTACCGC TATGCGTTT TGGGGTTGA TGGGGTGAGT	360
GAGGTCGCGA GCGTGGGGGG CTTTGTAAAG GATTATGAAG TAACGCTTCA AAACGATTCT	420
TTGATCCGTT ATAACATTGAG TTAGAACAA GTCGCTAACG CGATTTAAAAA TTCCAATAAC	480
GATACCGTG GGGCGTTAT TTTAGAAAAC GGGTTTGAAG AAATATAAG ATCGCATGGC	540
TATATCCAAT CTTAAACGA TTAGAAAGA ATTGTGGTT AAAAGAAGG GGCTATCCCT	600
TTAAAAATCA AAGATATAGC GAGCGTTAGG CTAGCGCCCA ACCCGCGCAG AGGGCGGGCT	660
AATCTAACG GCGATAAGGA AGTGGTGGGC GGGATTGTTA TGGTGCCTA TCACGCTGAC	720
ACTTTATAAGG TGCTTAAAGC CAATTAAGAAA AAAATGCCA CCTTACAAGC GAGTAACCC	780
GATGTGAAAAA TCACCAGCGT GTATGACAGG AGCGAATTGA TTGAAAAGG CATTGACAAT	840
TTGATTCACA CGCTCATAGA AGAAAGCGTC ATTGTGCTAG TCATTATTGC GATTTTCTTA	900
CTGATTCTCA GGAGCGCTTT AGTGGTGTATT ATCACTCTGC CTTTAAAGCGT GTGCATCAGT	960
TTCTTGCTCA TGGTTTATTG CAATATTGAA GCGGACATCA TGAGTTGGG GGGCATTGCG	1020
ATCGCTATAC GGGCGATGGT CGATGCGGG ATAGTGATGG TGGAGAACGC TCACAAGCAT	1080
TTGAAACACA TTGACACGAG AGACAACACT CAAAGGGTTA ATGCCATCAT GCAAGGGTT	1140
AAGCATGTGG GGGCGCGAT ATTTTTTGCC TTAATGATCA TCGTGGTTTC TTCTTGCC	1200
ATTTTCGCGC TCACCGGTCA AGAAGAAAAG CTTTTGCCC CTTTAGCTTA CACCAAAACC	1260
TTTGCCTATGC TAGTGGGAGC GCTGCTTCT ATTACGATAG TCCCTGTTT AATGGTATGG	1320
CTCATTAAG GGGGGATTTT AGAAGAGTCC GAAAGCCCCG TTAACGCTTT TTTCATGAAA	1380
ATTTATGGCG TGAGTTTGAG GGTGTTGCTT AAGTTCAAGAT ACGCTTTTTT AATAGCGAGC	1440
GTCTTAGGTT TAGGGGTTT AGTTGTAGCG TATAAAAAAC TCAACTGGGA ATTATATCCCC	1500
CAAATCAATG AAGGGTAAT CATGTATATG CCTGTAACCA TTAATGGCGT GGGTATTGAT	1560
ACCGCTTAC AATAATTGAA AAAAGTAAC GCTGCTATCA ACCAACTGGG TTTTGTCAA	1620
CAGGTTTTG GTAAAGTGGG CGCGCTAAC ACCAGCACCG ATGCCGCCGG TTTAGGAATG	1680
ATAGAACCT ACATTAATT AAAGCCGCAA AACGAATGGG AAGAAAAGCT CAGCTATAAA	1740
GAAGTTAGGG ACAATTGGA AAAACCCCTG CAATTAAGG CCTGACTAA TTCATGGACT	1800
TACCCCATTC GTGCGAGAAC GGACATGCTC TTAACCGGCA TTAGAACGCC CCTAGGCATC	1860
AAGCTCTATG GTAAACGACAC GGACAAATTAA CAAGAATTGG CGATCCTTAT GGAGCAACAG	1920
CTAAAACCC TCAAAGAGAG TTGTCGGC TTTGCGAGC GATCCAATAA CGGCTACTAC	1980
ATCACGCTGG ATTTGGAACG A	2001

## (2) INFORMATION FOR SEQ ID NO:1167:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167

CGCAACGTGG AAGCGCGTTA TTATTATGGG GACACTTCAT ACTTTTATT GCATGCGGGA	60
GTTTACAAG AGTTCGCTCA CTTTGGATCG AATGATGTGG CGTCTTTAAA CACCTTTAAA	120
ATCAAATGCCG CTCGCAGTCC TTTAACGACC TATGCAAGAG CGATGATGGG TGGGGAAATTG	180
CAATTGGCTA AAGAAGTGTT TTGAATTG GGCCTGGTTT ATTTGCACAA TTTGATTTC	240
AACGCAAGCC ATTTCGCTTC CAATTAGGA ATGAGGTATA GTTTC	285

(2) INFORMATION FOR SEQ ID NO:1168:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 633 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168

AAACCTACCA ATGTTGGGC TAACGCTATT GGGGGAGCGA GCTTGAATAG CGGCTCTAAC	60
GCTTCATTGT ATGGCACAAAG CGCCGGCGTA GACGCTTTCC TTAACGGGAA TGTGGAAGCC	120
ATTGTGGCG GTTTGGAAG CTATGGTTAT AGCTCCTTA GCAATCAAGC GAACTCTCTT	180
AACTCTGGGG CCAATAACGC TAATTTGGC GTGTATAGCC GTTTTTTGC CAACCACCT	240
GAATTGACT TTGAAGCTCA AGGGGCGCTA GGGAGCGATC AATCAAGCTT GAATTTCAAA	300
AGCACTCTAT TACAAGATT GAATCAAAGC TATAATTACT TAGCCTATAG CGCCACAGCA	360
AGAGCGAGTT ATGGTTATGA CTTCGGCTTT TTAGGAACG CTTTAGCTT AAAACCAAGC	420
GTGGCGTGA GCTATAACCA TTAGGTCTA ACCAACCTTA AAAGCAATAG CCAATCACAA	480
GTGGCTTAA AAAATGGCGC GAGCAGTCAG CATTATTCA ACCTAACGC AACGTGGAAG	540
CGCGTTATTAA TTATGGGAC ACTTCATACT TTATTTGCA TGCGGGAGTT TTACAAGAGT	600
TCGCTCACTT TGGATCGAAT GATGTGGCGT CTT	633

(2) INFORMATION FOR SEQ ID NO:1169:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 234 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169

AATAAAATCC TAGCCAGTGA GCTAGAATTAA	AAATTTTAA TCAAAGGAGT CATCATGGCA	60
CACCATGAAG AACAAACACGG CGGGCACCA CACCATCACC ACCACACACA CCACCACCAT		120
TATCATGGCG CGGAACACCA CCATCACCA CACAGCTCTC ATCATGAAGA AGGTTGTTGC		180
AGCACTAGCG ATAGTCATCA TCAAGAAGAA GGTTGTGCC ACGGGCATCA CGAG		234

## (2) INFORMATION FOR SEQ ID NO:1170:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1035 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170

GGGGTTTGA TTAGAACCCC CAAGCATTAA ACCAACGAAAG AGAGCGTGAA TTTAGGGGCT	60
TAATACACGC CCCCTTATTAA AGTGGATTGC GCTTACAAGC TTTTAAAAAA GCATGTTGGT	120
ATTGAAAATC ACACGCTTTT AGACACCGCA TGTGTAATA AAGAGTTTTT AAAGCTCCAC	180
CACCTAAAAA AAATAGGAGC GGATATTGAC CCTAAGTGTG ATGCTTTAAT AATAAACGCT	240
CTAGCCAATC CTAAAAGAGA AAATTATGGC ATTAGCCAAG ATGAACCTTT AATCATCGTG	300
GGCAATCCCC CCTATAACGA TAGAACTTCC TTTATCAAC AAGATATTAA AAATAAAGAT	360
TTCATTTTTG AGATAGACAA CGATTITGAAA TCCCGAGATT TAGGGATAAG TTTTTAAAAA	420
TCTTTTGCAA TTTTAAAGCC GGCGTTTATT TCGCGTGTAC ACCCTTTATC TTATCTCATC	480
AAAGAAGCTA ATTTTAAGCA ATTAAGCTA TTTAAGGATC ATTACAGGCT TTAGACGCT	540
TTTGTGTTT CTTCTAAATC TTTCACTAA AGTAACGAAT TTCTTATTGT GATAGCTTA	600
TATGAGCGAG GGCGAATGGA CTATGCAGGT ATTAGGCGTT TTGTTTTTCC AACTGATTGC	660
GATACGACGC TATGCTTAA CGATTITGAC TACATAGCCA ATTATGTTGA TAAATACCT	720
AACGCTAAA AGGTGGGGC ATGCGTGGGC TATTTTTTC CTATCGGAGA CATTAAACGCT	780
CTCAAACGCA ACAAAACTTT TTTAAACGGC CCAAGGAAA ATGCGGTGCG AATCAGTCAA	840
GATAAAATGA TTATTACCA ATATATCCAT TATTTAAGG AAATTGCTCC TAAAATCCT	900
TATTATTTTG GTAATTGGGAA TATTATCATT GATCATTTTG CTTTTTTAGA AATTAAAGAC	960
GCTTTTTAA AAGATAAAAG AGCGCGTTA GAATATTAA AAAATTGTT TCAAGGACAC	1020

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CCTTGTGAGT TTGAT

1035

## (2) INFORMATION FOR SEQ ID NO:1171:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 786 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...786

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171

AATATTTTAA AAAATTGTTT CAAGGACACC CTTGTGAGTT TGATTAAGT TAGTGGTGAT	60
AAAAAAAGTGA TTGAGGTTTC TATTCTTTA ACITCCATTG CAGGCAAAGC GCGTGTGAAA	120
ATCAGACATG CCTTTAGCGA TTATGGTATT TCAACAGCGA CTAGAAAAAT CCCTTTAGT	180
TTAAAGCATT ATGTAGAGTG GCAGATCGGT TATGATGTCC CCATTAAGA TAAAGAAAAA	240
TTTGAACTCA CTACTTTAAA AGATGAAAAA TATCATTTT TAGGGGCTAA TAATAAAGTA	300
AAAACTCTTT ATGAATTGAG CGAAATGATT TATTACGCTA AGCGATTGGG TTTAACAGT	360
TTAGAAAATT TAGAAAATAC TTIAAAAATT TTAGAAAAAC AAAAACAAATT TATAGAAGAT	420
AATTTTATGA TTACAAGAGA AAGATTTAGA TCGCATCAAT TTGGTGGCAT GGATTTGAA	480
CTCTTACGCA TTTCCTTATCC TTIGCTCATT CATTCTTTG ATGATAATGA GTTGAGCGAA	540
ATAGTTATTA AGGAACAACA ATATGGCTCT AAAACCCAAG CCATGCTGTA TTTTGCTTT	600
TCTATTTTGG AGTTAAAAC CGCTACCCCC TTATTAACAA GAACCGCTAT GCCCAAAGAA	660
CATGCCCTTT TGATTATCCA TGAAACCAAC GCTCTGTGT TTTTAGAAAT GCTTAAAATT	720
TTTGGACTTT TAAGCCAAGT GCACCATAAC GATGTGTTAA AGATTTAGA AAAAATACTT	780
CAAAT	786

## (2) INFORMATION FOR SEQ ID NO:1172:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1239 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...1239
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172

TTGAAGGCAT TAAACGACTG CATGGTATTT TTTCATAAGA AAATTATTTT AAATTTTATC	60
TATTCTTAA TGGTTGCTTT TTTATTCCAT TTATCCTATG GGGTTCTTTT AAAAGCCGAT	120
GGAATGGCTA AAAAGCAAC TCTTTTAGTG GGTGAAAGGC TTGTGTTGGGA TAAGCTCACG	180
CTGTTAGGGT TTTAGAAAA AAACCATATC CCCCAAAAAC TCTACTACAA TTTGAGCTCT	240
CAAGATAAAG AATTGAGTGC TGAAATCCAA AGCAATGTTA CCTACTACAC TTTAAGAGAT	300
GCAAATAACA CGCTCATTCA AGCCCTTATC CCTATTAGCC AGGATTTGCA AATCCATATT	360
TACAAAAAAAG GAGAGGATTA TTTTTAGAC TTTATCCCCA TTGTTTTTCAC TCGTAAAGAA	420
AGAACCTCTCC TTCTTTCTT ACAAAACTCG CCCTATCACG ATATTGTCAA AGCCACCAAT	480
GACCCCTTT TAGCCAACCA ATTGATGAAAC CGCTATTTAA AAAGCGTGCC TTTTAAACGC	540
CTAGTAAAAA ACGATAAAAT CGCTATCGTT TATACAAGGG ATTATCGTGT GGGGCAAGCG	600
TTTGGCCAGC CGACCATCAA AATGGCGATG GTTACGCTCTC GTTTCACCA ATACTATCTT	660
TTTCCCATT CAAACGGCG TTATTACGAT TCAAAAGCGC AAGAAGTGGC AGGGTTTTTA	720
CTAGAAACCC CGGTGAAATA CACCCGCATT TCTTCGCCTT TTCTGTATGG GAGGTTCCAT	780
CCTGTTTAA AAGTAAACG GCCTCATTAC GGCGTGGATT ATGCGGCTAA ACATGGCAGT	840
TTGATCCATT CTGCTTCAGA CGGCGTGTG GGTTTTATAG GGTTAAGGC GGGTTATGGG	900
AAGGTGGTTG AAATCCATT GAATGAATTG CGCTTGGTGT ATGCTCACAT GAGCGCGTTC	960
GCTAACGGAT TAAAAAAAGG CTCGTTGTT AAAAAGGGC AAATCATAGG AAGAGTGGGA	1020
AGCACGGGTT TAAGCACCGG GCCGCATTG CATTGGCG TGTTAAAAAA CTCCCCCCC	1080
ATTAATCCTT TAGGCTATAT CGCACCAGCT AAAACCAAGC TGATGGCAA ACAAAAGAGAG	1140
GTTTTTTAG AAAAGCTCA GTATTCTAAG CAAAATTAG AAGAACTTTT TAAAACCCAT	1200
TCTTTGAAA AAAATTCAATT TTATCTTTA GAGGTTTT	1239

## (2) INFORMATION FOR SEQ ID NO:1173:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 759 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...759
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173

GGATGCTTGA TGAAAAGCAT TTGCTCTTT ATGATTTTG TAGTTGTCA GTTAGAAGGC	60
AAAAAAATTTT CACAAGATAA TTTTAAGGTG GATTATAACT ACTATTTGCG CAAACAGGAT	120
TTGCACATCA TAAAAACGCA AAACGATTG TCCAATGCCT GGATCTCCC TCCACAAAAA	180
GCCCCAAAG AACATTCTT GGTGGATTT GCTAAAAAT ATTAAACAT GATGGATTAT	240
CTAGGCACTT ATTTTTGCC TTTTTATCAT AGTTTACCC CCATTTTCA ATGGTACAC	300
CCTAATATCA ACCCTTACCA ACCCAATGAG TTTAAGTTCC AAATCAGTT TAGAGTGCT	360
GTATTAGGC ATATTCTTG GACTAAAGGC ACGCTTTATC TGCCTTATAC CCAAACTAAC	420
TGGTTCAAA TTATAATGA CCCTCAATCC GCCCCCATGC GAATGATCAA TTTCATGCT	480
GAACTCATCT ATGTTTATCC TATTAATTTC AAACCTTTG GGGTAAAT AGGGAATT	540
TCTGAAATTG GGATAGGTG GCAGCACATT TCTAATGGTG TGGGGGTGC GCAATGTTAC	600
CAGCCTTTA ATAAAGAAGG TAATCCTGAA AACCAAGTTTC CAGGACAACC TGTAATGTT	660
AAAGATTATA ACGGGCAAAA AGATGTGCC TGGGGGGGT GTCGTTCGGT GAGCGGGC	720
AACGCCCTGT GTTTCGTTG GTGTGGAAA AGGGAGGCG	759

## (2) INFORMATION FOR SEQ ID NO:1174:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 272 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174

ATGTGAAATT AAAGGGCATG GATAAAGAAG AAAATGAAGA AAATAAAAATT AACCAAGCGA	60
ATGATAGCTA CGGCCAAAAA AGCCCTTCC AAAAGCTATG GATATTGTTT GGTGGGGCGT	120
TTTTAATT TCTTTTGCG GTTTTAGTGT ATTTTTTCTC GGCATTGAGC GGGGAAAAAG	180
TCTTACTGCC CGTCATTGGC GTTTAGAAA AAAACGCGCT AGAAGCCGGG CTGTTAAAGG	240
GGGATAGAAT CCTTCTATCA ACCATCAAAA AA	272

(2) INFORMATION FOR SEQ ID NO:1175:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 279 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175

AGAATTGAGT GGGGTAATAG GCATTGTCGG GCGTTAAGCC ATGCCAATAG CGTGAGCATG	60
CTTTTGTGT TTGGGGCGTT TTATCTATC AATCTAGGGA TTTTAAATT ATTACCCATT	120
CCAGCCTTAG ATGGGGCGCA AATGCTAGGG GTCGTTTTA AAAATATTT TCATATCGCT	180
TTGCCAACGC CCATACAAA TGCGTTGTGG CTAGGGGGG TGGGGTTTT GGTTTTGTC	240
ATGTTTTAG GGTTTTTAA TGACATTACT CGTTTGCTA	279

(2) INFORMATION FOR SEQ ID NO:1176:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1272 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...1272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176

AATTTAGGCG	GAGCGGCCAA	TGTGGCTAAT	AACCTTACCT	CTTTAAAAGC	TAAAGTC	60
TTATGCGGG	TAGTGGGAGA	TGATTTAAA	GGCAAGCATT	TCATTAGCAC	TTTAAATTCT	120
ATAAGGGATTG	ACACTTCAGG	TGTTTTATA	GATAAAACCC	GTTGCACCAC	GCTTAAAACG	180
CGCATCATCG	CGCAAACCCA	GCAAATCGTG	CGCGTGGATA	AGGAATCAA	AGACCCCTTA	240
AACGCTGATT	TAAGAAAGAA	TCTTTAGAT	TTTATCGAG	AAAAAATTCA	AGAAATAGAT	300
GGCGTGTATCC	TTTCAGATTA	CAATAAGGGT	GTGTGGATT	TTGAACTCAC	TCAAACCATC	360
ATCACGCTAG	CTAATAAGCA	TCATAAGCTC	ATTTATGCG	ACCTAAAGG	AAAGGATTAT	420
AGCAAATATT	CCCATGCGAG	TTTGATCACG	CCTAATCGCG	CTGAATTAGA	GCAAGCGCTC	480
CATTGAAAT	TAGACAGCCA	TGCGAATTAA	TCAAACGCC	TCCAAATTCTT	ACAAGAAACT	540
TATCATATCG	CTATGCC	AGTAACCTTG	AGCGAACAAAG	GCATCGCTTT	TTTAAAGAAAAA	600
GGCGAGTTAG	TCAATTGCC	CACTATCGCT	AAAAGAAGTTT	ATGATGTAAC	GGGGCAGGC	660
GATACGGTGA	TAGCGCTTT	AACGCTCTCT	TTATTGGAAT	CAAAAGCTT	GAAAGAAGCT	720
TGCGAGTTTG	CTAATGCGGC	TGCGGCGGTG	GTGGTGGTA	AAATGGGGAG	CGCGTTAGCG	780
AGTTTAAAG	AAATCGCTTT	GATTTGAAC	CAAACGCCACC	CTAAAATCCT	CCCTTTAGAA	840
AAGCTGTTAG	AAACTTTAGA	ACGCAACCAG	CAAAAAATCG	TTTCACCAA	TGGCTGTTT	900
GATATTCTCC	ATAAAGGGCA	TGCGAGCTAT	TTGAAAAGG	CTAAAGCTTT	AGGGGATATT	960
CTTGTGTTG	GGTTAAATAG	CGATAATTCC	ATTAAGGGC	TTAAGGGGA	TAAACGCC	1020
ATAGTGAGCG	AAAAGACAG	GGCGTTCTT	TTAGCGAGCT	TGCTTGGCGT	GGATTATGTT	1080
GTGGTGTITG	GAGAAGACAC	GCCCATAAAA	TTGATTCAAG	CCCTAAAGCC	TGATATTTTA	1140
GTCAAGGGAG	CGGACTACCT	CAATAAAAGAA	GTCATAGGGA	GCGAGTTGGC	TAAGAAACC	1200
CGTTTGATAG	AATTGAAAGA	AGGTTATTCC	ACAAGCGCTA	TCATAGAAAA	AATTAAAAGG	1260
ACACATAATG	AT					1272

(2) INFORMATION FOR SEQ ID NO:1177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 963 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION 1...963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177

GGATCCCTTA	TGGTGAATGT	GTTCCTCAAG	CAGCAAAAT	TCGTCATTAA	AAAACGCTTT	60
AATGACTTTA	ATGGTTTG	TATAGAAGAAA	AATGAAGTGT	TGTGGTTGA	ATTAATCAAC	120
CCTACGCCCA	ATGAATTAGC	CACTCTAACG	CAAGAACATCG	CTATCCACTA	CAACACGGAT	180
CATTCCCAAC	GAGTCTCATC	AGTTACCAAA	TACTGGGAAG	ACAGCTCCAG	CGTTACGATC	240

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AACCGTTTT	TCACCAACCA	GGATGAAAAT	GAGACTTCC	ACATGGAAAT	GGCGACCTT	300
ATTTTGCTA	ATAACATTCT	TTTCACGATT	TATTACGGGA	CTTAGAAT	CTTGATCT	360
ATCCAAAAAA	AGGTGTTGGC	TAGCCCTAAA	AAATTGAAAG	ACGGGTTTGA	TATTCTAAC	420
AAAATCTTIG	AAGTGTATT	TGAAAAAGGG	GTGGATGTT	TGGAATGGAT	CAACAAACAA	480
ACGAGCCTGT	TGCGCAAAA	CATCATTTC	AAAGAACCTT	CTACGCATGA	TGATATTTA	540
GTGCGCTTGT	CCAATTGCA	AGAATTAAAT	GTGGCTTAA	GGGATTCCTT	TTTGACAAA	600
CGGGCATT	TCACCGCTT	ATTAAGGAGC	AATAAAGTGG	ATAGCGATAC	AAAAATAAT	660
TTAAATATCA	TTTAACCAGA	TTTAGCTCT	TTGGTGGAGT	CTACAAACGGT	CAATCTCAC	720
TCGCTTGATA	ACATTCAAA	CCTGTTGCT	TCTCAAGTCA	ATGTGGAGCA	AAATAAAATC	780
ATTAACACTCT	TCACTGTGGC	GACTATGGCG	ATGATGCC	CCACATTGAT	TGGCACGATT	840
TATGGCATGA	ATTTAAATT	CATGCCGGAG	TTAGAATGGC	AATACGGGTA	TCTTTTGCG	900
CTGATTGTCA	TGGCGATTTC	TACGATTITG	CCGGTGAATT	ATTCAAAAAA	GAAGGGTGG	960
TTG						963

## (2) INFORMATION FOR SEQ ID NO:1178:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178

CCTTTCATGG	AATTTTTATC	CTCACTCTTA	GACGCTCTT	CTACACCGCA	TGGCATAGTC	60
TCCCTGGCTA	CGCTCACGCT	TTTAGAGATC	GTTCAGGGA	TTGATAATAT	CATTTTTATC	120
ACGGTGTGG	TTTATAAAACT	CCCCAAACAC	CAGCAAATA	AGCTCATGAT	TTTAGGCTTG	180
GGCTTAGCGA	TGATCACTCG	TATAGGGCTT	TTAGGGAGCT	TGTTTTTCAT	CAGGCCATTG	240
CAAAAGCCTT	TATTCGCTAT	AGCGGGCATG	AGCTTTTCAT	GGCGTGATGT	GGTGCCTGCTT	300
TTAGGGGGGG	CGTTTTGGC	TTTTAAGGCG	TTAGTGGAAAT	AAAAGAGCA	GATCTATCCT	360
AAAGAAAAAC	GCCAAGAAA	AGCGTTTGGC	TTTTTCATCA	CTTTAATAGA	AATCATGTTT	420
TTAGACATTG	TTTTTCTT	GGACTCCGTG	ATCACGGCTA	TTCGGATCGC	TAAACACTTA	480
GAAGTCATGG	CGCTTGCTAT	TATTTATCT	GTAATCGTGA	TGATGTTTT	TTCCAAAATC	540
GTTGGCGATT	TTATGAAA	GCATTATCGC	GTCAAACCTT	TAGCCTTGT	GTTCCTGCTC	600
GTTGTGGCG	TGTTTTGTT	TTAGAAGGC	TTGCATTTAC	ACATCAATAA	AAACTATTG	660
TATGCGGGTA	TTGGTTTGC	CTTGTCTATA	GAATGCTTGA	ATATTTTCAT	AGAAAAGAAA	720
ATGAAAAAAA	GT					732

## (2) INFORMATION FOR SEQ ID NO:1179:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179

GTTTATGGCT	TTTGGGCTTG	TGTTTTGTGC	TAGGGATTAA	AGTTTGGTTT	TGTTTATTTT	60
GCGAACAAA	GGGCAGTTCA	ATTTAGACAA	AACCATTCTT	TCCATTAGCG	CTATCAATGA	120
AATGAGCATG	ATTTAGGCC	TGTTCATGCT	CACAGCCGGG	AATTTCTTAG	GTGGGGTGTG	180
GGCGAATGAA	TCTTGGGGGC	GCTATTGGGG	GTGGGACCCCT	AAAGAAACTT	GGGCAGTTGAT	240
TTCTATTTC	GTCTATGCCT	TGATCTTGCA	TTTGCGTTTT	TTAGGCTCTC	AAAATTGGCC	300
CTTTATTTTA	GCGAGCAGCA	CGCTGCTAGG	GTTTTATTCCG	GTTTTAATGA	CTTATTTGG	360
CGTGAATTAC	TACCTTTCTG	GCTTGACACG	CTATGCCGCA	GGTGATCCTT	TGCCGATCCC	420
TACTTTTTA	TACTTTTIGG	TAGCGATAAC	TTTCGCTCTC	GTATCTGGC	GTATTTCAAA	480
CGCCATT						487

(2) INFORMATION FOR SEQ ID NO:1180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180

CGATATTCCG	ATCAGACGAA	TCTATTAGCC	CTAAATGCTG	CTATTGAAGC	CGCAAAGGCC	60
GGCGAGCATG	CTAGAGGCTT	TGCGGTGGTG	GCTGATGAAG	TTAGGAATTIT	AGCTGGGCC	120
ACTCAAAGT	CTTAGCCGA	AATCAATTCC	ACTATCATGG	TGATTGTCCA	AGAAATCAAT	180
GATGTGAGTT	CGCAAATGAA	TCTCAATTCC	AAAAAAATGG	AGCGCTTGAG	CGATATGAGT	240
AAAAGCGTGC	AAGAAACTTA	CGAAAAAAATG	AGTTCTAATT	TAAGCTCAGT	CGTTTTAGAC	300
AGCAATCAA	CCATGGACGA	TTACGCTAAA	TCCGGACACC	AAATTGAAGC	TATGGTAAGC	360
GATTTGCA	AAAGTGGAAAA	AGTGGCTCT	AAGACTTTGG	CTGATTCTTC	AGATATTTTA	420
AACATCGCTA	CGCATGTGAG	TGGAACGACC	ATGAATTAG	ACAAACAAGT	GAATTGTTT	480
AAAACT						486

(2) INFORMATION FOR SEQ ID NO:1181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

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- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...183
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181

ATTTGTTTAA AACTTAATCA GGGGGGAGTT TATCAAAAAA GGTTTGGATT GTTAAAGGTT	60
TCTGTGATCA CGCGTGTGTT TAATAGCGAA AAAACCATTG AAGACACCAT TCTTCCGTG	120
CTTAATCAAA CTTATAAAAA CATTGAATAC ATCATTATAG ATGGGGCTAG CGCGATAGCA	180
CTT	183

## (2) INFORMATION FOR SEQ ID NO:1182:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1992 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182

AATCATATTTG TCGCTGGCGT TGATTTGAT CGTGGCGTGA GCATTTAGG GGTGTCCTTA	60
AACAGCAGGG TGAAAGAGAT TTAAAAGAA AGCGCTCTGC ATTCAATGCA AGATAGTTG	120
CATTCAGG TTAAGGAAGT GCAAAGTGTG TTGAAAACA CTTATACGAG CATGGGCATT	180
GTCAAAGAAA TGCTCCCTGA AGACACCAAA AGAGAAATCA AAATCCAGTT GTTAAAAAAC	240
TTCATTTAG CCAATTGCGA TGTCGCTGGG GTGAGCATGT TTTTAAAGA CAGAGAGGAT	300
TTGAGATTGA CGCTTTACG AGATAACGAT ACGATCAAGT TGATGGAAA CCCGTCATTA	360
GGGAGTAACC CTTTAGTGC AAAAGCGATG AAAATAAAG AAATTTCTAA AAGCTTGCCT	420
TATTACAGGA AAATGCCAA CGGGGCGGAA CTTTATGGCG TGGATATTCT TTTACCACTA	480
TTCAAGGAAA CACCCAAGA AGTGGTGGG GTTCTGATGA TTTCTTTTC CATTGACAGC	540
TTCAGTAATG AAATCACTAA AAACAGGAGC GATTATTCTT TAATTGGCGT TAAAGGTAAA	600
GTCCTTTGA GCGCGAATAA AAGCTTGC ACAAATCCA TCACCGAAAT TTATAAAAGC	660
GTGCTAAAG CCACATATG AGTGATGGCT ATTTAGAAA ATGGCTCTAA AGCGACTTTA	720
GAATACCTGG ATCCCCTTAG CCATAAGGAG AATTTTTAG CCGTTGAAAC CTTTAAAATG	780
CTAGGCAAAA CAGAAACTAA AGACAATCTT AATTGGATGA TCGCTTTGAT CATTGAAAAA	840
GACAAGGTCT ATGAGCAAGT GGGATCGGTG CGTTTGTGG TGGTTGCGC GAGTGCTATC	900
ATGGTGTAG CCTTAATCAT AGCGATCACT CTTTTAATGC GAGCGATCGT GAGCAATCGT	960
TTCGAAGTCG TTCTCTGAC CTTCTCAT TTCTTAAAT TATTGAACAA TCAAGCCCAT	1020
TCTAGCGACA TTAAATTGGT TGAAGCGCA TCTAATGACG AATTAGGGCG CATGCAAACA	1080
GCGATCAATA AAAATATCTT GCAAACCAA AAAACCATGC AAGAAGACTG GCAAGCCGTC	1140
CAAGACACCA TTAAAGTGGT TTCAGATGTG AAACGGGGGA ATTTTGCCTG GCGCATCACG	1200
GCTGAACCCG CAAGCCCTGA TTGAAAGAA TTGAGAGACG CGCTAATGGA TCATGCACTA	1260
TTTGAAGAA AGCGTGGGAC TCACATGCCA AGCATTTCA AAATCTTGA AAGCTATTCT	1320

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GGCTTGGATT TTAGAGGGCG GATCCAAAAC GCTTCGGGTA GGGTGGAAATT GGTTACTAAC	1380
GCTTGGGC AAGAAATCCA AAAAATGCTA GAAACTTCGT CTAATTTGC CAAAGATCTA	1440
GCGAACGATA GCGCGAATT AAAAGAATGC GTGAAAATT TAGAAAAGGC TTCAAACCTCC	1500
CAACACAAAA GCCTGATGGA AACCTCCAAA ACGATAGAAA ATATCACCAC TTCCATTCAA	1560
GGCGTGAGCT CTCAAAGTGA AGCCATGATT GAACAAGGG AAGACATTAA AAGCATTGTA	1620
GAAATCTTA GAGATATTGC CGATCAAACG AATCTATTAG CCCTAAACGC TGCTATTGAA	1680
GCCGACAGAG CCCGCGAGCA TGGCAGAGGC TTTGCCGTGG TGGCTGATGAA GGTGAGGAAG	1740
CTCGCTGAAA GGACGCAAAA ATCCCTCAGT GAGATTGAAAG CCAATATTAA TATTCTCGTT	1800
CAAAGCATTG CAGACACGAG CGAAAGCATT AAAAACCGAG TTAAAGAAGT AGAAGAGATC	1860
AACGCTTCTA TTGAAGCCTT AAGATCGGTT ACTGAGGGCA ATCTAAAAAT CGCTAGCGAT	1920
TCTTAGAAA TCAGTCAAGA AATTGACAAA GTCTCTAACG ATATTTAGA AGATGTGAAT	1980
AAAAGCAGT TT	1992

## (2) INFORMATION FOR SEQ ID NO:1183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183

CGTGGTGAAT CCTATTTGAA AAGAGAAAATT GGATTGATGA GGGAAAATTTT TTCTTATATT	60
TCTAAGGTTTC TATTATTTAT TGGGGTGGTT TATGCGAGGC CTGATTCTAA AGTGGAGCC	120
TTAGAAGGGAA GGAAGCAAGA GTCTTCTTTG GATAAAAAAA TCCGCCAAGA ATTGAAGAGT	180
AAGGAATTGAA AGAATAAGGA ATTAAAGAAT AAGGATTGAA AAAATAAGA AGAAAAGAAA	240
GAAACAAAAG CCAAGAGAAA ACCCAGAGCA GAAGTCCATC ATGGGGAGCG CAAAAATCCC	300
ACTCCAAAGA TCACGCCCTCC TAAAATCAAAGGGAGTAGTA AGGGCGTTCA AAATCAAGGC	360
GTTCAAAACA ACGCCCAAA ACCTGAAGAA AAAGATACAA CCCCTCAAGC TACTGAAAAA	420
AATAAGGAAA CAACCCCTAG CTCTCAATTC AATTCCATTG TTGTTAATCC TAATAACGCT	480
ACCAACAAACA CCTCTGAAGA TAAGGCTGTA GGGGCCATT CATGCTTGT TAATGCTTCG	540
CCTATCACGC TGTATCAAAT CCAAGAAGAG CAAGAAAAT CTAAAGTGAG TAAGGCTCPAA	600
GCTAGGGATC GTTGTATCGC TGAACGCATT AAAACCAAG AAAATTGAGCG CTTAAAAATC	660
CATGTAGATG ATGACAAGCT AAACCAAGAA ATGGCGATGA TGGCGCAACA ACAAGGCATG	720
GATTAGGAC ATTCAAACAA GATGCTTATG GCTGAGGGGC ATTATAAACT CTATAGAGAT	780
CAACTAAAG AGCATTAGA ATGCAAGAA TTGTTGCGTA ATATTTTGCT CACGAATGTG	840
GATACCAAGCT CTGAACCCAA ATGCGCGAA TATTACACAA AACACAAGGA GCAATTCACT	900
ATCCCCACAG AAATAGAACAC CGTGCCTAC ACTTCCACCA ATCAAGAGGA TTTAGAAAGG	960
GCTATGGCG ACCCTAATTG GGAAGTCCCA GGGGTGAGTA AGGCCAATGAA AAAATAGAG	1020
ATGAAAACCC TAAACCTCA AATCGCCCAA GTCTTATTG CGCATGAGCA AGGCTCTTTC	1080
ACGCCGTTA TGAATGGGGG TGGGGGGCAG TTCATCACCT TTTATATCAA GGAAAAAAGG	1140
GGTAAAATG AAGTGAAGCTT CAGTCAGGCC AAGCAATTCA TCGCCAAAAA ATTAGTGGAA	1200
GAATCTAAGG ATAAGATTT AGAAGAGCAT TTGAAAAT TGCGCGTTAA GTCTAGGATT	1260
GTGATGATCA GAGAG	1275

## (2) INFORMATION FOR SEQ ID NO:1184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1008 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184

ATTTGTGCAAC ACTTCAATT	CCTCTATAAA GATTCTTAT	TTTCTATCGC TTTATTCACT	60
TTCAATTATCG CTCTTGTGAT	TTTATTAGAA CAGGCTAGAG	CGTATTCAC CCGAAAGAGA	120
AACAAAAAAAT TTTTGCAAAA	ATTCGCCCAA AATCAAAACG	CCTATGCGAG CAGCGAGAAT	180
TTAGACGAGC TTTTAAAGCA	TGCTAAAATT TCCAGTTGA	TGTTTTAGC TAGGCCGTAT	240
TCTAAAGCGG ATGTGGAAAT	GAGCATGAA ATCTTAAAG	GGCTTTTGAA TCGCCCCCTTA	300
AAAGATGAAG AAAAATCGC	TGTTTGTAGAT TTATGGCTA	AAATTATTTT TAGCGTGGGG	360
TATTTGAGA AAACAAAAGA	CACCGTAAA GAAATTTCGC	GCTTTTCCCCC AAGGAATGTG	420
GAAGCGTTGT TGAAGCTTTT	GCATCGTAT GAATTAGAAA	AAAGATTATTC AAAGCTTTA	480
GAAACTTTGG AATGTTTGG	AGAATTAGAG GTGCTAAAAA	TGAAACGAT TAAAAATTAC	540
CTCTATTTAA TGCATTTAA	AGAGAATAAG GAAGATGCGG	CTAAAATCTT GCATGTTCA	600
AAAGCGTCGT TAGATTGAA	AAAATCGCT CTGAATCACT	TAAAATCGCA TGATGAAAT	660
CTTTTTGGC AAGAAATTGA	TACAACCGAA CGGCTAGAAA	ATGTGATCGA TCTTTTATGG	720
GATATGAATA TCCCTGCTTT	TATTTTAAAG AAACATGCC	TTTGCAGGA CATCGCCGA	780
TCTCAAGGGT TGCTTTTGGG	TCACAAACCT TGCCAAATT	TTGAATTAGA GGTTTTAGC	840
GCTCTATTGCA ATAGCCCTAT	AAAAGCGAGT CTGACTTTG	AATACCGCTG CAAGCATG	900
AAACAAATCT TTCTTTTGA	AAGCCATAGG TGTCTGTGT	GTTACCAGTT AGCGTTATG	960
GATATGGTGC TAAAAATCTC	AAAAAAACG CATGCTATGG	GAGTGGAT	1008

(2) INFORMATION FOR SEQ ID NO:1185:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 765 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185

ATTAGAGGCG CAAAAACGGG	TCAAAACGAC CACTTAAAGG	GAATAATGAT GAAAAACAAA	60
CGCTCTAAA ATAGCCCTTA	TGTAACGCC	GACAACCTT ATCTAACGCT AGAAAAAGCT	120
TTAGGGTATT CTTTAAAGA	CAAGCGTTA	TTGGAGCAAG CCTTAACGCA TAAATCATGT	180
AAGCTCGCTT TAAACAAATGA	CGCCTTGGAA	TTTTGGCG ATGCGGTGTT GGGCTTGGTG	240

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ATAGGGGAGC	TGCTATAACCA	TAATTCTAT	CAATACGATG	AGGGCAAAC	CTCTAAATTA	300
AGGGCTTCTA	TNGTGAGCGC	GCATGGTTTC	ACTAAATTAG	CGAAAGCGAT	TGCTTTACAA	360
GATTATTGCG	CGCTTCTTC	TTCTGAAGAA	ATTTCTAAGG	GGAGGGAAA	ACCCCTCTATT	420
CTGTCAAGCG	CTTTGAGGC	TTTAATGGCT	GGGGTGTATT	TAGAACGAGG	GTTAGCTAAG	480
GTGCGTAAA	TCATACAAA	TTTACTCAAT	CGTGCTTACA	AGCCTTGGA	TTGGAGCAT	540
TTGTTATGG	ATTATAAAC	CGCTTGTGAG	GAATTGACCC	AAGCGCAGTT	TTGCGTGATC	600
CCCACCTACC	AATTACTCCA	AGAAAAAGGC	CCCGATCACC	ATAAAGAATT	TGAAATGGCT	660
CTATACATTC	AAGATAAAAT	GTATGCGACC	GCTAAAGCA	AGAGTAAAAA	AGAAGCCGAA	720
CAGCAATGCG	CTTATCAAGC	GCTTCAAAAA	CTTAAGGAAG	TCAAA		765

## (2) INFORMATION FOR SEQ ID NO:1186:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 429 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
  
- (ii) MOLECULE TYPE: DNA (genomic)
  
- (iii) HYPOTHETICAL: NO
  
- (iv) ANTI-SENSE: NO
  
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
  
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...429

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186

GCGCATCAAT	CATCTCGTGG	TGTTAGCATG	ATTTAGCAT	GCGATGTGGG	GTAAACGCC	60
ATTGGGATCG	CTGCGTTTT	AAACGGCGTT	ATCTGCCCTT	TGGAAGCGAT	TTTACGCCAC	120
AACAGGAATC	AAGCCTCTAG	GGATTTGAGC	GATTTATTGA	GAAAAAAAGA	CATTCAAGTG	180
CTGGTGGTGG	GCAAACCAA	CGAAAGCTAT	GCAGATACCC	ACGCCCGCAT	TGAGCATT	240
ATCAAGCTTG	TAGATTTAA	GGGCGAAATC	GTTTTATCA	ATGAAGATAAA	TTCTAGCGTA	300
GAAGCTTATG	AAAATTAGA	GCATTGGGT	AAGAAAATA	AGCGGATCGC	TACCAAAGAT	360
GGCCGGTTAG	ACTCTTGAG	CGCTTGTAGC	ATTTAGAGC	GCTATTGCCA	GCAGGTTTA	420
AAAAAGGGC						429

## (2) INFORMATION FOR SEQ ID NO:1187:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1731 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
  
- (ii) MOLECULE TYPE: DNA (genomic)
  
- (iii) HYPOTHETICAL: NO
  
- (iv) ANTI-SENSE: NO
  
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
  
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...1731

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187

AAGAAATGAAA	ATTTTATCAA	GGTTTTAATA	TTGGATTAA	AGGTATTATT	GCAACGGATT	60
GTTGATTIT	TCATCAAGCT	CAATAAAAAG	CAAAAATCG	CCCTGATCGC	AGCGGGGGTT	120
TTGATCACCG	CTTTACTCGT	TTTTTTATTG	CTCTATCCCT	TTAACAGAAA	AGACTACCGC	180
CAAGGGGGTT	ATGGGGTTT	ATTTGAAAGA	TTGGATTCTA	GGCATAACGC	CTTAATCTTA	240
CAACACCTCC	AGCAAAACCA	AATCCCTTAT	AAAGTCTAA	AAGACGACAC	CATTCTTGTC	300
CCTAAAGATA	AACTGTATGA	AGAAAGGATC	ACTCTGGCTT	CTCAAGGGAT	CCCTAAAACG	360
AGTAAAGTGG	GCTTTGAAAT	CTTTGACACT	AAAGACTTTG	GGGCGACTGA	TTTTGATCAA	420
AACATCCTAAC	TCATTGCGC	CATTGAGGGG	GAATTGTCGC	GCACGATTGA	AAGTTAAC	480
CCCATTCTTA	AAGCCAATGT	GCATATTGCA	ATCCCTAAAG	ACAGCGTGT	TGTGGCTAAA	540
GAAGTCCCTC	CTAGCGCTTC	AGTGATGCTC	AAGCTTAAAG	CTGACATGAA	GCTTTCACCC	600
ACTCAAATTT	TAGGGATTAA	AAATTTAATC	GCTCGAGCTG	TGCTCTAAACT	CACGATAGAA	660
AACGTAAAAA	TGCTGAATGA	AAATGGCGAA	TCAATAGGCG	AGGGCGATAT	ACTAGAAAAC	720
TCCAAAGAAT	TAGCCTTAGA	GCAATTGCGC	TACAAACAAA	ATTTGAAAAA	CATTTTAGAA	780
AATAAGATCG	TCATAATCTT	AGCCCCTATT	GTGGGGGTA	AAAACAAGGT	GGTCGCAAGG	840
GTCAATGCGG	AGTTTGATT	CAGCCAAAAG	AAAAGCACC	AAGAGACTTT	TGATCCCAAT	900
AATGTCGAA	GGAGCGAGCA	AAATTTAGAA	AAAAAAAAG	AAAGGCCCTCC	TAAAAAAACAA	960
GTTGGCGGTG	TGCCCCGGAGT	TGTGAGCAAT	ATTGGGCCTG	TGCAAGGATT	GAAGGACAAT	1020
AAAGAGCCAG	AAAAATACGA	AAAGTCTCAA	AACACGCCA	ATTATGAAGT	GGGTAAAAC	1080
ATTATCGAGA	TCAAGGGCGA	GTGGGCACC	TTAATGCGTT	TGAATGCCGC	GGTTGTGGTG	1140
GATGGCAAGT	ATAAAATCGC	GCTCGAAGAC	GGGGCAAACG	CTTCTAGAATA	CGAGCCTTTA	1200
AGCGATGAAT	CGCTTAAAAA	AATCAACGCC	CTAGTCAAAC	AAAGCCATTGG	TGATAATCAA	1260
AATAGAGGCG	ATGATGTGGC	GGTGAGTAAT	TTTGAGTTA	ACCCATATGGC	GCCTATGATT	1320
GACAACGCCA	CTTTCAGCGA	AAAATCATG	CATAAAACTC	AAAAAAATCTT	AGGCTCATTT	1380
ACGCCCTTAA	TCAAGTATAT	TTTGGTGTAT	ATAGTGTAT	TCATTTCTA	TAAAAAAAGTG	1440
ATCGTCCCT	TCAGCGAACG	CATGCTGAA	GTGGTCCCTG	ATGAAGATAA	GGAAGTGAAA	1500
TCCATGTTG	AGAAATGGA	CGAAGAAGAA	GATGAGTTGA	ACAAACTCGG	CGATTGAGG	1560
AAAAAAAGTAG	AAGATCAATT	AGGGCTTAAT	GCAAGCTTAA	GGCAAGAAGA	AGTAAGATAT	1620
GAAATTATTT	TAGAAAAGAT	TAGAGGAACC	CTTAAAGAGC	GTCCTGTATGA	AATGCCACG	1680
CTCTTAAAC	TCCTTAAATCAA	AGATGAAATC	TCTTCAGAC	GGCGAAAGG	T	1731

## (2) INFORMATION FOR SEQ ID NO:1188:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 597 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...597

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188

AAATGGTGCG	GTTATTGTGA	GGGGAGGAGC	GTTAGCCGTG	GATATTATCG	CTCAAGAAAA	60
CGCCCTTACCA	AAAACCATCA	TGCTTTCGCT	TGCACTTTGG	ATTTTATCTA	TCCCACGAAC	120
AACCATAAAAG	TGATCCAAGA	AATCGCGCAA	AACGGTTGAA	TTTTAAGCGA	ACATGAAAAG	180
GATTTCATGT	TTATTTAAAGG	TTTTTTTTTA	GTTAGAAATT	GTCTGGTGT	CGCTTTAAC	240
GACCCGGTGA	TTATCCCCCA	AGCGGATTAA	AAAACGGCT	CTATGACTAG	TGTGAGATTA	300
GCCCAGAAAT	ACCAAAAACC	CTTGTGTTGT	TTACCCCAAC	GCCTGAATGA	GAGCGACGGC	360
ACTAATGAGC	TTTTAGAAAAA	AGGGCAGGCT	CAAGGGATAT	TTAATATTCA	AAATTTTATA	420
AACACCCTT	TAAAAGATTA	CCATTAAAAA	GAAATGCC	AAATGAAAGA	TGAATTTTA	480
GAATATTGCG	CGAAAAACCC	TAGCTATGAA	GAAGCGTATC	TCAAATTGCG	GGATAAGCTT	540

TTAGAATACG AGCTGTTGGG TAAGATTAAG CGCATCAATC ATCTCGTGGT GTTAGCA

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## (2) INFORMATION FOR SEQ ID NO:1189:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 828 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...828
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189

AGGTAAAAAA TGGCAACCAA GCTTACCCCC AAACAAAAGG CTCATTAGA CGAACCTTCC	60
ATGAGTGAAA AAATCGCCAT TTTACTCATT CAAGTGGGGC AAGACACCAC AGGCGAGATT	120
TTAAGGCATT TAGACATTGA CTCTATTACA GAGATTCTA AGCAAATCGT GCAATTAAAC	180
GGCACGGACA AGCAAATCGG CGCGGCGGGT TTAGAGGAAT TTTTGCAT CTTTCAGTCT	240
AACCAATACA TCAATACCGG CGGTTTAGAA TACGCTAGGG AGCTTTAAC CAGGACTTTA	300
GGGAGCGAAG AACCCAGGAA ACTGATGGAC AAACCTACTA AAAGCTTGCA AACGCCAAAAA	360
AACTTCGCTT ATTATAGCAA AATCAAGCCC CAACAATCG CTGATTTCAT CATTAACGAA	420
CACCCCTCAA CCATCGCCTT GATTTGGGC CACATGGAAAG CCCCTAATGC GGCTGAAACT	480
TTGAGCTATT TCCCTGATGA AATGAAAGCC GAGATTTCA TTAGAATGGC GAATTAGGC	540
GAAATATCGC CCCAAGTGGT TAAAAGGGTT TCCACGGTGT TAGAAAACAA ACTAGAATCG	600
CTCACTAGCT ATAAAATTGA AGTGGGCGGC TTGAGAGCGG TGGCTGAAAT CTTAACCGC	660
TTGGGCCAAA AGAGTGCCA AACCACGCTC GCTCCATTG AAAGCGTGGA TAACAAACTC	720
GCCGGCGCGA TAAAGAAAT GATGTTCACT TTGAAAGATA TAGCCAAACT AGACAATTT	780
GCTATCATGA GAGATTAA AAGTGGGGGA TTAAAAAGA CTGGCTT	828

## (2) INFORMATION FOR SEQ ID NO:1190:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 582 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...582
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190

AGAAGTTTGG	GAAAAGGGCG	ACCAATGAAC	AAGAAAAATA	GCGTAATTTC	TGGTTTGATG	60
AATTTTTTA	GCGAAAAGAA	TGAGCGCTGG	CTGTTAGCCC	ACAGGCACAC	GAGGGGGTTT	120
GTGATAGTGG	CCTGGCTTTT	TAGGTTAAA	AGCATIGCGT	TTCTATTIT	AATCACTCTG	180
TIGGTTATTT	TAGTGGATAT	TTGGGTGAT	AGCGATGTGC	GCCAGTTTTT	ATTGGACACT	240
TCTAGCTCTT	TTATTTGGCT	TTAAATCGCT	TTACTAATCA	AGTGGGGCGT	GATTGTTATA	300
AGTGCACGCA	AATGCTACCA	ATTCAAGCCA	AAAATGTTTG	CGTTAATCCA	AAGAAAAAGG	360
CAAATCAGAG	AGAATTAAA	AAACCGCTCC	AATCGCAAAG	ATGCTAAAAA	TTTGAAAAA	420
CTCTCTAAC	TCGCTGAAGA	AATCATTTCA	AAAAAACAAAG	AAGAGTCCC	CCACAAAGAA	480
GATTCTAAC	ATGAAAACCA	CAAAGACAAG	CTTCTAACCA	TTACCGAAGA	AATGATTCTC	540
AAAAAACAAAG	AGGAACTGAA	AGCTAGAAAG	GATAAGGGGG	AT		582

## (2) INFORMATION FOR SEQ ID NO:1191:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1617 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191

CTTATGGATA	GAGCAAATT	TATATTGTT	ACAGGGGGCG	TGTTAAGCTC	TCTAGGGAAA	60
GGGATTTCAT	CTTCTTCAAT	CGCTACGCTT	TTGCAGCATT	GCAATTACCA	GGTTTCTATT	120
TTGAAGATTG	ATCCTTATAT	CAATATTGAT	CCAGGCCACCA	TGAGCCCTTT	AGAGCATGG	180
GAAGTGTG	TTACTAGCGA	TGGCGCTGAA	ACGGATTAG	ACATCGGGCA	TTATGAACGC	240
TTTTGAAACA	GGAAATTAAAC	GAGGTTGAAT	AATTTCACTA	CCGGGCAGAT	TTTTCAAGC	300
GTGATAGAAA	ATGAAAGGAA	AGGGAAATAT	TTAGGCAAAA	CCATTCAAAAT	CGTCCCCCAT	360
GTAACCGATG	AAATCAAAAG	GCGCATTAA	AGTGGGCTA	AGGGGTTGGA	TTTTTAATC	420
GTGGAAGTGG	GTGGAACCGT	GGCGATPATG	GAGGGCATGT	TTATGTGGA	ACCGATCCGC	480
CAGCTGAAAC	TGGAATTAGC	GAATAAAGCA	CTCATCAATA	TGCATGTAAAC	CTTGATGCC	540
TATATCCGTG	CCACTAGCGA	ACTAAGAAGC	AGACCCACGC	AAACACTCCGT	CCAGGAATT	600
CGGCGCTCTG	CGCTAACCCC	TCAAATCATT	TTGGCCGAT	CGCCTAACGCC	TTTGGATAAA	660
GAATTGAAAA	AGAAAATCGC	TTTGAGTTGC	GATGTGGAAC	AAGACAGCGT	GATTGTAGCC	720
ACAGACACTA	AAAGCATTAA	CGCATGCCCT	ATTCTTTCT	TGCAAGAAGG	CATTTTAAC	780
CCCATTGCCA	GACGCTTTAA	TTTGAAATAAG	TTGCAACCTA	AAATGGCGGC	TTGGAACACT	840
TTAGTAGAAA	AAATCATCGC	TCCTAAACAC	AAGGTCAAAA	TTGGTTTGT	GGGCAAGTAT	900
TTAAGCTAA	AAGAATCTTA	AAATCCTTG	ATTGAAGCCC	TAATCCATGC	GGGGGCGCAT	960
CTGGATACGC	AAGTCAATAT	TGAATGGCTG	GATAGCGAGA	ATTTTAATGA	AAAGACTGAT	1020
TTAGAGGGCG	TTGATGCGAT	TTTACTGCCG	GGGGCTTTG	GAGAAAGGGG	GATTGAGGGC	1080
AAAATTGCG	CCATTCAAAG	GGCTAGGTTA	GAAAAACTCC	CTTTTTAGG	GATTGTTTG	1140
GGCATGCAAT	TAGCGATCGT	TGAATTTGT	CCCAATGTTT	TAGGCTTGAA	AGGGGCTAAC	1200
TCTACGGAAT	TTAACCAACG	CTGCGAATAC	CCTGTGGTGT	ATTGATTGA	AGATTTATG	1260
GATCAAAACC	ACCAAAAACA	GGTGGCACCC	TATAATTCCC	CTTGTAGGAGG	CACCATGCGA	1320
TTAGGCGAAT	ACGAATGCGA	AATCATGCC	AATAGCTTGC	TAGAAAAAGC	CTATAAAAAG	1380
CCTAACATCA	AAGAAAGACA	CCGCCATCGT	TATGAAATCA	ACCCCAAATA	CCGCCAAGAG	1440
TGGAAAATA	AAGGCTTGAA	AGTGGTGGGC	TTTGGGGCGA	ATCATTGAT	TGAAGCGATT	1500
GAATTAGAAAG	ATCACCCGTT	CTTTGTGGG	GTGCAATTCC	ACCCGGAATT	CACCTCCAGG	1560
TTGCAAAGCC	CTAACCCSTAT	TATTTGSGAT	TTCATTAAGA	GGCCTCTTCA	TAATCC	1617

## (2) INFORMATION FOR SEQ ID NO:1192:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1107 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...1107
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192

ATATGGCGTG	GATGTGGAAG	CCATGACAGG	GTGCATGATG	AGTTTGTTT	TGCTCGTTAC	60
ACGAAGGCTA	ATTACGAAA	CACTTATTAC	GATACAGAGT	TTTCGCATTT	AAAAGAAGCG	120
AGCGCGTATT	TTCCGGACAT	TGATGAAGCG	AGCCTTTTA	CGGATTTGCA	AGATTATTT	180
AACTCATGGA	AAGAATTGTC	TTAAAACGCC	AAAGACTCCG	CTCAAAAACA	GGCTCTCGCT	240
CAAAAAACAG	AAGCTTTAAC	GCACAAACATT	AAAGACACCA	GAGAGAGGTT	AACGACCTTA	300
CAGCATAAAAG	CGAGCGAAGA	ATTAaaaAGC	GTCATTAAAG	AAAGTCATAG	CCTGGGTTCT	360
CAAATCGCTG	AGATCAACAA	ACGCATTAAA	GAAGTGGAAA	ACAACAAGAG	TTTAAAGCAT	420
GCGAATGAGT	TAAGGGATAA	GCGAGATGAA	TTAGAGTTTC	ATTTCGAGA	GCTTTTAGGG	480
GGGAATGTTT	TTAAAAGCAG	CATTAAAACC	CATTGCTCA	CAGATAAAGA	CTCAGCGGAC	540
TTTGTGAGA	GCTATAACCT	TAATATCGGG	CATGGGTCTA	ATATCATTTG	TGGCTCTATT	600
TTCCATCCCT	TAGTGGTTAA	AGAAATCCGAA	AATAAAGGGG	GTTGAAACCA	GGTTTATTTT	660
CAAAGCGATG	ATTTTAAGCT	CACTAATATT	ACCGACAAGC	TCAATCAAGG	GAAAGTGGGG	720
GCGTTATTGA	ATGTGTATAA	TGACGGCTCT	AAAGGGACTT	TAAGGGCAA	GTTGCAAGAT	780
TATATTGATT	TGGTGGATT	TTTGCTAGG	GGCTTGATAG	AATCCACGAA	TGCGATTTAC	840
GCTCAAAGCG	CGAGCCATCA	TATTGAGGGC	GAGCCTGTGG	AGTTTAATAG	CGATGAAGCC	900
TTTAAAGACA	CGAAATTACAA	TATCAAAAC	GGCTCGTTTG	ATTTAATCGC	TTACAACACC	960
GATGGTAAG	AAATCGCCAG	GAAAACCATT	GCTATCACCC	CCATTACAAC	CATGAACGAC	1020
ATTATCCAAG	TCATTAACGC	TAACACCGAT	GACAATCAAG	ACAACAACAC	CGAAAACGAT	1080
TTTGTGAAT	TATTTCACAG	CGAGCTT				1107

## (2) INFORMATION FOR SEQ ID NO:1193:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 813 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...813
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193

AAAAACAAAGC TCGTTTTAT GATAAAAGCG CGGTTAAAA AACGCCTTT AGGATCTAGG	60
GGCGCGTTG ATTTGAATAT AGACITAGAA ATTAAGAAG CAGAAGTTGT CGCTTTATTA	120
GGAGAAATCGG GAGCGGGTAA AAGCACGATC TTACGCATT TAGCAGGGCT TGAAGCGGTG	180
AGTAGCGGCT ATATTGAAGC CAATCATTCA GTATGGTTAG ACACTAAAA AAAGATTTT	240
TTAAAACCAC AACAGCGAAA ATACGGCTT GTGTTCAAG ATTACGCCCT ATTCCCTCAT	300
TTAACGTGT ATCAAAACAT CGCCTTGCT CACCCCTAAAG ATAATAAATAA AATCCACGAA	360
GTGTTACGCT TAATCGTTT AGAAAACCTA AGCCAGCAAA AAATTCCCAA ACTCTCTGGC	420
GGGCAAGGCC AACGAGTCGC TTTAGCAAA CCTAGATAAC GCCTTAAATCG CAGCCAAAAA TCTATTGCTT	480
TTAGATGAGC CTTTAAACGC CTTAGATAAC GCCTTAAAAA ACAGAGGTGCA ACAAGGTTG	540
CTTGTATTCA TCAAGCGTGA AAATTTAACG GTGTTATTGG TAAGTCATGA TCCAAACGAA	600
ATAACCAAAAC TCGCGCGAAC TTTCCTCTT TTAAACAATG GCCTTATTGA TCCTAATCAA	660
GAAAATCGGC TTTTTCAAA CCGCTTATTG GTAAAACCTC TCTTGAAGA TGAAAATTAT	720
TGCCATTATG AGGTCAATTCC TCAAACGATC AGTTTGCCTA AAGATTGTCT GAACCCAAC	780
TTTAAGCTTG ATTTCAATTCA AAACAAAAAA TTT	813

## (2) INFORMATION FOR SEQ ID NO:1194:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 213 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...213
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194

GGCTTATCCG CTACTATTCT TGGTATGTGG ATTATGTCTT CACTTTCTAG TTCATTCTT	60
CATTGCTCT TCTTCATCAA ATCAAACCT GGCCAACCTCT TAAAAGGTTG GGGTTCAAAA	120
ATCTTTTCA TAAATAGAAA GTTTGTTTA GCACAGTATA ATCCTAGCGT TTCAATTTT	180
ATTTACTCA ATAGGGTGTGTT TGGTGTGCGC GTT	213

## (2) INFORMATION FOR SEQ ID NO:1195:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 225 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature

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## (B) LOCATION 1...225

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195

ATTCAAGCGCT CGCACCCAGCT CTTTAATTG CAAGAAAAAA AAGGGATTCT TGGTTTTTA	60
CACCAAAAAA ATATCTTAAA TATTGCTCAA AATGACATCC ACCAGCTCCT TATTCTCATG	120
GTTGCTTTT CTATGTTAGC AACCCCTTTT ATTTAAAAT ACCTAGAAC TATCGCTCAA	180
TTTATTTGCA CCAAAAGAG CCAAGAAAAC GAGCCGGCTA AAAAAA	225

## (2) INFORMATION FOR SEQ ID NO:1196:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...351

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196

GGCTTGATGC GCATTATCAT AAGGTTACTT TCATTTAAAA TGAACGCTTT TTTAAAAC	60
GGCTCGCTT CTTTGATGGG GGGGCTTTGG TATGCTTTCA ATGGCGAAGG CTCTGAGATT	120
GTGCTATAG GGATTTTGT GTTGATCTG TTGTTTTTT TTATCCGCC TGTGAGTTTC	180
CAAGACCCAG AAAAACGAGA AGAATACATA GAACGGCTTA AAAAAAACCA TGAGAGGAAA	240
ATGATCTTAC AAGACAAGCA AAAAGAAGAG CAAATGCGCC TCTATCAAGC CAAAAAAGAG	300
CGAGAGAGCA GGCAAAACCA AGACCTTAAA GAACAAATGA AAAAAACTC A	351

## (2) INFORMATION FOR SEQ ID NO:1197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...327

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197

AGGAAAAAAA TGGAAATCAT TTTATTAATT GTTGCGGGGG TTGTGTTGTT TTATTTTAC	60
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AACACCCTCA AAGAATATTT GAAAAACCCC CTAACCCCTA AAACCAAAC CGAAGAATAC	120
GACTGAAAA ATGACCCCTA TTGCTGGTG CAATCTAGCC CCCTAGACAA ATTCAAGCAA	180
ACCCAAATAG GCGCGTATAT GCGTCTTTA AAATTTTAG ACATTCAAA AAACGCCCTG	240
GATAACGCTT TAAGAACGCT TTTATCCAT GAATTGGAGC AGCCCTTAAA CAGCGAACAG	300
CAAAATTAG GCCAAAGAGC TTCTCAA	327

## (2) INFORMATION FOR SEQ ID NO:1198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1629 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...1629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198

ATGCCTAATA ACGCTTTATT GCAAATCAA CAAGACACCC TAAGTCTCAT TGACGATT	60
AAAGTCATT CCAAGGATGC TGGTTTAGCG GGCAGCGCA ACGGATACAA GATCATCACG	120
CAATGCTTT TGTATAAATT CTTATGCCAT AAGTTGAAT TCTTTTTGAA ACAAAATTC	180
CCCAACAAAA CGATACGAGA CTACAAAGAC TTTAACGAGG AAGAAAAAGA ATATTTTTC	240
CTTACCTTAA CGCGATAAAA ACTCCCCAACTCGTTATG ATGAGCTTTTAAACTATCTT	300
TTTGGAAAAC ATTTTACGA TAACGATTAA CACCTAAAGC TAGATGCTAT TTTCATCGC	360
ATTCTAGCA ATAATGCCGA GCTTTTAAC ACCAAAAGCA CGGATGAAAC CACTATGCC	420
TTATTTGAAA CGCTCTACA ATACATTAAT GAAGGGCTA AAAGGGCTAA TTTTACAAGA	480
TCTTTATTAG ACAAAACTCAA AAATTTTAAAT TTCAAAACAG CTTTTTTAAA TTTCACAAAAC	540
CAACAAGGCT ATGACTTTT CGCCCCCATT TTGAAATACT TACTTTAAAGA TTACAATAAT	600
AAACAGGGAG GGACATACCC CGAACATACAC ACCCTTTAA GCATCGCTAG CATCATGCC	660
AAGCTTTAG TGAATAAACC CACTAAAGC GTCAAATCT ATGATCCAAG CGCTGGCAC	720
GGAACGCTTT TAATGGCATT AGCCCACCAA ATAGGCACCG ATTCTTGCAC CCTTTATGCC	780
CAAGACATTT CGCAAAATC CTTAAGAATG CTCAAACCTCA ACCTGATTTT AAACGACTTG	840
ACCCACTCTT TAAGACACGC CATTGAGGGAA AACACTTTGA CTAACCCCTA CCACTCCAAA	900
GACCACAAAG GAAAATGGA TTTCATCGT AGTAAACCCCC CTTTCAAATT GGATTTTICC	960
AACGAGCATG CCGAGATTTC GCAAAACAAA AACGATTTT TCTTAGGCGT GCCTAATATC	1020
CCTAAAAACG ATAAAGCAA ATGGCCATT TACACGCTCT TTTCCAGCA TTGCTGAAC	1080
ATGCTCAGTC CAAAGGTAA GGGAGCTATA ATCGTGCCAA CGGGATTCTATAGTCTAA	1140
AGCGGGGTAA ATAATAAGAA TGTCCGGCAT TTAGTGGATG AAAGGCTCGT TTATGGGTG	1200
ATTGCTATGC CCAGTCAGGT TTTCATCGA ACCGGCACTA ACGTGAGCAT CATCTTTTT	1260
CAAAAAACGC CAAGCGCAA GGAAGTGCAT TTGATTGACG CTCCAAACT CGGCGAAGAA	1320
TACACCGAAA ACAAAACAA AAAACGCCG TTAAGACCAA CGGATATGGA TTTCATTTA	1380
GAAACTTTC AAAATAAGC CCCAAATCG GATTTCGCG CTCTGGTTTC TTTTGATGAA	1440
ATTACAGAAA AAAATTATTC TCTAAACCCC GGGCACTT TCACATAGA AGACACGAGC	1500
GAGACAATCA GCCAAGCGGA GTTGTAAAAC TTGATGCAAC AATATTCAAG CGAACTAGCG	1560
AGCCTTTTG ATGAAAGCCA AAATTTGCAA CAAGAGATT TAGAAACTTT AAAACGGTT	1620
AGGTTTGAG	1629

## (2) INFORMATION FOR SEQ ID NO:1199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199

AAAGGGGATT	TCATGAAAGA	ACAAGAATGG	GATTTAACCG	CTTATTTGA	AAATAAAGAA	60
AGCGCAGAAG	AATTTTTAAA	AACCTTACAA	ACAGAAGTGC	AAGAATTGTA	GAACGCTTAT	120
CAAAATAACC	TTAAGAATTT	AGACGCTGCA	AAATTTGCCA	ACACTCTTAA	ACATTACGAA	180
AATTGTCAG	AAAAGATCTC	TAGAGCGATG	GCTTACGCTC	AATTACTTTT	TGCCAAGAAC	240
ACTAAAGAAG	CGAAGTTTA	TTTCGCAATGC	GAAATGGCTT	GTGCAAATAT	CCAACAACAC	300
CTTTTATTCT	TTGAAATTGA	ATTTAAGAAT	TTGGACGCCA	AAAAACAGCT	CGCTTTCATT	360
AAAAAATGCA	AAGATCATGC	TTTTATTTA	AAACATCTCA	TAGAAAAGAA	AAAGCACACC	420
CTAAATTAG	ATGAAGAAAA	GATCGCTCTA	GCCCTTCGC	CTGTGGGAGT	GGGTGCGTTT	480
AGCTTGTAA	TGGATGAACA	TTGTTTCT	TTGAAACATCT	CTTACATAG	AATAAACTTT	540
AAGCGAAGAA	TAAATTAG	CCCTCTTGCA	CAACCC			576

(2) INFORMATION FOR SEQ ID NO:1200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200

GCCAAAGAGC	TTCTCAATGA	GCCTGTGGAT	AAAAAAGAAA	ATTTGAAATC	CTTATGCCAA	60
GAAATGCCG	ACACACCGCA	TGGAGAATAC	ACCCAAAGCC	TGAAATTAGT	GGAATTCTT	120
ATGCTATTAG	CCTATGCTGA	TGGGATTTC	GACAGCAAAG	AAAAAGAATT	GTTTTTAGAT	180
GTGGGGCGT	TTTGCAGAT	AGACAATCAA	GATTTAACG	AGCTTATGA	CAATTTTGAA	240
CACTTCAATT	CAATAGAAAT	CCCTATGTC	TTAGAAGAAG	CAAAAAATCT	TTTGAAATC	300
CAAACCCACA	CCACCATGCA	AGATTTAGAA	AAAAAAGCTT	TGGATTTAAG	CGCCCCCTAT	360
TACCATAAAA	TGAATGACAA	CAAACGCTAC	AGCGAACAAAG	ATTTTATCTC	TTTGAAAAAA	420
ATCGCCCTCG	CTTCCCAC	TTTAGAAAAT	GATTTAAAAG	ACTCA		465

(2) INFORMATION FOR SEQ ID NO:1201:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1215 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...1215
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201

ATGCCCTTTT	AAAAAGCCCT	AGCATTTTT	GATGCCCT	TTTTAGAAAA	AGAAATTCA	60
AAGCGTTTTA	GGGATAATT	AGTTTTTTTC	AAATCTTATC	ACCTTAATCT	GTTAACGCC	120
CTCAATACGC	CTTTAAAAAA	TTACCAATTG	CTTTTGAAA	CAAACCATCT	TAATCTCTTA	180
CACACGCCCA	CGAACGCTT	AAGCTACCT	AAACATCAA	TGATAGAAC	CGCTTTTAAC	240
ATGGCTAAA	ACCCCTTGAA	TAATCCCAGA	TGGTCATTAG	ACAATAACCA	CCTCTCTT	300
CATTATTAA	AACTCAAAA	CAACCACAA	CTCCCCCTAA	CCCTTAAAGC	CACGCATGCC	360
ATCTCAAAC	TTTAGATAAA	TCATCAAACG	CCTTGCTCTT	TAAGAAATT	CCTACCCCT	420
ACCATGATTT	ATGGCGTTT	AGACGGCTTG	TTTTGGCTA	TTTACAGGC	TCAAAATTAC	480
CGCTTCCATT	CGCTTTATTT	GTGAGAA	AATTAGACT	TGTTTAAAT	CAGTTGCTAT	540
TTTGCCTGTT	ATGAAGATTT	GATTAAAAAA	GGGGCTAAAC	TTTTTATTCA	AGGGTTTTT	600
AACCTTAATG	AATTGAAAAT	GGATTTTTTG	AAACGCCCTA	TCACGCATTC	TTTTTTAAAG	660
CTAGAAATCA	TGCCCTATAA	AAGCGCTTTT	AATTGCGCA	TGGGAGAAAAA	CATTCAAAGC	720
TATTACAAAC	AACGCTTAAG	GGGTGGGG	AGTTTGAAG	ACGAATTGCT	AGGGGTAAG	780
AACACGCTTA	AAACACTTAC	CCTATGCCAA	ACCCAAAAAA	CCAAACCCAA	AAAAATTAAAC	840
GCCCCCATT	GGCTGCTGGG	TAATGGGCCA	AGCCTGGATT	TATTGTTAGA	TTTTTTAAA	900
GAAAATGAAG	AAAAATTCA	CATTTTTCA	TGGGAAACCG	CTTAAAGCC	TTTAAAAGCG	960
CATGGCGTTA	AAGTGGATT	TCAAATAGAA	GTGGAGCGA	TAGACTATCT	TAAGGAGGTT	1020
TTAGAAAGAG	CCCCCTAGA	AGACACCCCC	TTAATGGCG	CTAACATGCT	CAATCCTAAC	1080
GCTTTGATT	TAGCCAAAGA	AGCGTTGATG	TTTATGCGTG	GGGGGAGCCG	TTGCGCATAT	1140
AAGCCCTTG	ACTATAGAAT	ACCGAGCGCC	TTTGTGGGC	AATGCCGGGG	TGGCTTTAGC	1200
GGGTTTGATG	AGCGA					1215

## (2) INFORMATION FOR SEQ ID NO:1202:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1239 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION 1...1239

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202

AAGGGGTTAG	GTGGCAAAACA	TTTTGTTAA	AAGATTTAGG	GAAAATAGTC	60
GGCGCGCTA	CCCCACCTAC	CAATAACCCC	AAAAATTATG	GCAATAAAAT	120
ACCCCTAAAG	ATTTATCCAC	TTTACAAGGG	CGCTACATTA	AAAAGGCAG	180
TCACGATTAG	GGTTTAAATC	ATGCTCTGT	GTGTTGCTCC	CAAAGCATGC	240
TCTTCAGAG	CTCCCATAGG	TTATGTGGCA	ATTGTGAAA	AAAGGCTATG	300
GGTTTAAAAA	GTATTATCCC	TAACAAAAAA	ATTTATTTG	CACCAATCAA	360
AAATACTATA	AGGATAACAT	TTCCAACATA	GGGGCGGAA	CTACTTTAA	420
GGGGCTACTT	TAGGTCTTATT	CCAAGTAAAG	ATACCCCCCA	CTTATTACGA	480
ATCGCCCA	CACTTCTTAT	TTTAGATCAA	AAAATAGAGA	ACAACCATAA	540
CTTTACACA	AAATCTTGA	GCTCTTAT	GACCAAACT	TCGTCCGTTT	600
GATGAAAACA	ACAAACCTTA	TCAAACCTAG	GGCGGAAA	TGAAATTTC	660
AAACGCCCTA	TCCCTAACGA	TTTTAAAGTC	AAAACGCTAG	GGGAACCTAAT	720
TCCGGAAGTC	AGCCACCCAA	AAAGTTGTCAC	ATATACGAGT	ATAAAGAGGG	780
TTCATACAAA	ACAGAGATTA	TAGCTCTAAT	AATTATGTTA	CATATATTCC	840
AATAACAAGA	TTTGTATCA	ATATGATATT	ATGATGGACA	AATACGGAGA	900
GTGCGTTTTC	GACTTCAAGG	GGCTTATAAT	GTGCTTAA	GTAAAATTAG	960
CAATCCATGC	AGGAATATAT	ACCGAGTTAT	CTAAATTCAA	AACCTATAAA	1020
TCTAATGCTT	GCATGGCATC	TACGAGAGCA	TCACTAAATG	AAAATCATAAT	1080
ATGCTCCCCA	TACCAACCTAT	TAATCTTATA	CAAAAATACG	AAAAAATCGC	1140
ATAACAGCCA	TTATTAAAAA	CAATCAATCA	ACCCAAACCC	TAACCGCGCT	1200
CTACTCCCCC	TACTCTTAAA	ACAACAAGTC	AAACCACAA	CAGAGACTTT	1239

## (2) INFORMATION FOR SEQ ID NO:1203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...591

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203

GGTGTAACCTT	TAATTCAACCA	AGAAGGATTT	ATTATGATTA	AAAGAATTGC	60
AGCTTGAGCG	CGAGTTTAGC	GTAGCTGGC	GAAGTGAATG	GGTTTTTCAT	120
TATCAACAAG	GTCTTTATGG	CCCTTATAAC	AGCAATTACT	CTGATTGGCG	180
GACCTTTATG	TTTGAATTTC	CAAATTAGGT	TTTGAGGCT	TTGCCAATAA	240
GCTAGGGTGT	ATGGCTTTT	AGATGGTTT	AAACATTCAG	GGACTGAACA	300
AATTTCGCTCA	CCTATGGCGG	CGGTGGCGAT	TTGATTGTCA	ATCTCAATTCC	360
TTCGCTCTAG	GTCTCATTGG	TGGCGTTCAA	TTAGCCGAA	ACACTTGGAT	420
GATGTCATC	AAACCAGATT	CCAGTTCTTA	TGGAATTAG	GGCGAAGAT	480
GATCGCAGTG	CGTTGAAGC	GGGCGTGAAA	TTCCCTATGG	TAAATCAGGG	540
GTAGGGCTTA	TCCGCTACTA	TTCTTGGTAT	GTGGATTATG	TCTTCACTTT C	591

## (2) INFORMATION FOR SEQ ID NO:1204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...1098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204

TTTCGTTTT ATTCTTTAA ACCAAATCGA TCCTACTGGG GAAAGGTTTT TATGGTAAAC	60
AGCACACTT ATATTGTTAT TGCCGGCTTA TGGCTTGCTG TAGGCTTGG AATCTTTTA	120
AAGAAATTAG ACATGCCGT TATCATTTGC TACATTTGCA CAGGAACGGT CTTAGCGGCT	180
TTTTTAAAAA TTAATGATT TAAATTGTTG TCTGATATTG GTGAATTGGG TATCGTCTTT	240
TTAATGTTA TGATAGGCAT TGAGTTTAAT TTTGACAAGC TCAAGTCCAT CAAACAAGAA	300
GTGCTCGTTT TTGGGCTTTT ACAGGTGTTT TTATGCGCTT TAATCGTTT TTTATTGGGG	360
TATTGTTTC TGGGTCTTTC GCCCATTTT TCCCTGTTT TAGGCATGGG GCTTTCACTC	420
TCTTCAACCG CCATTGTTGT GAAATTCTT GAAGATTCCA AACAGCTTAG CACGCCATAG	480
GGAAAGAGCC CGGTGGGAT TTGATTTC CAAGATAATTG CAGCCATTCC CATGCTTTA	540
ATTTGACGA TTCTAGGCAG TAAGGATTCT CATGTCATT TGTCTCATTCT TAAAACCTT	600
ATTCAGCGG GGATTATTAA AATTCTTTA TTATGCGCTG AAAAAAAGG GGCTAATCTC	660
ATCTTAGAGC AAGCGAAAGA CACGCGCTTG CCTGAAATCT TTATAGGCAC GGTTTTAGTG	720
ATTGTTGCA GCGCGGCGGG GTTGAGCCAT TTTTTGGGT TTCTATGTC TTGGGGGGCG	780
TTCAATTGTC GCATGGCGAT TTCTAAATCG CGCTATAAAA TCAATGTCCA AGAAGAATTG	840
GCGCAATTAA AAAACCTCTT TTGGCCCTT TTTTCATTA CGATAGGGAT GCAGATTAAAT	900
GTGAGTTCTC TCATGGAGAA ATTCTTGTGTC GTCACTCTTT TACTCATTAA AGTGATGAGT	960
TTTAAGACTT TTATCATTAA TGCGCTATTG CGTTTTTTA GAGACGCTAA AACCGCCATC	1020
AAAACCGCTC TTCTTTGCG GCAAATTGGG GAGTTTCTT TCGTGATCTT TTAAATTCA	1080
GCGCTCGCAC CAGCTCTT	1098

(2) INFORMATION FOR SEQ ID NO:1205:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 726 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
 (B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205

TGTTTATGCG TGGGGGGAGC GCTTGCGCAT ATAAGCCCTT TGAGTATAGA ATACGCAGCG	60
CCTTTGTGG GCAATGCCGG GGTGGCTTTA GCGGGTTGAG TGAGCGATGA AATTTATTG	120
TGCGCTTAG ATTGCGCTTA TATCAAAGGG TTAAAAAACG ACGCTCAAAA TTCCTATTAT	180

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